

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 09:56:53 ; Search time 208.49 Seconds
(without alignments)
18060.838 Million cell updates/sec

Title: US-09-396-985B-1
Perfect score: 8579
Sequence: 1 aaatactcctctgcctcaaa.....caaaaaaaaaaaaaaaaaaa 4868

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ n2p model -DEV=xlh
-Q=/cgn2_1/USFTO_spool/US0396985/runat_28032005_155742_21135/app_query.fasta_1.85098
-DB=A.Geneseq_16Dec04 -QFMT=fastan -SUFIX=rag -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNIT5=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdt
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MTLEN=0 -MAXLEN=2000000000
-USER=US0396985 @CGN 1.1 4007 @runat_28032005_155742_21135 -NCPU=6 -ICPU=3
-NO MAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -IONGLOG
-DEV_TIMEOUT=120 -MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Geneseq_16Dec04:.*
2: geneseqp1980s:.*
3: geneseqp2001s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4355	50.8	839	6	ABU04773 Human exp
2	4355	50.8	839	6	ABU04774 Human exp
3	4355	50.8	839	6	ABU04775 Human exp
4	4355	50.8	839	7	ADCT8785 Human PRO
5	4355	50.8	839	7	ADDA8826 Human PRO
6	4335.5	50.5	837	2	AAW6361 Human DNA
7	4335.5	50.5	837	5	AAE16102 Human DNA
8	4335.5	50.5	837	6	ABU04776 Human exp
9	4328.5	50.5	837	5	AAE16116 Human DNA
10	4178	48.7	808	8	ADOS7782 Chimpanze

11	4167	48.6	808	8	ADOS7785 Gorilla t
12	4164	48.5	808	8	ADOS7803 Chimpanze
13	4141	48.3	799	2	AAW6352 Human DNA
14	4141	48.3	799	5	AAE16093 Human DNA
15	4141	48.3	799	5	ABE83162 Human DNA
16	4141	48.3	799	6	ABR42963 Human Tol
17	4141	48.3	799	7	ADB39121 Human Tol
18	4141	48.3	799	8	ADP56656 Human Tol
19	4141	48.3	799	8	ADP48597 Human Tol
20	4040	47.1	801	8	ADOS7788 Gibbon to
21	3918	45.7	795	8	ADOS7791 Rhesus mo
22	3892	44.5	795	8	ADOS7800 Hamadryas
23	3819	44.5	801	8	ADOS7797 Squirlrel
24	3794	44.2	738	8	ADP29455 Human sec
25	3501	40.8	745	8	ADOS7794 White-fac
26	1090	12.7	208	3	AAV88059 Human Tol
27	919	10.7	178	8	ADN12270 IL-1R/TLR
28	785	9.2	179	7	ADC42707 Murine To
29	629.5	7.3	661	2	AAW28510 Product o
30	629.5	7.3	661	2	AAW87556 B cell su
31	629.5	7.3	661	7	ADC38652 Human sec
32	629.5	7.3	661	7	ADP69098 Human MP5
33	628.5	7.3	650	3	AAV82527 Human RPI
34	615.5	7.2	661	2	AAW47274 Human B-c
35	603.5	7.0	784	2	AAW6350 Human DNA
36	603.5	7.0	784	5	ABE83161 Human DNA
37	603.5	7.0	784	8	ADN02005 Human inf
38	603.5	7.0	784	2	AAV05869 Human Tol
39	602.5	7.0	784	6	ABU61956 Human Tol
40	602.5	7.0	784	7	ADL15005 Human Tol
41	602.5	7.0	784	8	ADP56652 Human Tol
42	602.5	7.0	784	8	ADP48593 Human Tol
43	602.5	7.0	784	8	ADP23787 PEO polyp
44	602.5	7.0	784	8	ADQ39727 Human myo
45	602.5	7.0	784	8	ADQ39727 Human myo

ALIGNMENTS

RESULT 1	ABU04773 standard; protein; 839 AA.
ID	ABU04773;
AC	ABU04773;
XX	
DT	29-JUN-2003 (first entry)
XX	
DE	Human expressed protein tag (EPT) #1439.
XX	
KW	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW	protease; protease inhibitor; transporter; cytoskeletal protein;
KW	receptor; transcription factor; cancer; MHC;
KW	major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX	
OS	Homo sapiens.
XX	
PN	WO200278524-A2.
XX	
PD	10-OCT-2002.
XX	
PF	28-MAR-2002; 2002WO-US009671.
XX	
PR	28-MAR-2001; 2001US-0279495P.
PR	21-MAY-2001; 2001US-0292544P.
PR	08-NOV-2001; 2001US-0310801P.
PR	01-OCT-2001; 2001US-0326370P.
PR	04-DEC-2001; 2001US-0336780P.
PR	20-FEB-2002; 2002US-0358985P.
XX	
PA	(ZYCO-) ZYCOS INC.
XX	
PI	Chicz RM, Tomlinson AJ, Urban RG;

XX WPI; 2003-040607/03.
 DR New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 XX cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX Example 2; SEQ ID NO 1439; 134pp; English.
 PS
 XX The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 839 AA:
 SQ
 Alignment Scores:
 Pred. No.: 0 Length: 839
 Score: 4355.00 Matches: 839
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.76% Indels: 0
 DB: 6 Gaps: 0
 US-09-396-985b-1 (1-4868) x ABU04773 (1-839)

DB
 161 LeuIleGlnSerPheIleuProGluIrrPheSerAsnLeuThrAsnLeuGlnIleu 180
 QY 644 GACCTTCCAGAACAAAGTATTTATTCACAGACCTGCGGCTTACATCAA 703
 DB 181 AsnLeuSerSerAsnIleLeuIleSerIleIrrCysIrrAsnLeuValIleuIleGln 200
 QY 704 ATGCCCTACTCAATCTCTCTTACAGCTGTCCTGAAATCCATGATCACTTATCCAAACA 763
 DB 201 MetProIleuAsnLeuSerIleuAsnProIleuAsnProMetAsnPheIleGlnPro 220
 QY 764 GGTGCAATTTAAAGAAATAGGCTTCATAGCTGATTAAGAAATATTTGATAGTTA 823
 DB 221 GlyIlePheIleGluIleIrrGlnIleIrrIleuThrIleuAsnValIleuAsnPheSerIleu 240
 QY 824 AATGTAATGAAATCTTATTTACAGTCTGCTGCTTATGAAAGTCCATCTGTTGCTCG 883
 DB 241 AsnValIleuIrrCysIleGlnIleuIleuIleuIleuValIleuIleuValIleu 260
 QY 884 GGAGAAATTTAGAAATGAGAAATCTGAAAGTTTGAACAATCTGCTTACAGGAGCTG 943
 DB 261 GlyIlePheIleuAsnGlnIleuAsnIleuIleuIleuIleuIleuIleuIleuIleu 280
 QY 944 TSCAAATTTGACCAATGAAATTCGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 1003
 DB 281 CysAsnLeuThrIleGlnIleuPheIleuIleuIleuIleuIleuIleuIleuIleu 300
 QY 1004 ATTTGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1063
 DB 301 IleAsnLeuPheAsnCysLeuThrAsnValIleSerIlePheSerIleuValIleuIle 320
 QY 1064 GAAAGGTTAAAGACTTTCTTATATTTATTTATTTATTTATTTATTTATTTATTTATTT 1123
 DB 321 GluIrrValIleAsnPheSerIrrAsnIleGlnIleuIleuValIleuIleuIleuIleu 340
 QY 1124 AAATTTGACAGTTTCCCAATGAAATCTTCAAAAGCTTACCTTCACTTCC 1183
 DB 341 LysPheGlnIlePheProThrIleuIleuIleuIleuIleuIleuIleuIleuIleu 360
 QY 1184 AACAAAGTGGAAATGCTTTTTCAGAGTGAATTCACAAAGCTTGAAGTTTACATCTC 1243
 DB 361 AsnIrrGlnIleAsnIlePheSerIleuValIleuPheProSerIleuIleuIleuIleu 380
 QY 1244 AGTAAATAGGCTTGAATTTCAAGGTTGCTTCTCAAGATTTTGGACCAACAGC 1303
 DB 381 SerIrrAsnGlnIleuSerPheIleuIleuIleuIleuIleuIleuIleuIleuIleu 400
 QY 1304 CTAAAGTATTTAGATCTGAGCTTCAATGCTTATTTATTTATTTATTTATTTATTTATTT 1363
 DB 401 LeuIrrIleuAsnIleuSerPheAsnGlnIleIleuIleuIleuIleuIleuIleuIleu 420
 QY 1364 TTTGAAACAATGAAATCTGATTTCCAGCATTTCCAAATTTGAAATGAGTGAATTT 1423
 DB 421 LeuGlnIleuGlnIleuIleuAsnIleuIleuIleuIleuIleuIleuIleuIleuIleu 440
 QY 1424 TCAAGTATTTCACTCAAGAACTCATTTACCTTCAATTTCTCATCTACACACAGA 1483
 DB 441 SerValIleuSerIleuAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 460
 QY 1484 GTTGCTTTCAATGCAATCTTCAATGCTTTCACAGTCTTCAAGATTTGAAATGCTGAC 1543
 DB 461 ValIlePheAsnGlnIlePheAsnGlnIleuSerIleuIleuIleuIleuIleuIleuIleu 480
 QY 1544 AATTTCTTCCAGAAATCTTCTTCCAGATTTCTTCAAGATTTGAAATGCTGAC 1603
 DB 481 AsnSerPheGlnIleuAsnIleuPheProIleuIleuIleuIleuIleuIleuIleuIleu 500
 QY 1604 CTGACCTCTCAAGTCAATCTGAGAGCTTGTCTTCAAGATTTTAACTCACTCTCC 1663
 DB 501 LeuAsnIleuSerGlnCysGlnIleuGlnIleuIleuIleuIleuIleuIleuIleuIleu 520
 QY 1664 AGTCTTCAAGTATTTAAATTTAGACCAACAATCTTCTTCAATTTGATTAAGTTCTTAT 1723

D	b		521	SerLeuGlnValIleuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProtyr	540
Q	y		1724	AAGTGTCTGAACACTCCCTCCAGGTTTGGATTTCAGCTCTCAATCACAATAATGACTTCCA	1783
D	b		541	LysCysLeuAsnSerLeuGlnValIleuAspTrytSerLeuAsnHisIleMetThrSeryls	560
Q	y		1784	AAACAGCAACATCACACATTTTCCAGTAGTGCTAGCTTCTTAATCTTAATCAGAAATGAC	1843
D	b		561	LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnIleThrGlnAsnAsp	580
Q	y		1844	TTTTGCTTACTTGTGAAACACAGAGTTTCCGTGCATAGATCAAGACACAGAGCAGCTC	1903
D	b		581	PheAlaCysThrCysGluHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu	600
Q	y		1904	TTGGTGAAGTTGAACGAATGGAATGTGCCAACCTTCAGATPAACAGAGCATCGCTGTG	1963
D	b		601	LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal	620
Q	y		1964	CTGAGTTTGAATATACCTGTCCAGATGGAATAAAGACATCATTTGGTGTCCGTCTCAGT	2023
D	b		621	LeuSerLeuAsnIleThrCysGlnMetAsnYsthrIleIleGlyValSerValLeuSer	640
Q	y		2024	GTCGCTTGAGATCTGTGTGAGACAGTTCTGGCTTAAGTCTAATTTTACCCTGATGCTT	2083
D	b		641	ValLeuValValSerValAlaValLeuValTyrlzysPheTyrrPheHisIleuMetLeu	660
Q	y		2084	CTTGCTGGCTGCATAAAGATGATGTGTAAGGTGAACATCTATGATGCTTTGTATTCTAC	2143
D	b		661	LeuAlaGlyCysIleLysTyrglyYargglyGlnAsnIleTyrrAspAlaPheValIleTyrr	680
Q	y		2144	TCAAAGCCAGATTAAGAGATGGGTGAAGAATGACATGATGAAGAATTGGAAGAGGGGTG	2203
D	b		681	SerSerGlnAspGlnAspTrpValAlaArgAsnGluLeuValLysAsnLeuGlnGlnGlyVal	700
Q	y		2204	CCTCCATTTACGCTCTGGCTTCACTACAGAGACTTATTTCCCGGGTGGCCATTGGCTCC	2263
D	b		701	ProProPheGlnLeuCysLeuHisIstyrTrkAspPheIleProGlyValAlaIleAla	720
Q	y		2264	AACATCATCCATGAAGTTTCCATTAAGCCGAAGGTGATTTGTGTGGTGTCCAGAC	2323
D	b		721	AsnIleIleHisGlnGlyPheHisIleLysSerArgLysValIleValValSerGlnHis	740
Q	y		2324	TTTCATCCAGACCCGTGGTGTATCTTTGAATATGAGATTGCTCAGACCTGGCAGTTTGTG	2383
D	b		741	PheIleGlnSerArgTrpCysAlaPheGlnTyrgluIlealagInthrTrpGlnPheLeu	760
Q	y		2384	AGCAGTCGTGTGGATCATCTTCATCTTCCGTGCAGAGGTGGAGAAACCTCGTCAAG	2443
D	b		761	SerSerArgAlaGlyIleIlePheHisValLeuGlnLysValGlnLysThrLeuLeuArg	780
Q	y		2444	CAGCAGGTGAAGTGTACCGCTTCTCAGCAGGAACCTTACCTGAGTGGAGAGCAGT	2503
D	b		781	GlnGlnValGluLeuTyrrArgLeuLeuSerArgAsnthryrLneGlnTrpGlnAspSer	800
Q	y		2504	GTCCGTGGGGCGGCACATTTTGTGAGACAGCTCAGAAAAGCCGTGCTGGATGTGAATCA	2563
D	b		801	ValLeuGlyArgHisIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer	820
Q	y		2564	TGGATCCAGAAAGAAACAGTGGGTACAGGAATGGCAGGAAGCAACTATATC	2620
D	b		821	TrpAsnProGlnGlyThrValGlyThrIyCysAsnthrGlnGlnAlaThrSerIle	839
RESULT 2					
ID	ABU04774	standard; protein; 839 AA.			
XX	ABU04774;				
AC					
XX	29-JAN-2003	(first entry)			
DT					
XX					
DE		Human expressed protein tag (EPT) #1440.			
XX					
XM		Translational profiling; expressed protein tag; EPT; kinase; phosphatase;			

KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 PN W0200278524-A2.
 PM 10-OCT-2002.
 PD 28-MAR-2002; 2002MO-US009671.
 PE 28-MAR-2001; 2001US-0279495P.
 XX 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1440; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SO Sequence 839 AA;
 XX
 Alignment Scores:
 Pred. No: 0 Length: 839
 Score: 4355.00 Matches: 839
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.76% Indels: 0
 DB: Gaps: 0
 US-09-396-985B-1 (1-4868) x ABU04774 (1-839)
 QY 104 ATGATGTCGCGCTCGGCGCTGGCTGGAGCTCGATGCCAGGCATGAGGCTTCCTCTGCG 163
 DB 1 MeMeSeSerAlSeSerIrgJeuNlaIcIYhrIeuIIlePobIaWcIAlaPeIeISeSerCys 20
 QY 164 GTGAGACCGAAGAGCTGGAGAGCCCTGCGCTGGAGGTGTCTTAATATTAATTACTTATCAATGC 223
 DB 21 ValArgProGluSerTrrpGluProGlyValaIguValaIProaAnIIleHrTYrGInCys 40
 QY 224 ATGAGAGCTGAATTTCTCAAAAATCCCGACAACCTCCCTTCTCAACCAAGAACCTGGAC 283

Db 41 MetGluLeuAsnPhenylTylsileProAspAsnLeuProPheSerThrIlysAsnLeuAsp 60
QY 284 CTGAGCTTTAATCCCGGAGCAATTTAGGAGCATATGCTTCTCAAGTTCCGAGAACTG 343
Db 61 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 80
QY 344 CAGGTGCTGATTTATTCAGAGGTGAAATCCAGACAAATTGAGATGGGACATACAGAC 403
Db 81 GluValLeuAsnLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 100
QY 404 CTAGACCACTCTCTACCTTAATTTAGACGAAACCCCACTCCAGAGTTAGCCCTGGCA 463
Db 101 LeuSerHisLeuSerThrIleuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
QY 464 GCCCTTTCTGACTATCAAGTTTACAGAGCTGGTGGCTGGAGACAAATCTAGACTCT 523
Db 121 AlaPheSerGlyLeuSerSerLeuGlnIleuValAlaValGluThrAsnLeuAlaSer 140
QY 524 CTAGAGAACTTCCCGATTTGACATCTCAAACTTTGAGAACTTAAATGTGGCTCACAAT 583
Db 141 LeuGluAsnPheProIleGlyHisLeuIleThrLeuIleuGluLeuAsnValAlaHisAsn 160
QY 584 CTATCCCAATCTTTCAAAATTAACCTGAGATTTTCTATCTGACCAATCTTAGACACTTG 643
Db 161 LeuIleGlnSerPheIlyLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu 180
QY 644 GACCTTTCCAGCAACAGATTTCAAAATTTATTTAGCAGACTTGCGGGTTCTACATCAA 703
Db 181 AspLeuSerSerAsnIlyIleGlnSerIleTyrCysThrAspLeuAlaGValIleHisSerGln 200
QY 704 ATGCCCCCTACTCAATCTCTCTTTAGACCTGCTCCCTGAATCCTTAGAATTATTCACACA 763
Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
QY 764 GGTGCAATTTAAAGAAATTTAGGCTTCATAGCTGACTTTAAGAAATATTTTGATAGTTTA 823
Db 221 GlyAlaPheIlySerGluIleArgLeuHisIleIlyLeuThrLeuAlaAsnAsnPheAspSerLeu 240
QY 824 AATGTAATGAAAACTTGATTTCAAGCTGGCTGGTTTAGAAGCTCATCGTTGGTCTGCTG 883
Db 241 AsnValIleCysThrCysIleGlnGlyLeuHisIleGlyLeuGluValHisIleGlyLeuValLeu 260
QY 884 GGAAGAAATTTGAAATGAGAAACTTGGAAAGTTTGAACAAATCTGCTTAGAGAGGCTG 943
Db 261 GlyIleuPheArgHisGlnGlyIleAsnLeuGluIlyPheAspIlySerAlaLeuGluGlyLeu 280
QY 944 TGCATTTTGAACATTTGAGAAATTTCCGATTTAGCATTAACATCTACCTTCGATGATATT 1003
Db 281 CysAsnLeuThrIleGlnGluIlyPheArgLeuAlaTyrLeuAspIlyTyrIleuAspAspIle 300
QY 1004 ATTGACTTATTTAATGTTTGAACAAATGTTTCTCATTTTCCCTGGAGAGTGAATTT 1063
Db 301 IleAspLeuPheAsnIlyLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
QY 1064 GAAAGGCTAAAGACTTTTCTTATTAATTTGCGATGCAACATTTAGAAATTAAGTTAACTGT 1123
Db 321 GluArgValIlyAspPheSerTyrAsnPheGlyTyrGlnHisLeuGluIleuValAsnCys 340
QY 1124 AAATTTGAGACGTTTCCCACTTAACAACTCAATCTCTCAAAAGGCTTACTTTACTCTCC 1183
Db 341 LysPheGlyGlnPheProThrLeuIlyLeuIlySerLeuIlySerIlyArgLeuThrPheThrSer 360
QY 1184 AACAAAGGTGGAGATGCTTTTTCAGAGTTGATCTACCAAGCCTTGAGTTTCTAGACTCTC 1243
Db 361 AsnIlySerGlyIlyAsnAlaPheSerGluValAspLeuProSerLeuGluIlyPheLeuAspLeu 380
QY 1244 AGTAGAATGAGCTTGAAGTTTCAAAAGTGTGCTGTTCTCAAGTGAATTTTGGAGCAACAGC 1303
Db 381 SerArgHisGlnIlyLeuSerPheIlyGlyCysCysSerGlnSerArgPheGlyThrThrSer 400
QY 1304 CTAAAGTATTTAGATCTGAGCTCAATAGTGTTATTAACCATGAGTTCAAACTTCTTGAGC 1363
Db 401 LeuIlyTyrIleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420

QY 1364 TTGAACAACATGAAACATCTGATTTTCCAGACATTCCAATTTGAAACAAATGAGTAGTTT 1423
Db 421 LeuGluGlnLeuGluHisIleuAsnPheGlnHisIleSerAsnLeuIlyGlnMetSerGluPhe 440
QY 1424 TCAGATTTCTCTATCTCAAGAAACCTCATTTACCTTGACATTTCTCATCTCACACCA 1483
Db 441 SerValPheLeuSerLeuArgHisLeuIleTyrLeuAspIleSerHisThrHisThrArg 460
QY 1484 GTTGCTTTCAATGGACATCTTCATATGGCTGTGTCAGACTGGAAGTCTGAAAATGGCTGGC 1543
Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuIlySerAlaGly 480
QY 1544 AATTTCTTCCAGGAAAACTTCTTCCAGATATCTTCACAGACTGAGAAACTTGACCTTC 1603
Db 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgHisLeuThrPhe 500
QY 1604 CTGGACCTCTCTCAGTGTCACTGAGACGTTGTCTCCAAACAGCATTTAACTCATCTCC 1663
Db 501 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 520
QY 1664 AGTCTCAGGTACTAAATATGAGCCCAACAACTTCTTCAATTTGATAGTTAGTTCTCTTA 1723
Db 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 540
QY 1724 AAGTGTCTGAACCTCCCTCCAGGTTCTTGATTTACAGTCTCAATCACAATTAATGACTTCCAA 1783
Db 541 LysCysLeuAsnSerLeuGlnValLeuAspIlyrSerLeuAsnHisIleMetThrSerIly 560
QY 1784 AAACAGAACTACAGCAATTTTCCAGATAGCTTAGCTTTTAAATCTTCAATCTCAAGATGAC 1843
Db 561 LysGlnGluLeuGlnHisIlePheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1844 TTGCTTTGATCTTGTGAACACAGAGTTCTCGCAATGAGTACAGGACGAGGAGCTC 1903
Db 581 PheAlaCysThrCysGlnHisIleGlnSerPheLeuGlnThrIleLysAspGlnAspGlnLeu 600
QY 1904 TTGGTGAAGTTGAACGAATGGAATGTGCAACACTTCAGATTAAGCAGGACATGCTGTG 1963
Db 601 LeuValGluValGluArgMetGluCysValaThrProSerAspIlyGlnIlyMetProVal 620
QY 1964 CTGAGTTTGAATATCACTCTGTCAGATGAATTAAGCATCATTTGGTGTGCTCTCACT 2023
Db 621 LeuSerLeuAsnIleThrCysGlnMetAsnIlyThrIleGlyValSerValLeuSer 640
QY 2024 GTGCTTGATGATCTGTGTGAGCAGTTCTGCTATTAAGTCTTAATTTCACTGATGCTT 2083
Db 641 ValLeuValValSerValValAlaValLeuValTyrIlyPheTyrPheHisIleuMetLeu 660
QY 2084 CTGTGCTGCTGCAATTAAGTATGATGAGTGAACATCATGATGCTTTGTTATCTAC 2143
Db 661 LeuAlaGlyCysIleIlySerTyrGlyArgGlyIlyAsnIleTyrAspAlaPheValIleTyr 680
QY 2144 TCAGCCAGAGATGAGACTGGGTAGAGAAATGAGCTAGTAAAGATTTTGAAGAAAGGCTG 2203
Db 681 SerSerGlnAspGluAspIlyValArgAsnGluLeuValIlyAsnLeuGlnGlyIlyVal 700
QY 2204 CTTCCATTTCAAGCTCGCTTCACTACAGACTTAATTCCTCGGTGGCCATTTGGCTGCC 2263
Db 701 ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaIle 720
QY 2264 AACATCATCCATGAAGTTTCCATAAAGCCGAAAGGTGATTTGTTGTGCTCCAGAC 2323
Db 721 AsnIleIleHisGlnGlyPheHisIlySerAspArgIlyValIleValValIlySerGlnHis 740
QY 2324 TTCATCCAGAGCCGCTGGTGTATCTTTGAATATGAGATTTGCTCAGACTGGCAGTTTCTG 2383
Db 741 PheIleGlnSerArgIlyProCysIlePheGluTyrGluIleAlaGlnThrTrpGlnPheLeu 760
QY 2384 AGCAGTCGCTGCTGATCATCTTCAATTTGCTCCGCAAGGTGAGGAAGCCGCTCAGG 2443
Db 761 SerSerArgAlaGlyIleIlePheIleValLeuGlnIlyValGluIlyThrLeuLeuArg 780

QY 2444 CAGCAGGTGAGCTGTACCGCCCTTCTCAGCAGAAACCTTACTGAGTGGAGACAGT 2503
 DB 781 GlnGlnValGlnLeuValArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnAspSer 800
 QY 2504 GTCTCTGGGGGGGACATCTTCTGTGAGACGACTCAGAAACCCCTGCTGGATGGTAATCA 2563
 DB 801 ValLeuGlnYarGHisIlePheTrpArgArgLeuArgValAlaLeuLeuAspGlyLysSer 820
 QY 2564 TGGAAATCCAGAAAGAACAGTGGGTACAGATGCAATGGCAGAGAACACATCTATC 2620
 DB 821 TrpAsnProGlnIuGlnThrValGlnTyrGlnCysAsnTrpGlnIuAlaTrpSerIle 839

RESULT 3
 ABU04775
 ID ABU04775 standard; protein; 839 AA.
 XX
 AC ABU04775;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1441.
 XX
 KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KM protease; protease inhibitor; transporter; cytoskeletal protein;
 KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN MO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002MO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 XX
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-APR-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chiciz RM, Tomlinson AJ, Urban RG;
 XX
 DX WPI; 2003-040607/03.
 XX
 DR
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1441; 134p; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 839 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 839
 Score: 4355.00 Matches: 839
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 50.76% Indels: 0
 DB: 6 Gaps: 0

US-09-396-985b-1 (1-4868) x ABU04775 (1-839)

QY 104 ATGATGTGCTGCTCGGCGCTGGAGCTGTGATCCAGCCATGCGCTTCCTCTGCG 163
 DB 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 164 GTGAGACCAAGAAAGCTGGAGCCCTGCGTGGAGGTGCTTAAATTAATCAATGC 223
 DB 21 ValArgProGlnIuSerTrpGlnProCysValGlnValAlaProAsnIleThrTyrGlnCys 40
 QY 224 ATGAGCTGAATTTCTACAAATCCCGCAACCTCCCTTCAACCAAGCTGGAC 283
 DB 41 MetGlnLeuAsnPhetYrIlySileProAspAlaLeuProPheSerThrIlysaLeuAsp 60
 QY 284 CTGAGCTTAAATCCCTGAGGCACTTTAGGACAGCTATAGCTTCTTCAAGTTCCAGAACTG 343
 DB 61 LeuSerPheAsnProLeuAlrghIsleuGlySerTyrSerPhePheSerPheProGlnLeu 80
 QY 344 CAGGTGCTGAATTTATCCAGGTGTGAATCCAGACAAATGAAGATGGGCATATCAGAGC 403
 DB 81 GlnValLeuAsnProLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaTyrGlnSer 100
 QY 404 CTGAGCACCTCTCTACCTTAATATGACAGAAACCCATCCAGAGTTTACGCTGGGA 463
 DB 101 LeuSerHisLeuSerThrLeuIleThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
 QY 464 GCGTTTCTGAGACTATCAAGATTTAAGAAGCTGTGGTGGAGCAAAATCTAGCATCT 523
 DB 121 AlaPheSerGlyLeuSerSerLeuGlnIlybLeuValAlaValGlnThrAsnLeuAlaSer 140
 QY 524 CTAGAGAACTCCCAATGGAATCTCAAACTTGAAGAACTTAATGAGTCAAT 583
 DB 141 LeuGlnAsnPhetIroIleGlyHisLeuYsThrLeuYsGlnLeuAsnValAlaHisAsn 160
 QY 584 CTATATCAATCTTCAATTAATTAATGATATTTTCTTAATCTGACCAATCTAGAGCACTTG 643
 DB 161 LeuIleGlnSerPheIlysbLeuProGlnTyrPheSerAsnLeuThrAsnLeuGlnHisLeu 180
 QY 644 GACCTTCCAGCAACAAGATTCAAGATTATTTATGACAGACTTGCGGGTCTTACATCAA 703
 DB 181 AspLeuSerSerAsnIlySileGlnSerIleTyrCysThrAspLeuArgValLeuHisGln 200
 QY 704 ATGCCCTACTCAATCTCTTTAGACTGTGCTCCCTGAATCTATGAATTTATCAACCA 763
 DB 201 MetProLeuLeuAsnLeuSerIleLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 764 GGTGCAATTTAAAGAAATTTAGGCTTCTTAAGCTGACCTTTAAGAAATTTGATAGTTTA 823
 DB 221 GlyAlaPheIlyGlnIleArgLeuHisIlybLeuThrLeuArgAsnAsnPheAspSerLeu 240
 QY 824 AATGTAAATAAAACCTGTATTCAGAGTCTGGGTGTTTGAAGTCATGCTGTTGGTTCG 883
 DB 241 AsnValaMetIlybThrCysIleGlnGlyLeuAlaGlyLeuGlnValaHisArgLeuValLeu 260
 QY 884 GGAGAAATTTAGAAATGAAGAAACTTGAAGAAATTTGAACAAATCTGCTAGAGGCGCTG 943
 DB 261 GlyGlnPheArgAsnIuGlnIlybAsnLeuGlnIlybPheAspIlybSerAlaLeuGlnIlybLeu 280
 QY 944 TGCATTTTACCATTAAGAAATTTCCGATTTAGCATATTTAGCATCTTCACTCCATGATATT 1003
 DB 281 CysAsnLeuThrIleGlnIuPheArgLeuAlaTyrLeuAspIlybTyrLeuAspAspIle 300

QY 1004 ATGACTTATTTATTTGACAAATGTTCTTCATTTCCCTGGTAGTGACTATT 1063
DB 301 ILeAspLeuhenCysleuThrAnValSerSerPheSerleuValSerValThrIle 330
QY 1064 GAAAGGTTAAAGACTTTTCTTATTTGATGGGACATTTAGATTAGTTAACTGT 1123
DB 321 GlAArgValAspPheSerTyraSerPheGlyTyrP61nHsleuGluLeuValaAnCyS 340
QY 1124 AAATTTGACAGTTTCCCATTTGAAATCAATATCTCTCAAAAGGCTTACTTCAGCTTC 1183
DB 341 LysPheGlyGlnPheProHnLeuLysLeuLysSerleuLysArgLeuHnTrPheHnSer 360
QY 1184 AACAAAGTGGAATGCTTTTTCAGAAATGATCTACCAAGCTTGAGTTCTAGATCTC 1243
DB 361 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerleuGluPheLeuAspLeu 380
QY 1244 AGTAGAAATGGCTTGAATTCAAAGGTGCTGTTCTCAAGTAGATTTTGGACACACG 1303
DB 381 SerArgAsnGlyLeuSerPheLysGlyCysCysSerIleSerAspPheGlyThrHnSer 400
QY 1304 CTAAAGATTATAGTCTGAGCTTCATGAGTTCATGATTTATACCATGAGTTCAACTTGGGC 1363
DB 401 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1364 TTAGAACACTAGAACATCTGATTTCCAGCATTTCCAAATTTGAAACAATAGTAGTTT 1423
DB 421 LeuGlnGlnLeuGlnHsleuAspPheGlnHsSerHnLeuLysGlnMetSerGluPhe 440
QY 1424 TCAGTATTCCTATCACTCAGAAACCTCATTTACTGATTTCTCATCTACACACAGA 1483
DB 441 SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHnIleThrHsIleHnArg 460
QY 1484 GTTGCTTTCAATGGCATCTTCATGAGTTCAGAGTTCAGAGCTTGAAAGTGGCTGGC 1543
DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerleuGluValLeuLysMetAlaGly 480
QY 1544 AATTTCTTCCAGGAAATCTTCTCCAGATATCTTCCAGAGCTGAGAACTTGACCTTC 1603
DB 481 AsnSerPheGlnGlnValAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuHnTrPhe 500
QY 1604 CTGGACCTCTCTCAGTGTCACTGAGACAGTTGTCTCCAAACAGATTTAACTCATCTGC 1663
DB 501 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 520
QY 1664 AGTCTCAGGATCAATATAGAGCCACAAACACTCTTTCATGATGATGTTTCCCTAT 1723
DB 521 SerleuGlnValLeuAsnMetSerHnAsnAsnPhePheSerleuAspHnTrPheProTyr 540
QY 1724 AAGTGTCTGAATCCCTCCAGTTCCTGATTTACATGATGATGATGATGATGATGAT 1783
DB 541 LysCysLeuAsnSerleuGlnValLeuAspTyrSerleuAsnHsIleMetThrSerLys 560
QY 1784 AAACAGAACTACAGCAATTTTCCAGATGCTGAGCTTTCTTAACTCTTACTCAGATGAC 1843
DB 561 LysGlnGlnLeuGlnHsPheProSerSerleuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1844 TTTGCTTGTCTGTTGTAACCAAGATTTCTGTAAGATGATGATGATGATGATGATGAT 1903
DB 581 PheAlaCysThrCysGlnHsGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu 600
QY 1904 TTGGTGAAGTTGAACGAATGATGCAACCTTCAGATTAAGAGGAGCATGCTGTG 1963
DB 601 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 620
QY 1964 CTGAGTTGAATATCACCTGTCAAGATTAATGAACATCATGAGTGTGCTGCTCAGT 2023
DB 621 LeuSerleuAsnIleThrCysGlnMetAsnLysThrIleGlyValSerValLeuSer 640
QY 2024 GTGCTTGATGATCTGTGTAGACAGTCTGCTCATATAGTCTATTTTCCCTGATGCTT 2083
DB 641 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHsIleMetLeu 660
QY 2084 CTTCGCTGCTGATAAAGTATGTAGAGTGAGAAACATCTATGATGCTTGTATCTAC 2143

DB 661 LeuAlaGlyCysIleLeuTyrGlyArgGlyGluAsnIleTyrAspAlaPheValIleTyr 680
QY 2144 TCAGCCAGAGATGAGGACTGGGTAAAGGATGAGCTAGTAAAGATTTAGAAAGAGGGG 2203
DB 681 SerSerGlnAspGluAspTrpValArgAsnGluLeuValLysAsnLeuGluGlyVal 700
QY 2204 CCTCATTTCACTGCTGCTTCACTACAGAGACTTATTCCTGGTGGCCATTTGCTGCC 2263
DB 701 ProProPheGlnLeuCysleuHsIleTyrArgAspPheIleProGlyValAlaIleAla 720
QY 2264 AACATCATCATGAAGTTTCCATTAAGCCGAAGGTGATTTGTGTGCTCCAGAC 2323
DB 721 AsnIleIleHsGlnGlyPheHsIleLysSerArgLysValIleValValSerGlnHs 740
QY 2324 TTCATCCAGAGCCGCTGCTGATCTTTGAAATATGATGATGCTCAGACCTGGAGTTTCG 2383
DB 741 PheIleGlnSerArgTrpCysIlePheGlyTyrGluIleAlaGlnThrTrpGlnPheLeu 760
QY 2384 AGCAGTCGTGTGTATCATCTTCAATTTGCTGTCAGAAAGTGAGAGACCTGTCAAG 2443
DB 761 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuAspSer 780
QY 2444 CAGCAGTGAGCTGTACCGCTTTCAGACAGAACATTTACTGAGTGGAGAGACAGT 2503
DB 781 GlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGluTrpGluAspSer 800
QY 2504 GTCCGTGGGGCGGCAKATCTTTGAGAGAGACTCAGAAAGCCCTGCTGATGGTAAATCA 2563
DB 801 ValLeuGlyArgHsIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 820
QY 2564 TGGATTCAGAAAGAAACAGTGGGTACAGATGCAATTTGACAGAAACAATCTATC 2620
DB 821 TrpAsnProGluGlyThrValGlyThrGlyCysAsnTrpGlnGluAlaHsSerIle 839

RESULT 4
ID ADC78785 standard; protein; 839 AA.
XX
AC ADC78785;
DT 01-JAN-2004 (first entry)
XX
DE Human PRO protein #7.
XX
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
OS Homo sapiens.
PN
PN W02003034984-A2.
XX
PD 01-MAY-2003.
XX
PF 15-OCT-2002; 2002W0-US033070.
XX
PR 19-OCT-2001; 2001US-0340083P.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Gurney AL;
XX
DR WPI; 2003-481990/45.
DR N-PSDB; ADC78784.
XX
PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
PT medicament for diagnosing or treating cancer or inflammatory bowel
PT disorder e.g., ulcerative colitis or Crohn's disease.
XX
PS Claim 12; SEQ ID NO 14; 327pp; English.
XX
CC The invention comprises the amino acid and coding sequences of human PRO
CC proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
CC sequence represents a human PRO protein of the invention.

SQ Sequence 839 AA;

Alignment Scores:

Pred. No.:	0	839
Score:	435.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	50.76%	Indels:
DB:	7	Gaps:

US-09-396-985B-1 (1-4868) X ADC78785 (1-839)

QY	10	ATGATGCTGGCTCGCGGCTGGAGCTCGATGCCAGCATGAGCCCTCTCTCGC	163
Db	1	MechesteralaserAargueuAaIythrleuileproIaMeAlaPheleuSerCys	20
QY	164	GTGAGACCAGAAAGCTGGAGCCCTGCGTGAGAGTGTTCTTAATATTAATTATCAATGC	223
Db	21	ValArgProGlnSerThrGlnProCysValGluValAlaProAsnIleThrTyrgInCys	40
QY	224	ATGAGAGTGAAATTTCTAATAAATCCCGGACAAACCTCCCTCTCAACCAAGAACTTGAC	283
Db	41	MetClnleuAsnPheTyrgIleProAspAsnleuProPheSerThrIlyAsnleuAsp	60
QY	284	CTGAGCTTTAATCCCTGAGGCATTTTAGAGACTTACCTTCTTGAGTTTCCCAAGAC	343
Db	61	LeuSerPheAsnProleuAArgHleuulysertyrSerPhePheSerPheProGlnleu	80
QY	344	CAGGTGCTGGATTTATCCAGGTGTGAATCCAGACAAATTGAAGATGGGCAATACAGAC	403
Db	81	GlnValleuAspLeuSerThrCysGlnIleGlnThrIleGluAspGlyAlaTyrgInSer	100
QY	404	CTAAGCCACCTCTCAACTTAATATTAAGAGAAACCCATCCAAAGTTTAGCCCTGGGA	463
Db	101	LeuSerHlsleuSerThrleuIleleuThrGlyAsnProIleGlnSerleuAlaGlnIly	120
QY	464	GCTTTTCTGAGCTATCAAGTTTACAGAGCTGTGGCTGTGGAGACAAATCTAGCATCT	523
Db	121	AlaPheSerGlyLeuSerSerleuGlnIlySerleuValAlaValGlnThrAsnleuAlaSer	140
QY	524	CTAGAGAACTTCCCATTTGGAACATCTCAAACTTTGAAAGAACTTAATGTGGCTCACAAT	583
Db	141	LeuGlnAsnPheProIleGlyHlsleuulysThrleuIyGlnleuAsnValAlaHlsAsn	160
QY	584	CTTATCCAAATTTTCAATTAACCTGAGATTTTCTATCTGACCAATCTAGAGACCTTG	643
Db	161	LeuIleGlnSerPheIySleuProGlnTyrrPheSerAsnleuThrAsnleuGlnHlsleu	180
QY	644	GACCTTTCCAGCAACAAGATTCAAAGTATTTATTTAGCAGACCTTGCGGGTCTTACATCA	703
Db	181	AspLeuSerSerleuAsnIySleIleGlnSerIleTyrcysThrAspLeuArgValleuHlsGln	200
QY	704	ATGCCCCCTACTGCATCTCTCTTTAGACCTGTGCCGATCCGATTAACCTTATCCAAACA	763
Db	201	MetCProleuAsnleuSerleuAspLeuSerleuAsnProMetAsnPheIleGlnPro	220
QY	764	GGTGCACTTTAAGAAATTAGGCTTCATAGCTGCACTTTAAGAAATAATTTGATAGTTTA	823
Db	221	GlyAlaPheIySglnIleArgleuHlsIySleuThrleuAlaGlnAsnPheAspSerleu	240
QY	824	AATGTATGAATACTTGATTCAGAGCTTGGCTGGTTTGAAGTGCATCTGTTGGTCTTG	883
Db	241	AsnValMetCylsThrCysIleGlnGlyleuAlaGlyleuGlnValHlsArgleuValleu	260
QY	884	GGAGAAATTGAAATGAAAGAAACTTGAGAAAGTTTGACAATCTGCTTAGAGGAGCTG	943
Db	261	GlyIyIuPheArgAsnGlnGlyAsnleuGlnIySleuPheAspIySserAlaIeulGlnIyIeu	280
QY	944	TGCAATTTGACCAATGAAGAAATTCGATTAGCATATTAGACTTACTACCTCGATGATATT	1003

Db	261	CysanleuThrIleGlnGlnpheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle	300
QY	1004	ATTGACTATTAAATTTGTTTGACAAATGTTTCTTCATTGTTCCCGTAGAGTGACTATT	1063
Db	301	IleAspLeuPheAsnGlyLeuThrAsnValSerSerPheSerLeuValSerValThrIle	320
QY	1064	GAAGGGTAAGAAGCTTTTCTTTATATTGCGATGGCAACATTNGAATTAGTAAGT	1123
Db	321	GlnArgValIysAspPheSerTyrAsnPheGlyTyrGlnIleSLeuGlnLeuValAsnGly	340
QY	1124	AAATTGGACAGTTTCCACATTGAATAACTCAAACTCCAAAGGCTTACTTCCCTCC	1183
Db	341	LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysAspGlnThrPheThrSer	360
QY	1184	AACAAAGGTGGAAATGCTTTTTCAGAAAGTTGATCTACCAACCCCTGAAGTTCTAGATGTC	1243
Db	361	AsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeu	380
QY	1244	AGTGAAGAAATGGCTTGAGTTCAAAAGTTGCTGTTCTCAAGTATGATTTTGGACAAACAC	1303
Db	381	SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer	400
QY	1304	CTAAGATATTAGAATCTGAGCTTCAATGCGTGTATTACCAAGACTTCAAACTTCCTGGG	1363
Db	401	LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuTyr	420
QY	1364	TTAGAACACATAGAAACATCTGATTTCCAGACTTCCAAATTGGAACAATAGTGAAGTTT	1423
Db	421	LeuGlnGlnLeuGlnIleAspPheGlnIleSerAsnLeuLysGlnMetSerGlnPhe	440
QY	1424	TCAGTATTCCTATCACTACAGAAACCTCATTTTACCTTGACATTTCTCATACTCACACAGA	1483
Db	441	SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisIleThrArg	460
QY	1484	GTTGCTTTCATATGCGATCTTCAATGGCTGTGTCAGCTCCGAAGCTTGAATAATGGCTGGC	1543
Db	461	ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValIleLysMetGlnGly	480
QY	1544	AAATCTTCCAGAAAACCTTCCCTCCAGATATCTTCCACAGAGCTGAGAACTTGACCTTC	1603
Db	481	AsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPhe	500
QY	1604	CTGACCTCTCTCAGTGTCAACTGAGACAGTTGTCTCCACAGCAATTAACTCACTCC	1663
Db	501	LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer	520
QY	1664	AGTCTTCAGGTACTTAATATGAGCCACAACTTCTTTTATTGGATAGCTTCTTAT	1723
Db	521	SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr	540
QY	1724	AAAGTGTGAACTCCCTCCAGGTTCTTGATTTAAGTGTCAATGCATATATGACTTCCAA	1783
Db	541	LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys	560
QY	1784	AAACAGCAACTACAGCAATTTTCCAAAGTACTACTTCTTAAATCTTACTACAGATGAC	1843
Db	561	LysGlnGlnLeuGlnIleAspPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp	580
QY	1844	TTTGCTTGATCTTGTAAACACAGAGTTTCTGCAATGATCAAGACACAGAGCAGCTC	1903
Db	581	PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTyrIleLysAspGlnArgGlnLeu	600
QY	1904	TTTGATGGAAGTTGAACGAATGGAATGGCAACACTTCAGATTAAGCGAGGACCTGTG	1963
Db	601	LeuValGlnValGlnArgMetGlnCysAlaIleThrProSerAspLysGlnGlyMetProAla	620
QY	1964	CTGAGTTGATATCACCTGTCCAGATGAATTAAGACCAATCATGGTGTGTGCGTCTCAGT	2023
Db	621	LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer	640
QY	2024	GTCGTTTGAATATCTGTGTGTAAGCACTTCGCTCTATAAGTTCTAATTTTCACTGATGCTT	2083

Db 641 ValIeuValISeValIValIaValIleuValIyTrIlySpheTyRPhetiSleuMeIeu 660
Qy 2084 CTGCTGGCTGCATTAAGTATGTAGAGGTGAAAAACATCTATGATGCTTTGTTATCTAC 2143
Db 661 LeuAlaGlyCysIleuTyRyRgIyRgIyGluAsnIleTyRAspAlaPheValIleTyR 680
Qy 2144 TCAAGCAGATGAGAGCTGGTAAAGATGAGCTAGTAAGAATTAGAAAGAGGGGTG 2203
Db 681 SerSerGlnAspGluAspTrpValIArgAsnGluLeuValIAsnLeuGluGluValI 700
Qy 2204 CTTCACTTTCAGCTCTGCTTCACTACAGAGACTTATTCCTGGGTGTGGCATTGCTGC 2263
Db 701 ProProheGlnLeuCySleuHiStyRArgAspPheIleProGlyValIAlaIleAla 720
Qy 2264 AACATCATTCATGAAAGTTTCCATTAAGCGAAAGGTGATTTGTTGGTGTCCCGAC 2323
Db 721 AsnIleIleHISgluGlyPheHISlySerArgIySValIleValIValISerGlnHIS 740
Qy 2324 TTCATCCAGAGCCGCTGTGTATCTTGAATATGAGATTGCTCAGACCTGGCAGTTTCTG 2383
Db 741 PheIleGlnSerArgTrpCySlePheGlnTyRGlulIleAlaGlnThrTrpGlnPheIu 760
Qy 2384 AGCAGTGTGTGTATCATCTTTCATTTGCTCTGAGAAAGGTGAGAAAGCTTGTCTGAG 2443
Db 761 SerSerArgIaGlyIleIlePheIleValIleGlnIySValIgluTyRThrLeuArg 780
Qy 2444 CAGCAGGTGAGCTGTACCCCTTCTGAGAGAAACCTTACCTGGAGTGGAGAGACT 2503
Db 781 GlnGlnIValIgluLeuTyRArgLeuLeuSerArgAsnThrTyRleuGluTrpGluAspSer 800
Qy 2504 GTCTGGGGGGGACATCTTCTGTGAGAGAGACTCAGAAAGCCCTGTGATGTGAATCA 2563
Db 801 ValIeuGlyArgHISlePheTrpArgIleuArgIySAlaLeuLeuAspGlyLySer 820
Qy 2564 TGGATTCAGAAAGACAGTGGGTACAGATGCAATTGGCAGAAAGCAACATCTATC 2620
Db 821 TrpAsnProGluGluTyRThrValIgluTyRGlYCySAsnTrpGlnIuAlaThrSerIle 839

RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
XX ADD48826;
AC
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein AAF05316, SEQ ID NO 14536.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN MO2003016475-A2.
XX
PD 27-FEB-2003.
PF
XX 14-AUG-2002; 2002WO-US025765.
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
PI
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; AAF05316.

XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017p; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 839 AA;
SQ
Alignment Scores:
Pred. No.: 0 Length: 839
Score: 4355.00 Matches: 839
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.76% Indels: 0
DB: 7 Gaps: 0
US-09-396-985b-1 (1-4868) x ADD48826 (1-839)
Qy 104 ATGATGTCGTGCTCGGCTGTGGAGCTTGATCCAGGACCTTCTCTCTCTG 163
Db 1 MetMetSerIaSerArgIeuaIaGlyThrIleuIleProAlaMetAlaPheLeuSerCyS 20
Qy 164 GTAGACCAAGAAAGCTGGAGAGCCCTGTGGAGGTGTTCTTAATTTACTTAACAATGC 223
Db 21 ValArgProGluSerTrpGluProCySValIgluValIProAsnIleThrTyRGlNcyS 40
Qy 224 ATGAGACTGAAATTTCAAAATCCCGCAACCTCCCTTCAACCAAGAACTGTGAC 283
Db 41 MetGluLeuAsnHISheTyRlySleProAspAsnLeuProPheSerThrIySAsnLeuAsp 60
Qy 284 CTGAGCTTTAATCCCTGAGGACTTTAGAGAGCTATGACTTTCTTCAGTTCCAGAACTG 343
Db 61 LeuSerPheAsnProLeuArgHISleuGlySerTySerPhePheSerPheProGluLeu 80
Qy 344 CAGGTGCTGATTTATCCAGGTGTGAATCCAGCAATGAAGATGGGAGATTCAGAGC 403
Db 81 GlnValIeuAspLeuSerArgCySgluIleGlnThrIleGluAspGlyAlaTyRGlNser 100
Qy 404 CTAAAGCAGCTCTCTAATTAATTTAGACAGAAACCCATCCAGAGTTAGCCCTGGAG 463
Db 101 LeuSerHISleuSerThrIleuIleuThrGlyAsnProIleGlnSerIleuAlaLeuGly 120
Qy 464 GCCTTTTCTGAGACTATCAAGATTACAGAAAGCTGTGGCTGTGGAGCAAACTTGAATCT 523
Db 121 AlaPheSerGlyLeuSerSerIleuGlnIySleuValIAlaValIgluThrAsnLeuAlaSer 140

QY 524 CTAGAGAACTTCCCATTTGACATCTGAAAATTGAAAGAACTTAATGTCGACAAAT 583
 DB 141 LeuLysAsnProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 160
 QY 584 CTTATCCAACTTTGCAAAATTAAGTATTTTCTAATCTGACCAATCTAGACACTTG 643
 DB 161 LeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeu 180
 QY 644 GACCTTCCAGCAACAGATTCAAAGTATTTATTTGACAGACTGGGGGTTCTACACAA 703
 DB 181 AsnLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGln 200
 QY 704 ATGCCCTACTCAATCTCTTTAGACCTGCTCCGTAATCCTAATGAACTTATCAACA 763
 DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 764 GGTGCATTTAAGAAATTAAGCTTCATAGCTGACTTAAGAAATTAATTTGATAGTTA 823
 DB 221 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu 240
 QY 824 AATGTAATGAATACTTTATTAAGTCTGCTGCTGTTAGAAAGCTCATCGTTGCTCTG 883
 DB 241 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeu 260
 QY 884 GGAGAAATTTGAATAAGAACTTGAAGAAATTTGAACAATGCTGCTGAGAGGCTG 943
 DB 261 GlyGluPheArgAsnGluGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 280
 QY 944 TGCATTTGACCATTTGAAGAATTCGATTCGATTAAGTATTAAGTATTAAGTATTT 1003
 DB 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspLysTyrTyrLeuAspAspIle 300
 QY 1004 ATTGACTTATTTAATTTGTTGACAAAGTTTCTTCAATTTCCCGTGAGTGTGACTAT 1063
 DB 301 IleAspLeuPheAsnLysCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
 QY 1064 GAAAGGTTAAAGACTTTTCTTATTAATTTGCGATGCGACATTTAGAAATTTAGTTAACTG 1123
 DB 321 GluArgValLysAspPheSerTyrAsnPheGlyTyrPheGlnHisLeuGlnLeuValAsnCys 340
 QY 1124 AAATTTGACAGTTTCCACATTTGAACTCAATCTCTCAAAAGCTTACTTCACTTCC 1183
 DB 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
 QY 1184 AACAAAGGTGGAAATGCTTTTTCAGAACTGATTTACCAAGCTTGATTTCTAGATCTC 1243
 DB 361 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGlnPheLeuAspLeu 380
 QY 1244 AGTAGAAATGGCTTGAGTTCAAAAGTTGCTGTTCTCAAAAGTATTTTGGGACAACAGC 1303
 DB 381 SerArgAsnGlyLeuSerPheLysGlyCysCysSerIleSerAspPheGlyThrThrSer 400
 QY 1304 CTAAGATTTAATTAAGTCAATGCTTCAATGCTGTTATTAACCATGAGTTCAAACTTCTGGG 1363
 DB 401 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
 QY 1364 TTGGAACAACCTAGAACATCTGATTTCCAGCATTTCCAAATTTGAAACAATGAGTACTT 1423
 DB 421 LeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerSerAsnLeuLysGlnMetSerGluPhe 440
 QY 1424 TCAGTATTTCTATCACTCAAGAAACCTCATTTACTGATCTTCTCATCTCAACACAGA 1483
 DB 441 SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerThrIleHisArg 460
 QY 1484 GTTGCTTTCAATGAGCATCTTCAATGCTGCTGCTGCAAGTCTCGAAGCTTGAATGCTGCG 1543
 DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly 480
 QY 1544 AATTTCTTCCAGGAAACTTCTTCCAGATATCTTCCAGAGCTGAGAACTTGACCTTC 1603
 DB 481 AsnSerPheGlnGlnLeuAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500

QY 1604 CTGAGACTTCTCAAGTGTCAACTGAGACAGTGTCTTCCAAAGCATTTAACTCATCTCC 1663
 DB 501 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 520
 QY 1664 AGTTCTCAGGTACTAAATATGAGCCACACAACTTTCTTTCAATTTGATTAAGTTTCTTAT 1723
 DB 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 540
 QY 1724 AGGTGCTGAACCTCCCTCCAGGTTCTTGATTTACAGTCTCAATGACAAATGAGCTTCCAA 1783
 DB 541 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 560
 QY 1784 AAACAGAACTACAGCAATTTCCAAAGTATCTAGCTTTCTTAATCTTACTCATGAATAC 1843
 DB 561 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
 QY 1844 TTGCTTTGATCTTTGTAACCAAGAGTTTCTGCAATGATCAAGACCAAGGACGCTC 1903
 DB 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTyrIleLysAspGlnArgGlnLeu 600
 QY 1904 TTGCTGGAAGTTGAAGAAATGAATGAGCAACCTTCAAGTAAAGCAAGGCGCATGCTG 1963
 DB 601 LeuValGlnValGlnLysArgMetGlnCysAlaThrProSerAspLysGlnLysMetProVal 620
 QY 1964 CTGAGTTTGAATATCACTGCTCAGATGAATGAACCATCATCTAGTGTGTCGCTCAGT 2023
 DB 621 LeuSerLeuAsnHisIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 640
 QY 2024 GTGCTGTGATATCTGTGTTGAGCAGTTCTGCTATTAAGTTCTAATTTTCACTGATGCT 2083
 DB 641 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeu 660
 QY 2084 CTGCTGCTGCTGCAATAAGTATGTTAGAGTGGAAGAAATCATCATGATGCTTTGTTATAC 2143
 DB 661 LeuAlaGlyCysIleLysTyrGlyArgGlyGlyAsnIleTyrAspAlaPheValIleTyr 680
 QY 2144 TCAAGCCAGATGAGACTGGTGAAGAAATGAGCTGTAAGAAATTTGAAGAAAGGCGTG 2203
 DB 681 SerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlyVal 700
 QY 2204 CTTCAATTTCAAGCTGCTGCTTCACTACAGAGACTTTATTTCCGGTGTGCGCATGCTGCC 2263
 DB 701 ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 720
 QY 2264 AACATCATCCATAAGCTTTCCATAAAAGCCGAAAGGTATTTGTGTGCTGCCAGAC 2323
 DB 721 AsnIleIleHisGlnGlyPheHisLysSerArgGlyValIleValValValSerGlnHis 740
 QY 2324 TTGATCCAGAGCGGTGATCTTCTTGAATATGAGATTTGCTCAGACCTGGCAGTTTCTG 2383
 DB 741 PheIleGlnSerArgTrpCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPheLeu 760
 QY 2384 AGCAGTGTGCTGATTCATCTTCAATGCTCTGACAGAGTGGAGAAACCTGCTCAGG 2443
 DB 761 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg 780
 QY 2444 CAGCAGGTGAGCTGTACCGCTTCTCAGACGAAACATTACTGAGTGGAGACAGT 2503
 DB 781 GlnGlnValGlnLeuLysArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnLysSer 800
 QY 2504 GTGCTGGGGCGGACATCTTTGAGAGAGCTCAGAAAGCCGCTGAGTGGTAAATCA 2563
 DB 801 ValLeuGlyArgHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 820
 QY 2564 TGGAACTCAGAAAGAACAGTGGGTACAGAGATGCAATTTGACAGAAACATCTATC 2620
 DB 821 TrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnLysThrSerIle 839

RESULT 6

ID AAW86361
 ID AAW86361 standard; protein; 837 AA.
 AC AAW86361;


```

Db      420  G|G|I|n|e|u|g|i|n|h|s|e|u|a|p|h|e|g|i|n|h|s|e|r|a|n|e|u|y|s|g|i|n|e|s|e|r|g|i|n|p|h|e|s|e|r|
Qy      1427  G|T|A|T|T|C|C|A|C|C|G|A|A|A|C|T|T|A|C|T|T|G|A|C|A|T|T|T|C|T|C|A|T|T|C|A|C|C|A|G|G|T|
Db      440  V|a|P|h|e|u|s|e|r|e|u|a|g|a|n|l|e|u|l|e|r|y|l|e|u|a|s|p|i|l|e|s|e|r|h|s|t|h|r|s|t|h|n|g|y|a|l|
Qy      1487  G|C|T|T|C|A|A|T|G|C|A|T|T|C|A|T|G|G|T|T|C|A|G|T|C|C|A|G|T|T|C|T|G|A|A|A|G|G|T|G|C|A|T|
Db      460  A|a|P|h|e|a|n|s|i|l|y|l|e|P|h|e|a|n|g|i|l|e|u|s|e|r|S|e|r|i|e|u|i|n|v|a|l|l|e|u|y|e|t|h|a|a|g|i|y|a|n|
Qy      1547  T|C|T|T|C|C|A|G|A|A|A|C|T|T|C|T|C|C|A|G|A|T|T|C|C|A|G|A|G|C|T|G|A|A|A|C|T|T|G|A|C|T|T|C|T|G|
Db      480  S|e|r|P|h|e|i|n|g|i|u|s|P|h|e|u|P|r|o|a|s|i|l|e|P|h|e|r|i|g|i|u|e|u|a|r|g|a|n|l|e|u|t|h|r|P|h|e|u|
Qy      1607  G|A|C|T|C|T|C|A|G|T|C|A|C|T|G|A|G|A|C|A|T|T|G|T|T|C|C|A|C|A|G|A|T|T|T|A|C|T|A|C|T|C|C|A|G|T|
Db      500  A|s|P|h|e|u|s|e|r|i|n|C|y|s|i|n|l|e|u|g|i|n|l|e|u|s|e|r|P|r|o|t|h|r|a|P|h|e|a|n|S|e|r|l|e|u|S|e|r|
Qy      1667  C|T|T|C|A|G|T|A|T|A|A|T|A|T|G|A|C|C|A|C|A|C|A|C|T|T|C|T|T|C|A|T|G|A|T|G|A|T|G|T|T|C|T|T|A|G|
Db      520  L|e|u|g|i|n|v|a|l|l|e|u|s|e|r|h|s|a|n|a|s|P|h|e|s|e|r|l|e|u|a|s|p|h|e|r|P|r|o|t|h|r|y|l|y|s|
Qy      1727  T|G|T|G|A|A|C|T|C|C|T|C|C|A|G|G|T|T|T|G|A|T|T|A|G|T|C|C|A|T|C|A|T|A|T|G|A|C|T|T|C|C|A|A|A|A|
Db      540  C|y|e|l|e|u|a|n|s|e|r|l|e|u|g|i|n|v|a|l|l|e|u|a|s|P|y|S|e|r|l|e|u|a|n|h|i|s|i|l|e|w|e|t|h|r|S|e|r|y|e|l|y|s|
Qy      1787  C|A|G|A|A|C|T|A|G|A|C|A|T|T|T|C|C|A|G|A|G|T|C|T|T|C|T|T|A|A|T|C|T|A|T|C|A|G|A|T|G|A|T|T|T|
Db      560  G|i|n|g|i|l|e|u|i|n|h|s|P|h|e|r|P|r|o|s|e|r|S|e|r|l|e|u|a|l|P|h|e|u|a|n|l|e|u|t|h|r|g|i|n|a|s|P|h|e|
Qy      1847  G|C|T|T|G|A|C|T|T|G|A|A|C|C|A|G|A|G|T|T|C|C|T|C|A|T|G|A|T|G|A|C|A|G|A|C|C|A|G|A|G|C|A|G|C|T|T|G|
Db      580  A|a|C|y|e|t|h|r|C|y|s|e|i|u|h|s|i|n|s|e|r|P|h|e|u|g|i|n|t|h|r|i|l|e|y|s|a|s|P|i|n|a|g|i|n|l|e|u|
Qy      1907  G|T|G|A|A|G|T|G|A|C|G|A|T|G|A|T|G|C|A|C|C|T|T|C|A|T|A|G|A|C|G|G|C|A|T|G|C|T|G|C|T|G|
Db      600  V|a|I|G|i|u|a|I|u|a|r|g|e|t|G|i|u|C|y|a|l|a|t|h|r|P|r|o|s|e|r|a|s|P|y|s|i|n|g|i|y|e|t|P|r|o|v|a|l|l|e|u|
Qy      1967  A|G|T|T|G|A|A|T|C|A|C|C|T|G|C|A|G|A|T|G|A|A|A|C|A|C|A|T|T|G|T|G|T|G|G|T|C|C|A|G|T|G|
Db      620  S|e|r|i|e|u|a|n|h|e|r|C|y|s|i|n|e|l|a|s|h|l|y|e|h|r|i|l|e|g|i|y|a|l|S|e|r|v|a|l|l|e|u|S|e|r|v|a|l|
Qy      2027  C|T|T|G|A|T|C|T|G|T|G|A|G|A|G|T|T|C|T|G|C|A|T|A|G|T|T|C|A|T|T|T|C|A|C|G|A|T|G|C|T|T|
Db      640  L|e|u|v|a|l|S|e|r|v|a|l|a|a|v|a|l|l|e|u|v|a|l|l|y|l|y|s|h|e|r|y|l|P|h|e|h|s|b|e|u|e|l|e|u|
Qy      2087  G|C|T|G|C|T|G|C|A|T|A|A|G|T|G|T|G|A|G|G|T|G|A|A|A|C|A|T|T|A|T|G|C|T|T|T|T|A|T|C|T|A|C|T|C|A|
Db      660  A|a|g|i|y|C|y|e|i|l|e|y|s|t|r|g|i|y|a|r|g|i|y|l|u|a|n|h|l|e|r|y|a|s|p|h|a|l|P|h|e|v|a|l|l|e|r|y|s|e|r|
Qy      2147  A|G|C|C|A|G|A|T|A|G|A|C|T|G|G|T|G|A|G|A|T|G|A|G|C|T|G|T|A|A|A|A|T|T|G|A|A|A|G|G|G|T|G|C|T|
Db      680  S|e|r|g|i|a|s|P|i|u|a|s|P|t|r|P|V|a|l|a|r|g|a|n|g|i|u|d|e|u|v|a|l|l|y|s|a|n|e|u|g|i|u|g|i|y|a|l|P|r|o|
Qy      2207  C|A|T|T|C|A|G|C|T|G|C|T|C|A|C|A|G|A|C|T|T|A|T|T|C|C|G|G|T|G|G|C|A|T|T|G|G|C|C|A|C|
Db      700  P|r|o|P|h|e|i|n|e|u|C|y|e|u|h|i|s|t|r|y|a|r|g|a|s|P|h|e|i|l|e|P|r|o|i|y|a|l|a|i|l|e|a|i|a|a|a|a|n|
Qy      2267  A|T|C|A|T|C|A|T|G|A|G|T|T|C|A|T|A|A|A|G|C|G|A|A|G|G|T|G|T|G|T|G|T|G|C|C|A|G|A|C|T|T|C|
Db      720  I|l|e|i|l|h|i|s|i|g|i|u|g|i|P|h|e|h|s|y|s|e|r|a|r|g|i|y|e|v|a|i|l|e|v|a|l|a|l|S|e|r|g|i|h|i|a|P|h|e|
Qy      2327  A|T|C|A|G|A|G|C|G|G|G|G|T|A|T|T|G|A|T|A|G|A|G|A|T|T|G|C|T|C|A|G|A|C|T|G|C|G|C|T|T|G|A|G|C|
Db      740  I|l|e|i|l|S|e|r|a|r|g|t|r|P|C|y|i|l|e|P|h|e|i|g|i|u|r|g|i|l|e|a|i|n|h|r|t|r|P|g|i|n|P|h|e|l|e|S|e|r|
Qy      2387  A|G|T|G|T|G|G|T|A|T|C|A|T|T|G|C|T|G|C|A|G|A|G|G|T|G|A|G|A|C|C|T|G|C|A|G|G|C|A|G|
Db      760  S|e|r|a|r|g|i|a|s|i|l|e|i|l|e|P|h|e|i|l|e|v|a|l|l|e|u|g|i|n|y|s|a|i|g|i|u|y|s|t|h|r|l|e|u|S|e|r|a|r|g|i|n|
Qy      2447  C|A|G|T|G|A|G|C|T|G|A|C|C|C|T|T|C|A|G|A|G|A|C|A|C|T|T|A|C|T|G|A|G|T|G|G|A|G|A|C|A|G|T|G|C|

```

```

Db      780  G|i|n|v|a|l|G|i|u|e|u|t|r|a|r|g|i|e|u|s|e|r|a|r|g|a|n|h|r|t|h|r|l|e|u|g|i|u|r|g|i|u|a|s|P|e|r|v|a|l|
Qy      2507  C|T|G|G|G|G|G|G|C|A|C|A|T|T|T|G|G|A|G|A|C|T|C|A|G|A|A|A|G|C|C|T|G|G|A|T|G|G|T|A|A|T|C|A|T|G|
Db      800  L|e|u|g|i|y|a|r|g|h|i|s|i|l|e|h|e|r|t|r|P|a|r|g|a|r|g|e|a|r|y|a|l|a|l|e|u|e|u|a|s|P|i|y|l|y|s|e|r|t|r|P|
Qy      2567  A|A|T|C|A|G|A|A|G|A|C|A|G|T|G|G|T|A|C|A|G|A|T|G|C|A|G|A|T|T|G|C|A|G|A|C|A|C|A|T|T|A|T|C|
Db      820  A|a|n|P|r|o|G|i|u|g|i|y|h|r|a|l|G|i|y|h|r|g|i|y|C|y|a|a|n|h|r|P|o|i|n|d|i|u|a|h|r|S|e|r|i|l|e|
RESULT 7
AAE16102 standard; protein; 837 AA.
ID      AAE16102;
AC      AAE16102;
DT      26-MAR-2002 (first entry)
XX      XX
DE      Human DNAX Toll like receptor (DTLR) 4 #2.
XX      XX
KW      Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KM      interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX      XX
OS      Homo sapiens.
XX      XX
PN      WO200190151-A2.
XX      XX
PD      29-NOV-2001.
XX      XX
PF      23-MAY-2001; 2001WO-US016766.
XX      XX
PR      25-MAY-2000; 2000US-0207558P.
XX      XX
PA      (SCHE ) SCHERING CORP.
PI      Hardiman GT, Rock FL, Bazan JF, Kaetzelin RA, Ho SWK, Liu Y;
DR      WPI; 2002-083085/11.
XX      XX
DR      N-PDB; AAD26292.
XX      XX
PT      New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT      conditions exhibiting abnormal expression of the receptors of their
PT      ligands, particularly abnormalities manifested by immunological
PT      disorders.
XX      XX
PS      Claim 3; Page 41; 297bp; English.
XX      XX
CC      The invention relates to mammalian receptor proteins, e.g., primate,
CC      human DNAX Toll like receptor (DTLR) protein and their corresponding
CC      nucleic acids. The DTLR is useful for treating conditions exhibiting
CC      abnormal expression of the receptors of their ligands. Such abnormality
CC      is manifested by immunological disorders. In particular, the DTLR is
CC      useful for treating various disease or disorders associated with abnormal
CC      expression or abnormal triggering of response to a ligand. The DTLR is
CC      also useful as an immunogen for the production of antisera or antibodies
CC      specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC      receptor family members, for the DTLR or its various fragments. The
CC      purified DTLR can be used to screen monoclonal antibodies or antigen-
CC      binding fragments. The antibodies are useful for screening expression
CC      libraries for particular expression products. These are useful for
CC      detecting or diagnosing various immunological conditions related to
CC      expression of DTLR or cells that express it. The present sequence is
CC      human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
CC      Note: The present sequence SEQ ID NO 26 is stated to be similar to the
CC      sequence shown in page 240-243 (AAE16116). However these sequences differ
CC      at several locations
XX      XX
SQ      Sequence 837 AA:
XX      XX
Alignment Scores:
Pred. No.: 0
Score: 4335.50
Length: 837
Percent Similarity: 99.88
Matches: 837
Conservative: 0

```

Best Local Similarity: 99.88% Mismatches: 0
Query Match: 50.54% Indels: 1
DB: 5 Gaps: 1
US-09-396-985b-1 (1-4868) x AAE16102 (1-837)

QY 107 ATGTGCGCTCGCGCTGGGAGACTGTGATCCAGCCATGGCCTTCTCTCGCGTG 166
Db 1 MetSerLaserArgLeuAlaGlyThrLeuIleProLametaLapheLeuSerCysVal 20
QY 167 AGACCGAAGAGCGGAGCCCTCGCGAGAGTGTTCTTAATTAATTTCAATGATG 226
Db 21 ArgProGlnSerThrGluProCysValGlu--ValProasnIleThrTyGlnCysMet 39
QY 227 GAGCTGAATTTCTCAAAATCCCGACAACTCCCTTCTCAACAAGACTGACCTG 286
Db 40 GluLeuAsnPhenTyrrylsIleProAspAsnLeuProPheSerThrIrysAsnLeuAspLeu 59
QY 287 AGCTTAATCCCTGAGGCAATTTAGGCAAGCTTAATAGCTTTCAGTTTCCGAGAACTGACG 346
Db 60 SerPheAsnProLeuArgIleAsnGlySerTySerPhePheSerPheProGlnLeuGln 79
QY 347 GTCCTGATTTATCCAGGTGTGAATTCACAACTGAAGATGGGGCATTCAGAGCTTA 406
Db 80 ValLeuAspLeuSerArgCysGluIleGlnThrIleGlnAspGlyAlaTyrgInSerLeu 99
QY 407 AGCACCTCTCTCACTTAATTAATGACAGAAACCCCATCCAGAGTTTAAAGCCTGGAGCC 466
Db 100 SerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
QY 467 TTTTTCGACTATCAAGTTTACAGAAAGCTGGTGGCTGTGAGACAAATCTGACATCTTA 526
Db 120 PheSerGlyLeuSerSerLeuGlnTyLeuValAlaValGlnThrAsnLeuAlaSerLeu 139
QY 527 GAAACCTCCCGCATTTGGACATCTCAAAACTTTGAAGAATTAATGGGCTCAATCTT 586
Db 140 GluAsnPhenProIleGlyHisLeuTyThrLeuTySerGluLeuAsnValAlaHisAsnLeu 159
QY 587 ATCCAACTCTTCAATTAACCTGAGTATTTTCTAATCTGACCAATCTGAGAGCACTTGAC 646
Db 160 IleGlnSerPheTyLeuProGlnTyrrPheSerAsnLeuThrAsnHisLeuGlnHisLeuAsp 179
QY 647 CTTTCCAGCAACAGATTCAGAGTATTTAATGACACAGACTGGGGTCTTACATCAATG 706
Db 180 LeuSerSerAsnTyrrIleGlnSerIleTyrrCysThrAspLeuArgValHisGlnMet 199
QY 707 CCCCTACTCAATCTCTCTTGAACCTGTCCCTGAATCTTGAACCTTATCCAACCGAT 766
Db 200 ProLeuAsnHisLeuSerLeuAspLeuSerLeuAsnProMetAsnPhenIleGlnProGly 219
QY 767 GCATTTAAAGAAATTAAGGCTTCATAGCTGACTTAAGAATAATTTGATAGTTTAAT 826
Db 220 AlaPheTyrrGlnIleArgLeuHisTyrrLeuThrLeuArgAsnHisPheAspSerLeuAsn 239
QY 827 GTAATGAAAACCTTGATTAAGGCTTGCGCTGGTTTGAAGTCCATCGTTTGGTCTTGGA 886
Db 240 ValMetCysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValHisGly 259
QY 887 GAATTTGAATAAGAAACTTGGAAGAAAGTTTGAACAAATCTGCTTGAAGGGCTGTGC 946
Db 260 GluPheArgAsnGlnGlyAsnLeuGlnTyrrPheAspTyrrSerAlaLeuGlnGlyLeuCys 279
QY 947 AATTGACATTAAGAAATCCGATTAAGTACTGACTTAAGTACTGATGATATTAAT 1006
Db 280 AsnLeuThrIleGlnGlnPheArgLeuAlaTyrrLeuAspTyrrTyrrLeuAspAspIleTyr 299
QY 1007 GACTTATTAATTTGATTAAGAAATGTTTCTTCAATTTTCCCTGGTGAAGTGAATTAAG 1066
Db 300 AspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGln 319
QY 1067 AGGGTAAAGACATTTTCTTAATTTGATGACCAATTTGAATTAAGTAACTGTAA 1126
Db 320 ArgValTyrrAspPheSerTyrrAsnPhenGlyTyrrGlnHisPheGlnLeuValHisCysTyrr 339

QY 1127 TTGGAAGATTTCCACATTTGAAGAACTCAATCTCTCAAAAAGGCTTACTTTCACCTTCCAC 1186
Db 340 PheGlyGlnPheProThrLeuTyrrLeuTyrrSerLeuTyrrArgLeuThrPheThrSerAsn 359
QY 1187 AAAAGTGGAAATGCTTTTTCAGAAATGATCTTACAAAGCTTGAGTTTCTAGATCTCAGT 1246
Db 360 TyrrGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeuSer 379
QY 1247 AGAAATGGCTGAGTTTCAAGGCTGTCTTCCAAAGTAAAGTATTTGGACCAACGACCTTA 1306
Db 380 ArgAsnGlyLeuSerPheTyrrGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu 399
QY 1307 AAGTATTTAGATCTGAGCTTCAATGAGTGTATTAATCCATGATGATCAAACTTCTGGAGCTTA 1366
Db 400 TyrrTyrrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419
QY 1367 GAACAACTGACATCTTGATTTCCAGCAATTCGAATTTGAACAAATGAGTGATTTTCA 1426
Db 420 GluGlnLeuGlnHisPheAspPheGlnHisSerAsnLeuTyrrGlnMetSerGlnPheSer 439
QY 1427 GTATTGCTATCACTGAAACCTCATTTTACTTGAATTTCTGATCTGACACAGAGTT 1486
Db 440 ValPheLeuSerLeuArgAsnLeuIleTyrrLeuAspIleSerHisThrHisArgVal 459
QY 1487 GCTTTCAAATGGCATCTTCAATGGCTTGTCCAGTCTGGAAGTCTTGAATAATGGCTGGCAAT 1546
Db 460 AlaPheAsnGlyTyrrPheAsnGlyLeuSerSerLeuGlnValLeuTyrrMetAlaGlyAsn 479
QY 1547 TCTTTCAGAGAAAATCTTCTCCAGATATCTTCAACAGCTGAGAAACTTGAACCTTCTG 1606
Db 480 SerPheGlnGlnAsnPhenLeuProAspIlePheThrGlnLeuArgAsnLeuThrPheLeu 499
QY 1607 GACCTCTCAAGTGAACCTGAGAGCTTGTCTCCAAAGCAATTTAACTCACTCTCCAGT 1666
Db 500 AspLeuSerGlnCysGlnLeuGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSerSer 519
QY 1667 CTTCAAGTACTAAATTAAGACCAACAACAATCTTCTTCAATGGATAGCTTCTTAAAG 1726
Db 520 LeuGlnValLeuAsnMetSerHisAsnAsnPhenPheSerLeuAspThrPheProTyrrLe 539
QY 1727 TGTGTAACCTCCCTCCAGGTTCTTGATTAACGTCTCAATCACTAAATGACTTCCAAAAA 1786
Db 540 CysLeuAsnSerLeuGlnValLeuAspTyrrSerLeuAsnHisIleMetThrSerTyrrLe 559
QY 1787 CAGGAACCTCAGCAATTTTCCAGTACTGAGCTTCTTAAATCTTCTCAGAAATGACTT 1846
Db 560 GlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnHisAsnPhe 579
QY 1847 GCTTGTACTTGTGAACACAGAGTTTCTGCAATGATGATCAAGACCAAGGACGACTTGG 1906
Db 580 AlaCysThrCysGlnIleHisGlnSerPheLeuGlnThrIleTyrrAspGlnArgGlnLeuLeu 599
QY 1907 GTGGAAGTTGAACGAATGGAATGTGCAACACTTCAAGATTAAGCAGGCGATGCTGTGCTG 1966
Db 600 ValGlnValGlnArgMetGlnCysAlaThrProSerAspTyrrSerGlnGlyMetProValLeu 619
QY 1967 AGTTGAATATATCACTGCAAGTGAATGAACCATGATGCTGTGTCGGCTCAGAGTGG 2026
Db 620 SerLeuAsnIleThrCysGlnMetAsnTyrrHisIleGlyValSerValLeuSerVal 639
QY 2027 CTTGTAGTATCTGTGTAGACGTTCTGACTAATAGTCTAATTTTCAACGATGATCTTCTT 2086
Db 640 LeuValValSerValValAlaValLeuValTyrrTyrrPheTyrrPheHisLeuMetLeuLeu 659
QY 2087 GCTGGCTGCAATAAGATAGGTAGAGGTGAACCAATCATATGATGCTTGTGTATCTCACTCA 2146
Db 660 AlaGlyCysIleTyrrTyrrGlyArgGlyGlnAsnIleTyrrAspAlaPheValIleTyrrSer 679
QY 2147 AGCCAGATGAAGACCTGGGTGAAGGATGAGCTAGTAAAGATTTAAGAAAGGAGGCTGCT 2206
Db 680 SerGlnAspGlnAspThrValArgAsnGlnLeuValTyrrAsnLeuGlnGlnGlyValPro 699

QY 2207 CCATTTCAGCTCTGCCCTTCACTACAGAGACTTATTCCTCCGGTGTGCCATCTGCTCCAC 2266
 |||||
 Db 700 ProPheglnleuCySleuHtstYrArgAspPheIleProglYValAlaIleAlaIleAsn 719
 |||||
 QY 2267 ATATCATGTAAGGTTTCCATTAAGCCGAAAGGTGATTGTGTGGTCTCCAGCACTTC 2226
 |||||
 Db 720 IleIleIleGlnGlyPheHtstYsSerArgYValIleValValIleSerGlnHtstPhe 739
 |||||
 QY 2327 ATCCAGAGCCGCTGTGTATCTTGAATGATGAGATTGCTCAGACCTGCGAGTTTCTGAGC 2386
 |||||
 Db 740 IleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGlnHtstPheIlePheSer 759
 |||||
 QY 2387 AGTCGTCTGTATCATCTTCTTCTTCAGAGGTGAGAGACCTCTCAGGAG 2446
 |||||
 Db 760 SerArgAlaGlyIleIlePheIleValIleGlnIleValGlnIlePheSerGln 779
 |||||
 QY 2447 CAGGTGAGCTGTACCGCTCTTTCAGAGAGAACCTTACCTGAGGTGGAGACAGTCTC 2506
 |||||
 Db 780 GlnValGlnIleuYrArgIleuSerArgAsnHtstYrIleuGlnIlePheSerVal 799
 |||||
 QY 2507 CTGGGGGCGGACATCTTCTGAGAGCAGTCAAGAAAGCCCTGCTGATGTAATCATG 2566
 |||||
 Db 800 LeuGlyArgHtstIlePheHtstPArgYLeuArgYValIleuSerGlyLysSerTyr 819
 |||||
 QY 2567 AATCCAGAAAGAACAGTGGGTACAGATGCAATTGGCAGGAAACATCTATC 2620
 |||||
 Db 820 AsnProGlnIleYrValGlnIleGlyCysAsnHtstPheIleGlnIleHtstSerIle 837
 |||||

RESULT 8
 AB004776
 ID AB004776 standard; protein; 837 AA.
 XX
 AC AB004776;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1442.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicz RM, Tomlinson AJ, Urban RG;
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukaemia.
 XX
 PS Example 2; SEQ ID NO 1442; 134p; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a

CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 837 AA;
 SQ

Alignment Scores:

Pred. No.:	0	Length:	837
Score:	4335.50	Matches:	837
Percent Similarity:	99.88%	Conservative:	0
Best Local Similarity:	99.88%	Mismatches:	0
Query Match:	50.54%	Indels:	1
DB:	6	Gaps:	1

US-09-396-985b-1 (1-4868) x AB004776 (1-837)

QY 107 ATGCTGCTCTGCGCTGCTGAGCTGTGATCCAGACCTCTCTCTGCGG 166
 |||||
 Db 1 MetSerAlaSerArgIleuAlaGlyHtstIleProAlaMetAlaPheIleuSerCysVal 20
 |||||
 QY 167 AGACCAAGAAAGCTGGAGCCCTGCGAGGTGCTTCTTAATTTACTTTATCATGATG 226
 |||||
 Db 21 ArgProGlnSerTyrPheGlnProCysValGlu---ValProAsnIleHtstYrGlnCysMet 39
 |||||
 QY 227 GAGCTGAATTTTCAGAAATCCCGCAACCTCCCTTCAGACCAAGAACTGAGCCTG 286
 |||||
 Db 40 GlnIleuAsnPheHtstYrIlePheProAsnIleuPhePheSerHtstYrAsnIleuAsn 59
 |||||
 QY 287 AGCTTAAATCCCTGAGGCAATTAGCAGATATAGCTTCTTCAAGTTCCAGAACTGAG 346
 |||||
 Db 60 SerPheAsnProIleuArgHtstIleuGlySerTyrSerPhePheSerPheProGlnIleuGln 79
 |||||
 QY 347 GTGCTGATTTATCCAGGTGTGAATCCAGCAATTTGAAGATGGGCAATTCAGAGCTTA 406
 |||||
 Db 80 ValIleuAspIleuSerArgCysGlnIleGlnHtstIleGlnAspIleValIleArgIleuSerIleu 99
 |||||
 QY 407 AGCCACCTCTCTACCTTAATTTATGACAGAAACCCATCCAGAGTTTAAAGCCCTGGAGGCC 466
 |||||
 Db 100 SerHtstIleuSerHtstIleuIleuHtstIleuArgAsnProIleGlnSerIleuAlaIleuGlyAla 119
 |||||
 QY 467 TTTTCTGACTATCAAGTTTACAGAGCTGTGGCTGTGGAGCAAAATCTAGCATCTCTA 526
 |||||
 Db 120 PheSerGlyIleuSerIleuGlnIleuValAlaValGlnHtstIleuAlaSerIleu 139
 |||||
 QY 527 GAGAACTTCCCACTTGAGCACTCAAACTTTGAAGAACTTATATGTGCTCACAATCTT 586
 |||||
 Db 140 GlnAsnPheProIleGlyHtstIleuYrHtstIleuGlnIleuAsnValAlaHtstIleu 159
 |||||
 QY 587 ATCCAACTTTTCAATTTTCTGAGTATTTTCTCAATCTGACCAATCTAGGCACTTGAGC 646
 |||||
 Db 160 IleGlnSerPheHtstIleuProGlnIleuYrPheSerAsnIleuHtstIleuGlnIleuAsp 179
 |||||
 QY 647 CTTTCAGAACCAAGATTAAGTATTTATGACAGACTTGCGGGTTCTACATCAATG 706
 |||||
 Db 180 IeuserSerAsnHtstIleGlnSerIleYrCysHtstAspIleuArgValIleuHtstIleuGlnMet 199
 |||||
 QY 707 CCCCTACTCAATCTCTCTTTTACAGCTGTGCCGTAATCTTATGAACTTTATCCAAAGGT 766
 |||||
 Db 200 ProIleuAsnIleuSerIleuAspIleuSerIleuAsnProMetAsnHtstIleGlnProGly 219
 |||||

QY 767 GCATTAAAGAAATAGGCTTCAATAGCTGACTTAAAGAAATATTGATGATTTAAAT 826
 |||||
 Db 220 AlaPheLysGluLeuLeuLeuHISlybLeuThrLeuArgbAsnHbheAspSerLeuAsn 239
 |||||
 QY 827 GTAATGAAAATTGATTCAGAGGCTGGCTGTTTGAAGCTCCATCGTTGGTTGGGA 886
 |||||
 Db 240 ValMetLysThrCysIleGlnGlnLysLeuAlaGlyLeuGluValHISArgLeuValLeuGly 259
 |||||
 QY 887 GAATTTAGAAATGAGGAAATCTGGAAAGTTGACAAATCGCTCTGAGGGCCGTGC 946
 |||||
 Db 260 GluPheArgAsnGlnGlnLysLeuGluLysPheAspLysSerAlaLeuGlnGlnLysCys 279
 |||||
 QY 947 AATTGACCATTAAGAAATCCGATTAGCATTAAGTACTACTACTGATCTGATTAATAT 1006
 |||||
 Db 280 AsnLeuThrIleGlnGlnPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAlaIleIle 299
 |||||
 QY 1007 GACTTATTATATTGTTGACAAATGTTTCTTCAATTTCCCTGGTGAAGTGTGACTATTGAA 1066
 |||||
 Db 300 AspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGlu 319
 |||||
 QY 1067 AGGGTAAAGACTTTTCTTATATTCCGATGGCAACTTAAAGTAACTGTA 1126
 |||||
 Db 320 ArgValLysAspPheSerTyrAsnPheGlyTyrGlnHISLeuGlnLeuValAsnCysLys 339
 |||||
 QY 1127 TTGGAAGTTTCCCATTAAGAACTCAATCTCTCAAAAGGCTTACTTCACTTCCAA 1186
 |||||
 Db 340 PheGlnGlnPheProThrLeuLysbLeuLysSerLeuLysArgLeuThrPheThrSerAsn 359
 |||||
 QY 1187 AAAGTGGGAATGCTTTTCAAGAAATTGATCTACAAAGCTTGAATTTGAGTCTCAGT 1246
 |||||
 Db 360 LysGlnGlnLysbLysAsnLysPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeuSer 379
 |||||
 QY 1247 AGAAATGGCTGATTTCAAGAGTGGCTTCTCAAGTAAATTTGGGCAACAGGCTTA 1306
 |||||
 Db 380 ArgAsnGlnLeuSerPheLysGlyCysCysSerGlnSerAspPheGlnTyrHISerLeu 399
 |||||
 QY 1307 AAGTATTAGATCTGAGCTTCAATGATGTTATTAACATGAGTTCAACTTGGGCTTA 1366
 |||||
 Db 400 LysTyrLeuAspLeuSerPheAsnGlnValIleThrThrSerSerAsnPheLeuGlnLys 419
 |||||
 QY 1367 GAAACAATAGAACATCTGATTTCCAGATTTCCAGATTTGAAACAATGAGTGAAGTTTCA 1426
 |||||
 Db 420 GlnGlnLeuGlnHISLeuAspPheGlnHISerAsnLeuLysGlnMetSerGlnPheSer 439
 |||||
 QY 1427 GTATTCCTATCACTCGAAGAACTCATTAATCTGAGATTTCTCATTACTCAACAGAGT 1486
 |||||
 Db 440 ValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHISThrHISThrArgVal 459
 |||||
 QY 1487 GCTTTCATGAGCATCTTCAATGAGCTTGCAGATCTCGAAATCTTGAATAATGAGTGCAT 1546
 |||||
 Db 460 AlaPheAsnGlnIlePheAsnGlnLysSerSerLeuGlnValLeuLysMetAlaGlyAsn 479
 |||||
 QY 1547 TCTTTCAGAGAAATCTTCTTCCAGATATCTTCAAGAGCTGAGAAATCTGACCTTCTG 1606
 |||||
 Db 480 SerPheGlnGlnLysbPheLeuProAspIlePheThrIleLeuArgAsnLeuThrPheLeu 499
 |||||
 QY 1607 GACCTCTCAGAGTCACTGAGCACTGAGTCTTCCACACATTAATCTCACTCTCAGT 1666
 |||||
 Db 500 AspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSerSer 519
 |||||
 QY 1667 CTTCAGGTAATTAATAGCAACAACAATCTTCTTCAATGATGATGTTTCTTATAG 1726
 |||||
 Db 520 LeuGlnValLeuAsnMetSerHISAsnAsnPhePheSerLeuAspThrPheProTyrLys 539
 |||||
 QY 1727 TGTCTGAAGTCCCTCCAGGTTCTTGATTAAGTCAATCAATCAATATGACTTCAAAAA 1786
 |||||
 Db 540 CysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHISIleMetThrSerLysLys 559
 |||||
 QY 1787 CAGGAATAGACATTTTCCAGAGTCTGATTTCTTAAATCTTAACTCAAGAAATGAGTCTT 1846
 |||||
 Db 560 GlnGlnLeuGlnHISpheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
 |||||
 QY 1847 GCTTGACTTGTAACACAGAGTTTCTGCAATGATCAAGACAGAGGAGCTCTTG 1906
 |||||

Db 580 AlaCysThrCysGlnHISGlnSerPheLeuGlnTyrIleLysAspGlnArgGlnLeuLeu 599
 |||||
 QY 1907 GTGGAAGTTGAAAGCAATGGAATGTGCAACACTTCAAGAAACAGGAGGCTGCTGCG 1966
 |||||
 Db 600 ValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlnMetProValLeu 619
 |||||
 QY 1967 AGTTGAATATCACTCGTGCAGATGAATAGAACCATCATCATGATGGTGGCTCTCAGTGTG 2026
 |||||
 Db 620 SerLeuAsnHISLeuThrCysGlnMetCysLeuLysThrIleIleGlnValSerValLeuSerVal 639
 |||||
 QY 2027 CTGTGATCTGTGTGTAGCACTTGTGCTGATTAAGTCTTATTTCACTGATCTTCTT 2086
 |||||
 Db 640 LeuValAlaSerValValAlaValLeuValTyrLysPheTyrPheHISLeuMetLeuLeu 659
 |||||
 QY 2087 GCTGGCTGATTAAGTAAGTGTAGAGTGAACCACTATAGAGCCCTTGTATCTATCTCA 2146
 |||||
 Db 660 AlaGlyCysAlaLeuLysTyrGlnArgGlnLysbLeuIleTyrAspAlaPheValIleTyrSer 679
 |||||
 QY 2147 AGCCAGATGAGGACTGGGTTAAGAAATGAGCTAGTAAAGAAATTTAGAAAGAGGCTGCT 2206
 |||||
 Db 680 SerGlnAspGlnAspTyrValArgAsnGlnLeuValLysbAsnLeuGlnGlnValPro 699
 |||||
 QY 2207 CCATTTCACTCTGCTTCACTACAGAGACTTTATCCCGTGTGGCAATTGCTGCCAAC 2266
 |||||
 Db 700 ProPheGlnLeuCysLeuHISLysTyrArgAspPheIleProGlnValAlaIleAlaAlaAsn 719
 |||||
 QY 2267 ATCATCCAGAAAGGTTTCCATTAAGAAAGCGAAAGGATGTTGGTGGTCCAGCACTTC 2326
 |||||
 Db 720 IleIleHISGlnGlnLysbHISLysSerArgLysValIleValValValSerGlnHISpHe 739
 |||||
 QY 2327 ATCCAGAGCCGCTGCTGTATCTTTGAATAGAGATTTCTCAGACCTGAGGAGTTTCTGAG 2386
 |||||
 Db 740 IleGlnSerArgTyrCysIlePheGlnLysGlnIleAlaGlnThrIlePheLeuSer 759
 |||||
 QY 2387 AGTGTGCTGTATCATCTTCAATGCTTCTGCAAGAGTGTGAGAAAGCTGCTCAGGCG 2446
 |||||
 Db 760 SerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLysArgGln 779
 |||||
 QY 2447 CAGGTGAGCTGTACCGGCTTCTCAGAGAAACACTTACCTGAGTGGAGGAGCACTGTG 2506
 |||||
 Db 780 GlnValGlnLeuLysArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnLysSerVal 799
 |||||
 QY 2507 CTGGGCGGCACTCTTCTGAGAGCACTCAGAAAGCCCTGCTGATGGTAAATCATG 2566
 |||||
 Db 800 LeuGlnArgHISLeuPheThrArgArgLeuArgLysAlaLeuLeuAspGlnLysSerTyr 819
 |||||
 QY 2567 AATCAGAAAGAACAGTGGGTACAGGATGCAATTTGSCAGAGCAACATCTATC 2620
 |||||
 Db 820 AsnProGlnGlnTyrValGlnTyrGlnCysAsnTyrGlnGlnAlaThrSerIle 837
 |||||

RESULT 9

AAE16116 standard; protein; 837 AA.

ID AAE16116;

AC AAE16116;

DT 26-MAR-2002 (first entry)

DE Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.

XX Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;

KM Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

XX key difference 211

XX FT misc-difference 211 /label= Unknown

XX FT /note= "Encoded by AAY"

XX PN

XX MO200190151-A2.

PD 29-NOV-2001.
 XX 23-MAY-2001; 2001WO-US016766.
 PF 25-MAY-2000; 2000US-0207558P.
 XX (SCHE) SCHERING CORP.
 PA Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
 PI WPI; 2002-083085/11.
 DR N-PSDB; AAD26306.
 XX New DMAX Toll like receptor (DTRL) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 PS Claim 3; Page 240-243; 297pp; English.
 XX The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DMAX Toll like receptor (DTRL) protein and their corresponding
 CC nucleic acids. The DTRL is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTRL is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTRL is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTRL or its various fragments. The
 CC purified DTRL can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression
 CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTRL or cells that express it. The present sequence is
 CC human DTRL4 protein, alternative version. The DTRL4 gene is located on
 CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
 CC be similar to the sequence shown in page 41 (AAE16102). However these
 CC sequences differ at several locations
 XX
 XX Sequence 837 AA:
 Alignment Scores:
 Pred. No.: 0 Length: 837
 Score: 4328.50 Matches: 836
 Percent Similarity: 99.76% Conservative: 0
 Best Local Similarity: 99.76% Mismatches: 1
 Query Match: 50.45% Indels: 1
 Gaps: 1
 DB: 5
 US-09-396-985b-1 (1-4868) x AAE16116 (1-837)
 QY 107 ATGTCTGCTCGGCGCTGGAGACTGTATCCAGCCATGCGCTCTCTCGGCG 166
 DB 1 MetSerAlaSerArgLeuAlaGlyThrLeuIleProIaMetAlaPheLeuSerCysVal 20
 QY 167 AGACGAGAAGCGGGAGCCCTCGTGGAGGTGCTTCTATATCTTATCAATGANG 226
 DB 21 ArgProGlnSerIleProCysValGln--ValProAsnIleThrTyrglnCysMet 39
 QY 227 GAGCTGAATTTCTCAAAATCCCGACAACTCCCTTCTCAACAAGAGCTGACCTG 286
 DB 40 GluLeuAsnPheTyrlsIleProAspAsnLeuProPheSerThrIryAsnLeuAspLeu 59
 QY 287 AGCTTTAATCCCTGAGGCACTTTAGGAGCTATAGCTTCTTCAGTTTCCAGAACTGACG 346
 DB 60 SerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeuGln 79
 QY 347 GTCTGGAATTTATCCAGGTGTAATCCAGCAATGAATGAAGGGGATATCAGAGCTTA 406
 DB 80 ValLeuAspLeuSerIleGlyGlnIleGlnThrIleGlnAspGlyAlaTyrglnSerLeu 99
 QY 407 AGCACCTCTCTAATTAATATGACAGAAACCCATCCAGATTTAGCCCTGGAGGCC 466

DB 100 SerHisLeuSerThrLeuIleuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
 QY 467 TTTTGGAGCTATCAAGTTTACAGAGCTGGTGGCTGGAGCAATCTAGATCTCTA 526
 DB 120 PheSerGlyLeuSerSerLeuGlnLeuValAlaValGlnThrAsnLeuAlaSerLeu 139
 QY 527 GAGAACTTCCCACTTGACATCTCAAAACTTTGAAAGAACTTATGAGTGCACAACTT 586
 DB 140 GluAsnPheProIleGlyHisLeuTyrlleuLeuGluLeuAsnValAlaHisAsnLeu 159
 QY 587 ATCCAAATCTTTCAATTAATTAACCTGAGATTTTCTAATCTGACCAATCTAGACCTTGAC 646
 DB 160 IleGlnSerPheLeuSerProGluTyrlPheSerAsnLeuThrAsnLeuGlnHisLeuAsp 179
 QY 647 CTTTCAGACAAACAAGTATTAATTTATTTATGACAGACTGGGGGTTCTACATCAATG 706
 DB 180 LeuSerSerAsnHisLeuGlnSerIleTyrglyThrAspLeuArgValLeuHisGlnMet 199
 QY 707 CCCCTACTCAATCTCTCTTGTAGACTGTCCCTGAATCTTGAACCTTTATCCAGCAGGT 766
 DB 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeu***PrometAsnPheIleGlnProGly 219
 QY 767 GCATTTAAAGAAATTAAGCTTCTAATAGCTGACTTTAAGAATAATTTGATTAAT 826
 DB 220 AlaPheTyrglnIleArgLeuHisIlyLeuThrLeuArgAsnAsnPheAspSerLeuAsn 239
 QY 827 GTAAATGAATCTGTATTTCAAGGTCTGGCTGTTTGAAGTCCATGCTTGTCTTGGGA 886
 DB 240 ValMetLeuThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeuGly 259
 QY 887 GAATTTAGAAATGAAGAAACTTGAAGAAATTTGAACAAATCTGCTAGAGGCGCTGTGC 946
 DB 260 GluPheArgAsnGlnIleAsnLeuGlnIlysrPheAspIlySerHisAlaLeuGlnGlyCys 279
 QY 947 AATTGACCAATGAGAATTCGATTTAGCAATTAAGTACTTACCTGATGATTAATTT 1006
 DB 280 AsnLeuThrIleGlnGlnIlePheArgLeuAlaTyrlLeuAspTyrlTyrlLeuAspIleIle 299
 QY 1007 GACTTATTAATTTGTTGACAAATGTTTCTCAATTTCCCTGGTGGAGTGCATATTGAA 1066
 DB 300 AspLeuPheAsnIlyLeuThrAsnValSerSerPheSerLeuValSerValThrIleGln 319
 QY 1067 AGGGTAAAGACTTTCTTATATATTCGAGTGGACCAATTTAGTAATTAATCTGA 1126
 DB 320 ArgValIlyAspPheSerTyrlAsnPheGlyTyrlGlnHisLeuGlnLeuValIlyAsp 339
 QY 1127 TTGGACAGTTTCCCACTTGAATCAATCTCTCAAAAGGCTTACTTCACTTCCAAC 1186
 DB 340 PheGlyGlnPheProThrIleuTyrlleuTyrlSerLeuIlyAspGlnPheThrSerAsn 359
 QY 1187 AAGGTGGGAATGCTTTTTCAGAGTTGATCTACAGAGCTTGAGTTTCTAGATCTCAGT 1246
 DB 360 IlyGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnIleuAspLeuSer 379
 QY 1247 AGAAATGGCTGAGTTTCAAGGTGCTGTTTCAAGGATTTTGGGCAACACAGCTTA 1306
 DB 380 ArgAsnGlyLeuSerPheLeuGlyCysGlySerGlnSerAspPheGlyThrThrSerLeu 399
 QY 1307 AAGTATTTAGATCTGAGCTTCAATGAGTGTATTAATCCATGATGATCAATCTTGGGCTTA 1366
 DB 400 IlyTyrlLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419
 QY 1367 GAACAATGGAACATTTGATTTCCAGCATTTCCAAATTTGAAACAAATGAGTGAATTTCA 1426
 DB 420 GluGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuIlyGlnMetSerGlnPheSer 439
 QY 1427 GTATTCCTTCACTGAGAAACCTCAATTTACTTGAATTTCTCATCTGACACCAAGAT 1486
 DB 440 ValPheLeuSerLeuAsnIlyTyrlLeuAspIleSerHisThrHisThrArgVal 459
 QY 1487 GCTTTCAATGAGATCTTCAATGAGCTTGTGCACTTCAAGTCTTGAATAATGCTGGCAAT 1546

```

Db      460 AlaPheAsnGlyllePheAsnGlyLeuSerSerLeuGluValleuIysMeAlaGlyAsn 479
QY      1547 TCCTTCCAGGAAAACCTTCCAGATATCTTCCAGAGAGTTGAGAACTTGACCTTCG 1606
Db      480 SerPheGlnIleuAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPheLeu 499
QY      1607 GACCTCTCTCAGTGCACACTGAGAGAGTTGTCTCAACAGACATTTAACTCACTCTCCAGT 1666
Db      500 AspLeuSerGlnCysGlnLeuGlnLeuSerProThrIlePheAsnSerLeuSerSer 519
QY      1667 CTTCAAGTACTAAATATGAGCCACACAACTTCTTTCAATGATACGTTTCTTATAG 1726
Db      520 LeuGlnValleuAsnMetSerIleAsnAsnPhePheSerLeuAspThrPheProTyrLys 539
QY      1727 TGTGTGAACCTCCCTCCAGGTTCTTGAATACAGTCTCAATCACTCAATATGACTTCCAAA 1786
Db      540 CysLeuAsnSerLeuGlnValleuAspTyrSerLeuAsnIleIleCtnrSerLysLys 559
QY      1787 CAGAACTACAGCATTTTCCAGATAGTCTAGCTTTCTTAATCTTACTCAGAAATGACTTT 1846
Db      560 GlnGluLeuGlnIlePheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
QY      1847 GCTTTGATCTTTGAAACACAGAGTTCTCTCAATGATGATCAAGACAGGAGCTCTTG 1906
Db      580 AlaCysThrCysGlnIleAsnSerPheLeuGlnIleThrIleLysAspGlnArgGlnLeu 599
QY      1907 GTGGAAGTTGAAGAAATGGAATGGAACCTTCAATATGAGAGGAGGAGGAGCTGTGCTG 1966
Db      600 ValGluValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProValLeu 619
QY      1967 AGTTGAAATATCACTGTCAAGATGAATAGACATCATGAGTGTGTGCTCAGATGTG 2026
Db      620 SerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValleuSerVal 639
QY      2027 CTTGTAGTATCTGTGTGAGAGATTCTGTCTATATGATTCTATTTTCACTGATGCTTCT 2086
Db      640 LeuValValSerValValAlaValleuValTyrLysPheThrPheIleAsnLeuLeu 659
QY      2087 GCTGGCGTCATTAAGTATGTAAGTGAAGGAAACCTATATGATGCTTGTATCTATCTCA 2146
Db      660 AlaGlyValIleLysTyrGlnArgGlyGlnAsnIleTyrAspAlaPheValIleTyrSer 679
QY      2147 AGCCAGAGATGAGAGCTGGTAAAGGAATGAGCTAGTAAGAATTTGAAGAAGAGGGGTCT 2206
Db      680 SerGlnAspGlnAspTyrValArgAsnGlnLeuValLysAsnLeuGlnGlyValPro 699
QY      2207 CCATTTCAGCTCTGCTTCACTACAGAACTTATTTCCCGGTGTGGCCATTGTCTGCCAAC 2266
Db      700 ProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaIleAsn 719
QY      2267 ATCATTCATGAAGGTTCCATTAAGCGCAAGGTAATGTTGTGTGTCCTCCAGCACTTC 2326
Db      720 IleIleHisGlnGlyPheHisLysSerArgLysValIleValValSerGlnHisPhe 739
QY      2327 ATCCAGAGCCGCTGTGTATCTTGAATATGAGATTGCTCAGACTGCGCAATTTCTGAGC 2386
Db      740 IleGlnSerArgTyrCysIlePheGlnTyrGluIleAlaGlnIleThrPheGlnPheLeuSer 759
QY      2387 AGTCGTGCTGTATCATTTCTTCAATTTGCTCTGAGAAAGTGAAGAAAGCTTGTCTCAG 2446
Db      760 SerArgLysGlyIleIlePheIleValleuGlnIleValGlnLysThrLeuLeuArgGln 779
QY      2447 CAGGTGAGGCTGTACCGGCTTTCAGAGAGAAACCTTACCTGAGTGGAGAGACAGTCTC 2506
Db      780 GlnAlaGlnLeuValArgLeuLeuSerArgAsnThrTyrLeuGlnIleThrPheGlnAspSerVal 799
QY      2507 CTGGGGGGGACATCTTCTGAGAGAGACTCAGAAAAGCCCTGCTGAGTGGTAATCAATG 2566
Db      800 LeuGlnIleArgHisIlePheThrPheArgLeuArgLysAlaLeuLeuAspGlyLysSerThr 819
QY      2567 AATCCAGAGAAACAGTGGGTACAGATGCATTTGGCAGAGAAAGCAACATCATTC 2620
Db      820 AsnProGlnGlyThrValGlyThrGlyCysAsnThrPheGlnIleAlaThrSerIle 837

```

```

RESULT 10
AD057782
ID AD057782 standard; protein; 808 AA.
XX
AC AD057782;
XX
DT 12-AUG-2004 (first entry)
XX
DE Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KM sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX
OS Pan troglodytes.
XX
PN W02004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003MO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
DR WPI; 2004-400726/37.
DR N-PSDB; AD057780, AD057781.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
PS Example 1; SEQ ID NO 3; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents chimpanzee TLR4.
XX
SQ Sequence 808 AA;
XX
Alignment Scores:
Pred. No.: 0 Length: 808
Score: 4178.00 Matches: 805
Percent Similarity: 99.88% Conservative: 2
Best Local Similarity: 99.63% Mismatches: 1
Query Match: 48.70% Indels: 0
DB: 8 Gaps: 0
US-09-396-985b-1 (1-4868) x AD057782 (1-808)
QY      197 GTGGTTCCTTAATTTTCTTATCATGAGAGCTGAATTTTCAAAAATCCCGACAAC 256
Db      1 ValValProAsnIleThrTyrGlnCysMetGlnLeuAsnIleThrLysIleProAsn 20
QY      257 CTCCTCTTCAACCAAGAACTGAGCTTGAATTCCTGAGGCAATTTAGGAGC 316
Db      21 LeuProPheSerThrTyrAsnLeuAspLeuSerPheAsnProLeuArgHisLeuGlySer 40
QY      317 TATAGCTTCTTCAATTTCCAGAACTGACAGTGTGATTTATCCAGTGTGAATTCAG 376
Db      41 TyrSerPhePheSerPheProGlnLeuGlnValleuAspLeuSerArgCysGlnIleGln 60

```

QY 377 ACAATTGAAGTGGGCGATATCAGAGCCTAAGCCACTCTCTACCTTAATATTGACAGGA 436
Db 61 ThrileulaspjylalatyrglnserleuserhstleuserthrleullelethrGly 80
QY 437 AACCCCATCCAGAGTTTAAAGCCCTGGAGACCTTTTCTGAGATATCAAGTTTACAGAGCTG 496
Db 81 AsnProileglnserleuallaleuglYAlapheserGlyleuserSerleuglnlyleu 100
QY 497 GTGGCTGTGGAGCAAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAACT 556
Db 101 ValAlavalglutrranleuAlasrleuileglnserPheylsleuProglutryPhe 120
QY 557 TTGAAAGACTTAATGTGGCTCACAACTTATCCAACTTTCAAAATTAAGTATATTTT 616
Db 121 LeuylsleuleuamvalAlahlsanleuileglnserPheylsleuProglutryPhe 140
QY 617 TCTAATCTGACCAATCTTAGAGCACTTGACCTTTCCAGCAACAAGATTCAAAATTTAT 676
Db 141 SerAsnleuthrAsnleuGlunhlsleuAspleuserSerAsnlyslleGlnserliletyr 160
QY 677 TGGACAGACTTGGGGGTTCTTACATCAAAATGCCCTACTCAATCTCTCTTAGAGCTTCC 736
Db 161 CysThrAspleuArGValleuHlsGlnmecProleuAsnleuSerleuAspleuser 180
QY 737 CTGAATCCTATGAACCTTTATCCAAACAGTGACATTTAAAGAAATTTAGAGCTTCAATAGCTG 796
Db 181 LeuAsnProleuAsnleuPheileglnProglYAlapheylsleuileahgluehNlslyleu 200
QY 797 ACTTAAAGAAATATTTGATAGTTTAAATGTATGAAACTTGTATTTCAAGCTCTGGCT 856
Db 201 ThrleuArGAsnAsnPheserleuAsnValhmeltyrthrCyslileGlnlyleuAla 220
QY 857 GGTTTAGAATCCATCTTTGGTTCTGGAGAAATTTGAAATGAGAAACTTGGAAAG 916
Db 221 GlyleuGlunValhsarGleuValleuGlunPheArGAsnGlnlyAsnleuGlnlys 240
QY 917 TTGACAAATCTGCTCTAGAGGGGCTGTGCAATTTGACCATTTGAGAAATCCGATTGCA 976
Db 241 PheAspleyserralaleuGlnlyleuCyAsnleuThrilleGlnlyleuPheArGleuAla 260
QY 977 TACTTAGACTACTCTCGATGATATTTAGCTTATTTATTTGACAAATGTTTCT 1036
Db 261 TytleuAspleyrrlyrleuAspAsplelleleAspleuPheAsnCyseuThrAsnValSer 280
QY 1037 TCAATTTCCCTGGTGTGAGTGTGACTATTTGAAAGGTTAAAGACTTTTCTTAATTTGGG 1096
Db 281 SerPheSerleuValSerValThrilleyservalylsAspPheSerTyAsnPheGly 300
QY 1097 TGGCAACATTTAGATAGTTAACTGTAAATTTGGAAGTTTCCCACTTGAAGAACTCAA 1156
Db 301 TrpGlnhlsleuGlunleuValAsnCylyPheGlyGlnPheProthrleuLysleuLys 320
QY 1157 TCTCTCAAAAAGGCTTACTTCACTTCCAAAGAGTGGAATGCTTTTTCAGAAATGAT 1216
Db 321 SerleuLysArGleuThrPheThrSerAsnlyleGlyGlyAsnAlapheSerGlyValAsp 340
QY 1217 CTACCAAGCTTTAGATTCTAGATCTCAGTAAAGATGCTTGAAGTTCAAGTTGCTGT 1276
Db 341 LeuProSerleuGlunPheleuAspLeuSerArGAsnGlyleuSerPheylsGlyCyCs 360
QY 1277 TCTCAAGGTAGTTTGGGACCAACAGCTTAAAGATTAGATTGAGCTTCAATGGGTT 1336
Db 361 SerGlnSerAspPheGlyThrlnrSerleuLysTyrrleuAspleuserPheAsnGlyVal 380
QY 1337 ATTACATGAGTTCAAACTTCTGGGCTTAGAAACAATAGACATCTGATTTCCAGAT 1396
Db 381 lilethrleuserSerAsnPheleuGlyleuGlnGlnleuGlunhlsleuAspPheGlnhls 400
QY 1397 TCCAAATTTGAAACAATGAGTGAATTTCAATTTCTATCACTCAGAAACTCTGATTTAC 1456
Db 401 SerAsnleuLysGlnmetSerGlnPheSerValPheleuSerleuArGAsnleuLiletyr 420

QY 1457 CTGACATTTCTCATACTCACACAGAGTTGCTTTCAATGAGCATTTCAATGGCTTGCC 1516
Db 421 LeuAsplelserhsthrhsthrArgValAlaPheAsnlylilePheAsnGlyleuSer 440
QY 1517 AGTCTGAGAGTCTTGAATAATGGCTGGCAATTTCTTTCCAGAAAACTTCTTCCAGATATC 1576
Db 441 SerleuGlunValleuLysmetAlaGlyAsnSerPheGlnlyleuAsnPheleuProAspIle 460
QY 1577 TTCAAGAGCTGGAAGAACTTGACCTTCCAGAGCTCTCTCAGGTGCAACTGGAGCACTTG 1636
Db 461 PheThrGlunleuArGAsnleuThrPheleuAspleuserGlnCyGlnleuGlnleu 480
QY 1637 TCTCAACAGCACTTAACTCACTCTCCAGTCTTCCAGTACTTAATATAGACCACAAC 1696
Db 481 SerProthrAlapheAsnserleuserSerleuGlnValleuAsnmetSerhlsAsn 500
QY 1697 TTTCTTTCAATGATACGTTTCTTATTAAGTGTGAACTCCCTCCAGGTTCTTGATAC 1756
Db 501 PhePheSerleuAspThrPheProtyrlyrCyseleuAsnserleuGlnValleuAspTy 520
QY 1757 AGTCTCAATCAATATGACTTCCAAAACAGAACTAAGACATTTCCAAAGTCTTA 1816
Db 521 SerleuAsnhsstleuethrSerlyleGlnGlnleuGlnhlsPheProSerSerleu 540
QY 1817 GCTTCTTAAATCTTACTCAGATGACTTGTGTTGATCTTGTGAACACAGAGTTTCTG 1876
Db 541 AlapheleuAsnleuThrGlnAsnAspPheAlaCyethrCyseGlnhlsGlnserPheleu 560
QY 1877 CAATGATCAAGACCAAGAGGAGCTTTGGTGGAAATTTGAACGAATGAATGTGACAA 1936
Db 561 GlnThrPilleysarGlnArGlnleuLeuValGlnValGlnArGmetGlnCyAlaThr 580
QY 1937 CTTTCAGATPACAGAGGCGATGCTGTGCTGATGATTAATACCTCTCAGATGAATAG 1996
Db 581 ProSerAspLysGlnGlymetProValleuSerleuAsnillethrCysGlnmetAsnLys 600
QY 1997 ACCATCAATGGTGTGTGCTGCTCAGTGTGCTTGTATCTGTGTAGAGAGTTCTGCT 2056
Db 601 ThrilleleGlyAlaSerValleuserValleuValAlaSerValAlaAlaValleuVal 620
QY 2057 TATAGTTCTATTTTCACTGATGCTTCTTGTGCTGCTGCTCAATAAGATGAGTGA 2116
Db 621 TyrlyPheTyrrPhehlsleuMetleuLeuAlaGlyCysliletyrtyrGlyGlyGln 640
QY 2117 AACATCTAGATGCTCTTGTATCTACTCAAGCAGATGAGACATCGGTAAGAAATGAG 2176
Db 641 AsnilletyrAspAlaPheValilletyrSerSerGlnAspIlyAspIlyrValArGAsnGln 660
QY 2177 CTAGTAAAGAAATTTAGAAAGAGGGGCTCCATTTCAAGCTTGCTTCACTCAGAGAC 2236
Db 661 LeuValLysAsnleuGlnGlnlyValProProPheGlnleuCyseuHlsTyrrArGAsp 680
QY 2237 TTTATTCGCGTGTGCACTTGCTGCAACATCATCATCAAGATTTCCATAAAGCCGA 2296
Db 681 PheileProglYAlaAlaileAlaAlaAsnillehlsGlnlyPhehlslySerArG 700
QY 2297 AAGGATATTGTTGGTGTGCCAGCACTTCATCAAGGCCGCTGGTGTATCTTGAATAT 2356
Db 701 LysValilleValAlaValaSerGlnhlsPheilleGlnserArGtyrCysllePheGlytyr 720
QY 2357 GAGATTTGCTCAGACCTGGGAGTTTCTGAGAGCGAGTGGATCAATCTTCAATGTCCTG 2416
Db 721 GlnilleAlaGlnhthrtrPglnPheleuserSerArGAlaGlylilePheilleValleu 740
QY 2417 CAGAAAGTGAAGAAAGCCTGTCTCAGCAGCAGTGAAGCTGTACCGCTTCCACAGAG 2476
Db 741 GlnlyValGlnlyserThrleuArGArGlnValGlnleuLyrrArGleuLysArG 760
QY 2477 AACACTTACTGAGAGTGGAGAGCAAGTGTCTGGGGCGGCAACTTCTTGAGAGCACTC 2536
Db 761 AsnThrTyrrleuGlnlytrPglunspSerValleuGlyArGhlsillePheThrPArGAspleu 780
QY 2537 AGAAAAGCCCTGTGATGATGATAATCATGGAATCCAGAAAGAAACATGGGTTACAGATG 2596

|||||
DB 781 ArglyAlaIeuLeuaspGlysserTPasPProGluGlyThrValGlyThrGlyCys 800
QY 2597 AATTGGCAGAGCAACATCTATC 2620
DB 801 AsnTrpGlnGluAlaThrSerIle 808
RESULT 11
AD057785
ID AD057785 standard; protein; 808 AA.
XX
AC AD057785;
XX
DT 12-AUG-2004 (first entry)
XX
DE Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS Gorilla gorilla.
XX
PN WO2004042365-A2.
XX
PD 21-MAY-2004.
XX
PF 03-NOV-2003; 2003WO-US036247.
XX
PR 01-NOV-2002; 2002US-0423113P.
XX
PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI Messier W;
XX
XX WPI; 2004-400726/37.
DR N-PSDB; AD057783, AD057784.
XX
PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
in treating sepsis and asthma, by comparing the TLR4 polynucleotide
sequence of the Old World monkey with that of a human.
XX
PS Example 1; SEQ ID NO 6; 111pp; English.
XX
CC The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents gorilla TLR4.
XX
SQ Sequence 808 AA.
Alignment Scores:
Pred. No.: 0 Length: 808
Score: 4167.00 Matches: 803
Percent Similarity: 99.75% Conservative: 3
Best Local Similarity: 99.38% Mismatches: 2
Query Match: 48.57% Indels: 0
DB: 8 Gaps: 0
US-09-396-985b-1 (1-4868) x AD057785 (1-808)
QY 197 GTGGTCTCAATATTAATCAATGATGAGTGAATTTTCACAAAATCCCGAGAAC 256
DB 1 ValValProAsnIleTrpGlnCysMetGluLeuAsnPheTrpIleProAspAsn 20
QY 257 CTCCTTCTCAACCAAGAACCTGACCTGAGCTTTATCCCTGAGGCAATTAGGAGC 316

|||||
DB 21 LeuProPheSerThrIlyAsnIleuAspLeuSerPheAsnProLeuArgIleuGlySer 40
QY 317 TATAGCTTTTCAAGTTTCCCAAGACTGCAGGCTGTGATTTTCCAGGCTGTAATCCAG 376
DB 41 TyrSerPhePheSerPheProGluLeuGlnValIleuAspLeuSerArgCysGluIleGln 60
QY 377 ACAATGAAGATGGGCAATATCAGAGCCCTAACCCACTCTCTCACTTAATATTGACAGA 436
DB 61 ThrIleGluAspGlyAlaIleTyrGlnSerLeuSerHisLeuSerThrIleuIleuThrGly 80
QY 437 AACCCATCAGAGTTTACCCCTGGAGCCCTTTTCTGACATACAGTTTACAGAACTG 496
DB 81 AsnProIleGlnSerIleuAlaIleuGlyAlaPheSerGlyLeuSerSerIleuGlnIlySer 100
QY 497 GTGGCTGTGAGACCAATCTAGCATCTCTAGAGAACTTCCCATTTGGAATCTCAAAACT 556
DB 101 ValAlaValAlaGluThrAsnLeuAlaSerLeuGluAsnPheProIleGlyHisLeuIlyTrp 120
QY 557 TGAAGAAGACTTAATGTGGCTCACAATCTTATCCAACTTTTCAAAATTACCTGAGTATTT 616
DB 121 LeuIlySGluLeuAsnValAlaHisAsnLeuIleGlnSerPheIlySerProGluIlyTrp 140
QY 617 TCTAATCTGACCAATCTAGAGCACTTGAACCTTTCAGGACAGAACTTCAAGTATTTAT 676
DB 141 SerAsnLeuThrAsnLeuGluIlyTrpLeuAspLeuSerSerAsnIlyIleGlnSerIleTrp 160
QY 677 TGCACAGACTTGGGGTTTACATCAAAATGCCCTACTCAATCTCTTACCACTGCTGC 736
DB 161 CysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
QY 737 CTGAATCTATGAACTTTATCCAAACAGAGTGCACTTTAAAGAAATTAGGCTTCAAGCTG 796
DB 181 LeuAsnProMetThrPheIleGlnProGlyAlaPheIlyGluIleArgLeuHisIlySer 200
QY 797 ACTTTAAGAAATTAATTTTGAATAGTTTAAATGTATGAAGAACTTGTATCAAGCTGTGCT 856
DB 201 ThrLeuArgAsnAsnPheAspSerLeuAsnValIleIlyThrCysIleGlnIlyLeuAla 220
QY 857 GGTTTGAGAGTCCATGTTGGTTCTGGGAGAAATTTAGAAAGAACTTGGAAGAAG 916
DB 221 GlyLeuGluValAlaArgArgLeuValLeuGlyGluPheArgAsnGluIlyAsnLeuGluIly 240
QY 917 TTTGACAAATTCGCTTAGAGGGCTGTGCAATTTGACATTGAAGAAATTCGATTAGCA 976
DB 241 PheAspIlySerAlaIleuGluIlyLeuCysAsnLeuThrIleGluIleuPheArgLeuAla 260
QY 977 TACTTAGCTACTACCTCGATGATATATTGACTTTATTTAATTTGTGACAAATGTTTCT 1036
DB 261 TyrLeuAspTyrTyrIleuAspPheIleIleAspLeuPheAsnCysLeuThrAsnValSer 280
QY 1037 TCAATTTCCCTGGTGAAGTGTGACTATTTGAAAGGTTAAAGACTTTCTTATAATTTCCGA 1096
DB 281 SerPheSerIleuValSerValThrIleGluArgValIlyAspPheSerTyrAsnPheGly 300
QY 1097 TGGCAACATTTAGAAATTAAGTAACTGTAAATTTGACAGTTTCCCATTTGAAGAACTCAAA 1156
DB 301 TrpGlnHisLeuGluLeuValAlaCysIlyAspPheGlyGlnPheProThrLeuIlySer 320
QY 1157 TCTCTCAAAAGCTTACCTTCACTTCCAACAAGGTGGGAATGCTTTTTCAGAAAGTTGAT 1216
DB 321 SerLeuIlyArgLeuThrPheThrSerAsnIlyGlyIlyAsnAlaPheSerGluValAsp 340
QY 1217 CTACCAAGCTTGAGTTTCTAGATCTCAGTAAAGAAAGGCTTGAGTTTCAAAAGTTCTCT 1276
DB 341 LeuProSerLeuGluIleuPheuAspLeuSerArgAsnGlyLeuSerPheIlySGlyCys 360
QY 1277 TCTCAAGGATTTTGGGACCAACAGCCTAAAGATATTGATGTGAGCTTCAATGGTGT 1336
DB 361 SerGlnSerAspPheGlyThrThrSerLeuIlyTyrLeuAspLeuSerPheAsnGlyVal 380
QY 1337 ATTACATGAGTTCAAACTTCTTGGCTTAGAACCACTGAACATCTGATTTCCAGCAT 1396


```

Db      381  ILethrMetSerSerAenPheLeuGlyLeuGluLeuGluHISleuAaspPheGlnHIS 400
QY      1397  TCCATTGGAACAAATGAGTGGTTTCACTATTTCTCACTCAGAAACCTGATTAC 1456
Db      401  SerMetLeuysgInMetSerGlnPheSerValPheLeuSerLeuAghAenIleTyr 420
QY      1457  CTTCAGATTCTTCATCTACACACAGAGTTGCTTTCAATGGCATCTTCAATGGCTTGTCC 1516
Db      421  LeuApsIleSerHISThrHISThrArgValAlaPheAenGlyIlePheAenGlyLeuSer 440
QY      1517  AGTTCGAGAGCTTGAAAAATGCTGGCAATCTTTCCAGGAAACCTTCTCCAGATTC 1576
Db      441  SerLeuGluValLeuAysMeCAlaGlyAasnSerPheGlnGluAanPheLeuProAaspIle 460
QY      1577  TTCACAGAGCTGAGAACTTCACTTCGAGACCTCTCTGAGTCGCACTGAGACAGTTG 1636
Db      461  PheThrGluLeuAghAenLeuThrPheLeuAaspLeuSerGlnGlnLeuGluGlnLeu 480
QY      1637  TCTTCAAACAGATTAACTCACTCTCCAGTCTTCAAGTAAATATGAGCCACACAC 1696
Db      481  SerProThrAlaPheAasnSerLeuSerSerLeuGlnValLeuAanMetSerHISAsn 500
QY      1697  TTCTTTTCATTGATAGCTTCTTATTAAGTGTCTGAACCTCCCTCCAGGTTCTGATTAC 1756
Db      501  PheSerSerLeuAaspThrPheProTyrLeuCySleuAasnSerLeuAargValLeuAaspTyr 520
QY      1757  AGTCTCAATGACATATGATGATCTTCCAAAACAGAACTCAAGCATTTTCCAAAGTACTA 1816
Db      521  SerLeuAasnHISIleMetThrSerLeuAysGlnLeuGlnHISProSerSerLeu 540
QY      1817  GCTTTCTTAAATCTTACTCAGAAATGACTTGTGTGATCTTGTGAAACACAGAGTTTCTGTG 1876
Db      541  AlaPheLeuAasnLeuThrGlnAanAaspPheAlaCysThrCysGlnHISGlnSerPheLeu 560
QY      1877  CAATGATCAAGACCAAGAGCAGCTCTGTGTAAGTGAAGTAAGAAATGTCGACAA 1936
Db      561  GlnThrPheLeuAaspGlnAargGlnLeuLeuValGluValGluAargMetGluCysAlaThr 580
QY      1937  CCTTCAGATAGAGCAGGAGCATGCTGTGCTGAGTTGAATTCACCTCTCAGATGAATAG 1996
Db      581  ProSerAaspLysGlnGlyMetProValLeuSerLeuAasnIleThrCysGlnMetAasnLys 600
QY      1997  ACCATCATGAGTGTGCTGCTCCAGTGTGCTTGTAGTATCTGTTGAGCAGTTCTGTGTC 2056
Db      601  ThrIleIleGlyAlaSerValLeuSerValLeuValSerValAlaAlaValLeuVal 620
QY      2057  TATTAAGTTCTAATTTTCACTGATGCTTCTGTGCTGCTGCAATAAAGTAGTAGAGTGA 2116
Db      621  TyrCysPheTyrPheHISLeuMetLeuAlaGlyCysIleTyrGlyAargGlyGlu 640
QY      2117  AACATCTAATGATGCTTTGTTATCTACTCAAGCCAGAGATGAGACCTGGGTAAAGATGAG 2176
Db      641  AsnValTyrAaspAlaPheValIleTyrSerSerGlnAaspGluAaspTyrValAargAasnGlu 660
QY      2177  CTAGTAAAGATTATGAGAAAGGGGCTCTCATTTGAGCTGCTCTTCACTACAGAGAC 2236
Db      661  LeuValLysAasnLeuGlnGluGlyValProPhePheIleuCySleuHISThrAargAasp 680
QY      2237  TTTATTTCCGGTGTGCGCATGCTGCTCCAAACATCATCAAGTAAGTTTCCATAAAGCCGA 2296
Db      681  PheIleProGlyValAlaIleAlaIleAlaAsnIleIleHISGlnGlyPheHISLysSerArg 700
QY      2297  AAGGTGATGTTGTGGTGGTCCCGACACTTCATCCAGACCGCGTGTATCTTTGAATAT 2356
Db      701  LysValIleValValValSerGlnHISPheIleGlnSerArgTyrCysIlePheGluTyr 720
QY      2357  GAGATTGCTGAGACCTGCGCAGTTTCTGAGCAGTGTGCTGGTATCATTTGATGCTCTG 2416
Db      721  GluIleIleIleGlnThrPrgInPheLeuSerSerArgAlaGlyIleIlePheIleValLeu 740
QY      2417  CAGAGGTGAGAAAGACCTGCTGAGCAGCAGAGGTGAGCTGTACCGCTTCTCAGCAGG 2476
Db      741  GlnLysValGluLysThrLeuLeuAargGlnGlnValGluLeuTyrAargLeuLeuSerArg 760

```

```

QY      2477  AACATTACCTGGAGTGGAGAGACAGTGTCTGGGGCGGACATCTTCTGAGACGACTC 2536
Db      761  AsnThrTyrLeuGluTyrPrgInAaspSerValLeuGlyArgHISIlePheThrPargArgLeu 780
QY      2537  AGAAAGCCCTGCTGTGATGGTAAATCATGGAATCCAGAAAGACAGTGGGTACAGATGC 2596
Db      781  ArgLysAlaLeuLeuAaspGlyLysSerTyrAasnProGluGlyThrValGlyThrGlyCys 800
QY      2597  AATTGGAGGAGACGACATCTATC 2620
Db      801  AsnTyrGlnGluAlaThrSerIle 808

RESULT 12
AD057803
ID   AD057803 standard; protein; 808 AA.
AC   AD057803;
DC   12-AUG-2004 (first entry)
DE   Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX   XX
XX   toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX   immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX   sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX   Pan troglodytes.
XX   WO2004042365-A2.
XX   21-MAY-2004.
XX   03-NOV-2003; 2003MO-US036247.
XX   01-NOV-2002; 2002US-0423113P.
XX   (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX   PA
XX   Measler W;
XX   PI
XX   WPI; 2004-400726/37.
XX   DR   N-PSDB; AD057801, AD057802.
XX   PT   Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX   PT   in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX   PT   sequence of the Old World monkey with that of a human.
XX   PS   Disclosure; SEQ ID NO 24; 11pp; English.
XX   CC   The invention relates to a novel method for identifying a nucleotide
XX   CC   change in a TLR4 polynucleotide sequence of an old world monkey
XX   CC   comprising comparing the TLR4 polynucleotide sequence of the Old World
XX   CC   monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX   CC   method of the invention has antibacterial, immunosuppressive, and
XX   CC   antiasthmatic activity. The method is useful in identifying a nucleotide
XX   CC   change in a TLR4 polynucleotide sequence of an old world monkey where the
XX   CC   change may be associated with reduced sensitivity to Gram-negative
XX   CC   bacterial infection. The methods, agents and composition are useful in
XX   CC   treating sepsis, severe sepsis or septic shock and asthma. The present
XX   CC   sequence represents chimpanzee TLR4.
XX   SQ   Sequence 808 AA.

Alignment Scores:
Pred. No.: 0
Score: 4164.00
Percent Similarity: 99.63%
Best Local Similarity: 99.38%
Query Match: 48.54%
DB: 8
Gaps: 0
Length: 808
Matches: 803
Conservative: 2
Mismatch: 3
Indels: 0
Gaps: 0
US-09-396-985b-1 (1-4868) x AD057803 (1-808)

```

QY 197 GTGGTTCCTAATATTAATTACTATCAATGCATGAGCTGAATTTCTACAAATCCCGACAAC 256
Db 1 ValValProAsnIleThrTyrgInCysMetGluLeuAsnPhetTylysIleProAspAsn 20
QY 257 CTCCCTCTCTCAACCAAGAACTGAGACTTGAGCTTTAATCCCTGAGGCACTTTAGGCAAC 316
Db 21 LeuProPheSerThrTyrsAsnLeuAspLeuSerPheAsnProLeuAlaGHisLeuGlySer 40
QY 317 TATAGCTTCTCAATTCCTCCAGAACTGCAGATGTGTGATTTATCCAGGTGTGAATTCAG 376
Db 41 TyrSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIleGln 60
QY 377 ACAATTGAAGATGGGGCATATCAGAGCTTAAGCCACTCTCTAATCTTAATATTGACAGCA 436
Db 61 ThrIleGluAspGlyAlaTyrgInSerLeuSerHisLeuSerThrLeuIleLeuThrGly 80
QY 437 AACCCCATCCAGATTTAGCCCTGGGAGCCTTTTCTGCACTATCAAGTTTACAGAGCTG 496
Db 81 AsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnTyrsLeu 100
QY 497 GTGGCTGTGGAGCAAACTTAGCATCTCTAGAGAACTTCCCATTTGGACATCTCAAAACT 556
Db 101 ValAlaValGluThrAsnLeuAlaSerLeuGluAsnPhetProIleGlyHisLeuTyrsThr 120
QY 557 TTGAAGAAGCTTAATGTGCTCACAATCTTATCCAACTTTCAAAATTACCTGATATTTT 616
Db 121 LeuTyrsGluLeuAsnValAlaHisAsnLeuIleGlnSerPheTyrsLeuProGluTyrsPhe 140
QY 617 TCTAATCTGACCAATCTAGAGCACTTGAGCACTTTCCAGCAACAGATTCAAGATTTAT 676
Db 141 SerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnTyrsIleGlnSerIleTyrs 160
QY 677 TGACAGACTTGCGGGTCTTACATCAATGCCCTTACTCATCTCTTTAGACTGCTGC 736
Db 161 CysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
QY 737 CTGAATCTCTATGAACCTTTATCCAAACAGGTGCAATTTAAGAAATTAGCTTCAATAGCTG 796
Db 181 LeuAsnProMetAsnPhetIleGlnProGlyAlaPheTyrsGluIleArgLeuHisAlaTyrsLeu 200
QY 797 ACTTTAAGAAATTAATTTGATAGTTTAATGTAATGAAACTGTATTCAGAGCTGCGCT 856
Db 201 ThrLeuArgAsnAsnPhetAspSerLeuAsnValMetTyrsThrCysIleGlnGlyLeuAla 220
QY 857 GGTTAGAAGTCCATGCTTGGTCTGCGAGAAATTTGAATGAGGAAACTTGGAAG 916
Db 221 GlyLeuGluValHisArgLeuValLeuGlyGluProPheArgAsnGluGluAsnLeuGluTyrs 240
QY 917 TTTGACAAATCTGCTTAGAGGGGCTGTGCAATTTGACATTTGAAGAAATTCGATTAGCA 976
Db 241 PheAspTyrsSerAlaLeuGlnGluTyrsLeuCysAsnLeuThrIleGlnGluProPheArgLeuAla 260
QY 977 TACTTAGACTACTACCTCGATGATATTATTTAGACTTATTTAATGTTTGAACAAATGTTTCT 1036
Db 261 TyrsLeuAspTyrsTyrsTyrsLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnValSer 280
QY 1037 TCAATTTCCCTGGAGTGTGACATTTGAAGGTTAAAGACTTTTCTTAATTTTCGA 1096
Db 281 SerPheSerLeuValSerValThrIleTyrsSerValIleTyrsAspPheSerTyrsAsnPhetGly 300
QY 1097 TGGCAACATTAGATTTAGTTAACTGTAAATTTTGACAGTTTCCACATTTGAACCTGAAA 1156
Db 301 TrpGlnHisLeuGluLeuValTyrsCysAlaTyrsPheGlyGlnPheProThrLeuTyrsLeuTyrs 320
QY 1157 TCTCTCAAAAAGGCTTACTTCACTTCCAAACAAAGTGGGAATGCTTTTTCAGAAAGTTGAT 1216
Db 321 SerLeuTyrsArgLeuThrPheThrSerAsnTyrsGlyGlyAsnAlaPheSerGluValAsp 340
QY 1217 CTACCAAGCTTGAGTTTCTAGATCTCAGTAGAAATGGCTTGAGTTTCAAGGTTGCTGT 1276
Db 341 LeuProSerLeuGluProPheLeuAspLeuSerArgAsnGlyLeuSerPheTyrsGlyCysCys 360

QY 1277 TCTCAAGATGATTTTGGGACAACACAGCTTAAAGTATTTAGATCTGACGTTCAATGGTGT 1336
Db 361 SerGlnSerAspPheGlyThrThrSerLeuTyrsTyrsLeuAspLeuSerPheAsnGlyVal 380
QY 1337 ATTAACATAGATTTCAAACTTTCTGGGCTTAGAAACATCTAGAACATCTGGATTTCCAGCAT 1396
Db 381 IleThrMetSerSerAsnPhetLeuGlyLeuGlnGluLeuGlnHisLeuAspPheGlnHis 400
QY 1397 TCCAAATTTGAACAAATGATGATGTTTTCAGTATCTCTATCTCACTCAGAAACCTCATTTAC 1456
Db 401 SerAsnLeuTyrsGlnMetSerGluProPheSerValPheLeuSerLeuArgAsnLeuIleTyrs 420
QY 1457 CTTGACATTTCTCAATCTCACACACAGAGTTGCTTTCAATGGCATCTTCAATGGCTTGC 1516
Db 421 LeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 440
QY 1517 AGCTCGAAGTCTTGAAAATGGCTGGCAATCTTTCCAGGAAACCTTCTTCCAGATATTC 1576
Db 441 SerLeuGluValLeuTyrsMetAlaGlyAsnSerPheGlnGluAsnPhetLeuProAspIle 460
QY 1577 TTCAAGAGCTGAGAAACTTGACCTTCTGAGCTCTCTCAAGTGTCAACTGAGCAGTTG 1636
Db 461 PheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnLeu 480
QY 1637 TCTCAACAGCACTTTAACTCACTCTCAGTCTTCAGGTACTAATATGAGCCACAAC 1696
Db 481 SerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsn 500
QY 1697 TTTCTTTTCATGGATACGTTTCTTTCTTAAGTGTCTGAATCTCCTCCAGGTTCTTGATATAC 1756
Db 501 PhePheSerLeuAspThrPheProTyrsCysLeuAsnSerLeuGlnValLeuAspTyrs 520
QY 1757 AGCTCAATCACTAATGACTTCCAAAAACAGGAACCTACAGACTTTTCCAACTAGCTCA 1816
Db 521 SerLeuAsnHisIleIleMetThrSerTyrsGlnGluLeuGlnHisPheProSerSerLeu 540
QY 1817 GCTTTCTTAAATCTTACCTGAAATGACTTGTCTTGTAGTGTGAACACAGAGTTTCTGT 1876
Db 541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
QY 1877 CATGATCAAGGACCAAGAGGCAAGCTCTTGCTGGAGAGTTGAACGAATGGAATGTGCACA 1936
Db 561 GlnTrpIleTyrsAspGlnArgGlnLeuLeuValGluValGluArgMetGluCysAlaThr 580
QY 1937 CCTCAGATPAGAGGAGCAATGCTGCTGCTGAGTTGATATATCACTGTCAGATGAATAG 1996
Db 581 ProSerAspTyrsGlnIleMetProValLeuSerLeuAsnIleThrCysGlnMetAsnTyrs 600
QY 1997 ACCATCATTTGGTGTGCTGCTCAAGTGTCTTGAATCTGTGTAGACAGTTGTGTC 2056
Db 601 ThrIleIleGlyValSerValLeuSerValLeuValSerValAlaValAlaVal 620
QY 2057 TATAAGTTCTATTTTCACTGATGCTTCTTGCTGCTGCATTAAGATAGTGTAGAGTTGAA 2116
Db 621 TyrsLeuPheTyrsPheHisLeuMetLeuAlaGlyCysAlaLeuTyrsTyrsGlyArgGlyGln 640
QY 2117 AACATCTAGATGCTCTTGTATCTACTCAAGGCAAGAGGAGGAGCTGGGAAAGAAATGAG 2176
Db 641 AsnIleTyrsAspAlaPheValIleTyrsSerSerGlnAspGluAspTrpValAlaGlnGln 660
QY 2177 CTAGTAAGAAATTTAGAAAGGGGTGCTCCATTTCAAGTCTGCTTCACTACAGAGAC 2236
Db 661 LeuValTyrsAsnLeuGlnGluGlyValProProPheGlnLeuTyrsLeuHisTyrsArgAsp 680
QY 2237 TTTATTTCCGGGTGTGCTGCTGCTGCAACATATCATGAGAGTTTCCATTAAGCCGA 2296
Db 681 PheIleProGlyValAlaIleAlaIleAlaAsnIleIleHisGlnGlyPheHisTyrsSerArg 700
QY 2297 AAGGATATGTTGTGTGTGCCAGCACTTCAATCAGAGGCGCGTGATCTTTGAATAT 2356
Db 701 TyrsValIleValAlaValSerGlnHisPheIleGlnSerArgTrpCysIlePheGluTyrs 720
QY 2357 GAGATTTGCTCAGACTTGAGCAATTTCTGACAGATCGTGTGTATCATTTCAATTTGTCTGT 2416

Db 721 GUILLEAGLHNRHTRPGINPHELEUSERSERARGLAAGLYLEILEPHELEVALLEU 740
 QY 2417 CAGAGGTGGAGAAAGCCCTGCTCAGCAGCAGGTGAGCTGTAACCGCTTCTCAGCAGG 2476
 Db 741 GlnlyValaIgluylsrThrleuLeuArgGlnValaIgluLeuYrArgleuLeuSerArg 760
 QY 2477 AACACTTACCTGAGAGGAGGAGCAGGTCTCGGGGGGCAACATCTTCTGAGACGACTC 2536
 Db 761 AsnThrIylLeuGlnIulrPgIuAspSerValleuGlyArgHisIlePheThrPArgArgLeu 780
 QY 2537 AGAAAGCCCTGCTGAGTGTAAATCATGGAATCCAGAAAGAACAGTGGGTACAGATGC 2596
 Db 781 ArglyAlaIleuLeuAspGlyIysSerTrpAsnProGluGlyThrValaIgluThnGlyCys 800
 QY 2597 AATTGGCAGAGCAACATCTATC 2620
 Db 801 AsnTrpGlnGlnIulalThrSerIle 808
 RESULT 13
 AAM86352
 ID AAM86352 standard; protein; 799 AA.
 XX
 AC AAM86352;
 XX
 DT 15-MAR-1999 (first entry)
 XX
 DE Human DNAX toll-1-like receptor DTLR4.
 XX
 KM DNAX toll-1-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
 KM interleukin 1 receptor; phosphate metabolism; innate immunity response;
 KM modulate inflammatory function; morphological effect;
 KM immunological disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO9805047-A2.
 XX
 PD 12-NOV-1998.
 XX
 PF 07-MAY-1998; 98WO-US008979.
 XX
 PR 07-MAY-1997; 97US-0044293P.
 PR 22-JAN-1998; 98US-0072212P.
 PR 05-MAR-1998; 98US-0076947P.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
 XX
 DR WPI, 1999-059670/05.
 DR N-PSDB; AAV80666.
 XX
 PT Human DNAX toll-1-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
 XX metabolism, modulate inflammatory function or innate immunity responses.
 XX
 PS Example; Page 115-117, 171pp; English.
 XX
 CC The present invention specifically describes human DNAX toll-1-like
 CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
 CC in the present invention. Also described are: (1) a fusion protein
 CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
 CC an antibody or antibody fragment which specifically binds to a DTLR
 CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
 CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
 CC host cell comprising the vector of (4). The host cell of (5) can be used
 CC to produce the DTLR proteins. The DTLR proteins can be used to alter
 CC phosphate metabolism, to modulate inflammatory function, innate immunity
 CC responses or morphological effects. The DTLR proteins can be used in the
 CC treatment of conditions exhibiting abnormal expression of the receptors
 CC of their ligands. These abnormalities are typically manifested by
 CC immunological disorders
 CC

SQ Sequence 799 AA;
 Alignment Scores:
 Pred. No.: 0
 Score: 4141.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 48.27%
 DB: 2
 Gaps: 0
 US-09-396-985b-1 (1-4868) x AAM86352 (1-799)
 QY 224 ATGAGCTGAATTTCTCAAAATCCCGCAACACCTCCCTTCTCAACCAAGAACTGGAC 283
 Db 1 MetGluLeuAsnPhenylrIylsrIleProAspAsnLeuProPheSerThrIylsAsnLeuAsp 20
 QY 284 CTGAGCTTTAATCCCTGAGGCAATTTAGGCACTATAGCTTTCAGTTTCCAGAACTG 343
 Db 21 LeuSerPheAsnProLeuArgHisLeuGlySerTrpPhePheSerPheProGluLeu 40
 QY 344 CAGGTGCTGATTTATCCAGGTGTGAATCCAGAACTGAAGATGGGGCATTCAGAGC 403
 Db 41 GlnValleuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaIylrGlnSer 60
 QY 404 CTAGCCACCTCTCTACCTTAATATGACAGAAACCCCATCCAGAGTTTAGCCCTGGGA 463
 Db 61 LeuSerHisLeuSerThrLeuIleLeuThrIylAsnProIleGlnSerLeuAlaIleGly 80
 QY 464 GCCTTTTCTGACTATCAAGTTTACAGAGCTGTGGCTGTGAGACAAATCTAGCATCT 523
 Db 81 AlaPheSerGlyLeuSerSerLeuGlnIylsLeuValAlaValaIgluThrAsnLeuAlaSer 100
 QY 524 CTGAGAACTTCCCTTGGACATCTCAAACTTGAAGAACTTGAATGTGGCTCCCAAT 583
 Db 101 LeuGluAsnPhenylProIleGlyHisLeuIylsrThrLeuIylsrGluLeuAsnValAlaHisAsn 120
 QY 584 CTATCCAACTTTCTCAAAATTAACCTGAGTATTTTCTATCTGACCAATCTAGAGCACTTG 643
 Db 121 LeuIleGlnSerPheIylsrLeuProGluIylrPheSerAsnLeuThrAsnLeuGlnHisLeu 140
 QY 644 GACCTTTCCAGCAACAGATTCAGATTAATTTATGACAGACTTGGGGTTCATCATCA 703
 Db 141 AspLeuSerSerAsnIylsrIleGlnSerIleIylrCysThrAspLeuArgValaIleuHisGln 160
 QY 704 ATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGAATCTTGAACCTTATCCACCA 763
 Db 161 MetProLeuLeuAsnLeuSerIleuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
 QY 764 GTGCAATTTAAAGAAATTAAGCTTCAATAGCTGACTTAAGAAATATTTTGAATAGTTTA 823
 Db 181 GlyAlaPheIylsrGlnIleArgLeuHisIylsrLeuThrLeuArgAsnAsnPheAspSerLeu 200
 QY 824 AATGTAATGAAACCTGTATTCAGGCTGTGGCTGTTTAGAAGTCCATCGTTTGGTCTG 883
 Db 201 AsnValMetIylsrThrCysIleGlnIylsrValaIgluLeuIylsrValaHisArgLeuValleu 220
 QY 884 GGAATTTTGAATGAAATGAGAAACCTTGAAGAAAGTTTGACAAATCTGCTCTAGAGGGCTG 943
 Db 221 GlyGluPheArgAsnGlnIylsrValaLeuGlnIylsrPheAspIylsrSerAlaIleuGlnIylsr 240
 QY 944 TGAATTTGACCAATGAGAAATCCGATTGACATCTTACATCACTCACTCGATGATATT 1003
 Db 241 CysAsnLeuThrIleGlnIylsrPheArgLeuAlaIylsrIylsrIylsrIylsrIylsrIylsr 260
 QY 1004 ATGACTTATTAATTTGACAAATGTTTCTTCATTTTCCCTGGTGAAGTGTGACTATT 1063
 Db 261 IleAspLeuPheAsnCysIleuThrAsnValSerSerPheSerIylsrValThrIle 280
 QY 1064 GAAAGGTTAAAGACTTTTCTTATTAATTTGAGATGGCAACATTTGAATTAAGTTAACTGT 1123
 Db 281 GluArgValIylsrAspPheSerIylsrAsnPheGlyTrpGlnHisLeuGlnIylsrValaHisCys 300
 QY 1124 AATTTGACAGATTTCACATTTGAAGAACTCAAAATCTGTCAAAAGGCTTACTTCATCTCC 1183

```
Db      ||| 301 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 320
Qy      ||| 1184 AACAAAGTGGGAATGCTTTTTCAGAAATGATATCAACAAGCTTGAATTTTCAGATCTC 1243
Db      ||| 321 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340
Qy      ||| 1244 AGTAAAGAAAGGCTTGAGTTTCAAGGTTGCTTCAAGTGAATGATTTTGGGACAACAGC 1303
Db      ||| 341 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
Qy      ||| 1304 CTAAATATTATAGATGATGAGCTTCAATGAGTTATTAACATGAGTTCAAACTTTGGG 1363
Db      ||| 361 LeuLysTyrlLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
Qy      ||| 1364 TTAGAACAACTAGAACATCTGGATTTTCAGACATTTCCAAATTTGAAACAAATGAGTGT 1423
Db      ||| 381 LeuGluGlnLeuGlnIleLysLeuAspPheGlnIleSerAsnLeuLysGlnMetSerGluPhe 400
Qy      ||| 1424 TCAGTATTCCTATCAGTCAAGAAACCTTATTACTTGAATTTCTCATTACTCAACACAGA 1483
Db      ||| 401 SerValPheLeuSerLeuAspGlnLeuIleTyrlLeuAspIleSerThrIleuArgAsnLeuThrPhe 420
Qy      ||| 1484 GTTGCTTTCAATGGCATCTTCAATGGCTTGTCCAGTCTCGAAGTCTTGAAGTGGCTGGC 1543
Db      ||| 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 440
Qy      ||| 1544 AATCTTTTCCAGGAAAATTCTTCCAGATATCTTCCAGACAGCTGGAGAAAATTGACCTTC 1603
Db      ||| 441 AsnSerPheGlnIleuAsnPheLeuProAspIlePheThrIleuArgAsnLeuThrPhe 460
Qy      ||| 1604 CTGACAGCTCTCAGAGTCAACTGGAGCAGTTGCTCCAGACAGATTTAATCTCACTCTCC 1663
Db      ||| 461 LeuAspLeuSerGlnCysGlnLeuGluLeuSerProThrAlaPheAsnSerLeuSer 480
Qy      ||| 1664 AGTCTTCAGGTAATAATATAGACCAACAACATCTTCTTCAATGATAGATTCCTTAT 1723
Db      ||| 481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeuAspThrPheProTyrl 500
Qy      ||| 1724 AAGTGTCTGAATCCTCCAGGTTCTTGATTACAGTTCATCAATCAATAGATCTTCCAA 1783
Db      ||| 501 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 520
Qy      ||| 1784 AAACAGGAATCTACAGCATTTTCCAGATGCTAGCTTCTTAATCTTATCTCAAGATGAC 1843
Db      ||| 521 LysGlnIleuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
Qy      ||| 1844 TTGCTTTGTACTTGTGAACACACAGAGTTTCTCGAATGATCAAGACAGAGCAGCTC 1903
Db      ||| 541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeu 560
Qy      ||| 1904 TTGGTGAAGTGAACGAATGGAATGTGCAACACTTCAGATTAAGCAGGCGACCTGTG 1963
Db      ||| 561 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnIleMetProVal 580
Qy      ||| 1964 CTGAGTTTGAATATCACCTGTCAGATGAATAAGCACTCATTTGGTGTGGTCTCAGT 2023
Db      ||| 581 LeuSerLeuAsnIleThrCysGlnMetCAsnLysThrIleIleGlyValSerValLeuSer 600
Qy      ||| 2024 GTGCTGTAGATATCTGTGTAGACAGTTCTGGTCTAATAGTTCTAATTTTCACTGATGCTT 2083
Db      ||| 601 ValLeuValValSerValValAlaValLeuValTyrlTyrPheThrIleMetSerLeu 620
Qy      ||| 2084 CTGCTGGCTGCATAAAGTATGTAGAGGTGAAGAAAACCTATGATGCTTGTATTATCTAC 2143
Db      ||| 621 LeuAlaGlyCysIleLysTyrlGlyArgGlyGlyAsnIleTyrlAspAlaPheValIleTyrl 640
Qy      ||| 2144 TCAAGCCAGATGAGACTGGGTGAAGAAAGAGCTATGAAGATTTTGAAGAGAGGAGT 2203
Db      ||| 641 SerSerGlnAspGlnAspTrpValArgAsnIleuValLysAsnLeuGluGluVal 660
Qy      ||| 2204 CCTTCATTTGAGCTGCTGCTTCACTACAGAGACTTTATTCCTCCGCTGTGCACATTCGCTCC 2263
```

```
Db      ||| 661 ProProPheGlnLeuCysLeuHisIleTyrlArgAspPheIleProGlyValAlaIleAla 680
Qy      ||| 2264 AACATCATCCATGAAGTTTCCATAAAGCCGAAAGGTGATTTGGTGGTGTCCGACAC 2323
Db      ||| 681 AsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValSerGlnHis 700
Qy      ||| 2324 TTCATCCAGAGCCGCTGTGTATCTTTGAATATGAGATTTGCTCAGACCTGGCAGTTTCTG 2383
Db      ||| 701 PheIleGlnSerArgTrpCysIlePheGlnTyrlGluIleAlaGlnThrTrpGlnPheLeu 720
Qy      ||| 2384 AGCAGTGTGCTGTGATCATCTTCATTTCTTCGACAGAGTGGAGAGAACCTGCTCAG 2443
Db      ||| 721 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuAsnArg 740
Qy      ||| 2444 CAGCAGTGAAGCTGTAACGCCCTTCTCAGAGGAACACTTACCTGAGTGGAGACAGT 2503
Db      ||| 741 GlnGlnValGlnLeuTyrlArgLeuSerArgAsnThrTyrlLeuGluTrpGluAspSer 760
Qy      ||| 2504 GTCTTGCGGCGGACATCTTCTGAGACGACTCAGAAAAGCCCTGTGATGGTAAATCA 2563
Db      ||| 761 ValLeuGlyArgHisIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 780
Qy      ||| 2564 TGGATTCAGAAAGAACAGTGGGTACAGATGCAATTTGGCAGAGACCAACTTATTC 2620
Db      ||| 781 TrpAsnProGluGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle 799

RESULT 14
AAEL6093
ID AAEL6093 standard; protein; 799 AA.
XX
AC AAEL6093;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX Toll like receptor (DTLR) 4 #1.
XX
KW Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KM Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS Homo sapiens.
XX
PN WC200190151-A2.
XX
PD 29-NOV-2001.
XX
PE 23-MAY-2001; 2001MO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Hardman GT, Rock FL, Bazan JF, Kastellein RA, Ho SWK, Liu Y;
XX
XX WPI; 2002-083085/11.
XX
DR N-PSDB; AAD26283.
XX
PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
PS Claim 1; Page 35; 297pp; English.
XX
CC The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antibodies or antibodies
CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
```

CC purified DTR can be used to screen monoclonal antibodies or antigen-binding fragments. The antibodies are useful for screening expression CC libraries for particular expression products. These are useful for CC detecting or diagnosing various immunological conditions related to CC expression of DTR or cells that express it. The present sequence is CC human DTR4 protein. The DTR4 gene is located on chromosome 9q32-33

XX Sequence 799 AA;

Alignment Scores:

Pred. No.:	0	Length:	799
Score:	4141.00	Matches:	799
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	48.27%	Indels:	0
DB:	5	Gaps:	0

US-09-396-985B-1 (1-4868) x AAE16093 (1-799)

```

QY 224 ATGAGCTGAATTTCTACAAATCCCGACACCTCCCTTCTCAACCAAGAACTTGAC 283
    |||
Db 1 MetGluLeuAsnGlyTrpGluPheProAspAsnLeuProPheSerThrTrpAsnLeuAsp 20

QY 284 CTGAGCTTAAATCCCTGAGGCAATTGAGCATTAGCTTTCTTCACTTTCCCAAGAACTG 343
    |||
Db 21 LeuSerPheAsnProLeuArgHisLeuGlySerTrpSerPhePheSerPheProGluLeu 40

QY 344 CAGGCTCTGATTTATTCAGAGTGTGAATTCAGACAACTTGAAGATGGGGCAATCAGAGC 403
    |||
Db 41 GlnValLeuAspLeuSerArgCysGluLeuThrLeuGluAspGlyAlaTrpGlnSer 60

QY 404 CTAAAGCACCTCTCTACCTTAATATTGACAGAAACCCCATCCAGAGTTAGCCCTGGA 463
    |||
Db 61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80

QY 464 GCCTTTTCGACTATCAAGTTTACAGACGCTGGCTGTGAGACAAATCTTACGACTT 523
    |||
Db 81 AlaPheSerGlyLeuSerSerLeuGlnValAlaValGluThrAsnLeuAlaSer 100

QY 524 CTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAAAGACTTAAATGGGCTCACAAT 583
    |||
Db 101 LeuGluAsnGlyProIleGlyHisLeuGlyThrLeuGlyGluLeuAsnValAlaHisAsn 120

QY 584 CTATCCCAATCTTCAATATTAACCTGAGTATTTTCTAATCTGACCAATCTTGAACCTTG 643
    |||
Db 121 LeuIleGlnSerGlyLeuSerLeuProGluTrpPheSerAsnLeuThrAsnLeuGluHisLeu 140

QY 644 GACCTTTCAGACAAAGATTCAAGATTATTTATTTGACAGACTTGCGGTTCTTACATCAA 703
    |||
Db 141 AspLeuSerSerAsnGlyHisLeuSerIleTrpCysThrAspLeuArgValIleuHisGln 160

QY 704 ATGCCCTTACTCAATCTCTCTTTAGACCTGTCCCTGAAATCTTATGAACTTTATTCACCA 763
    |||
Db 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180

QY 764 GGGCACTTTAAAGAAATTAGGCTTCAATAGCTGACTTAAAGAAATATTTTGAATGTTA 823
    |||
Db 181 GlyAlaPheLeuGlyIleArgLeuHisLeuThrLeuArgAsnLeuPheAspSerLeu 200

QY 824 AATGTATGAAATCTGTATTCAGAGCTGTGGCTGTTTGAAGTCCATCTTTGGTCTTG 883
    |||
Db 201 AsnValMetLeuSerThrCysIleGlnGlyLeuAlaGlyLeuGluValHisAspGluValLeu 220

QY 884 GGAAGATTTTGAATGAGAAACTTGGAAAGTTTGAACAATCTGCTTGAAGGGCTG 943
    |||
Db 221 GlyGluPheArgAsnGlyGluAsnLeuGluTrpPheAspLysSerAlaLeuGluGlyLeu 240

QY 944 TGAATTTGACCTTGAAGAAATCCGATTAGCACTTACTTAACTACTGATGATAT 1003
    |||
Db 241 CysAsnLeuThrIleGluGluPheArgLeuAlaTrpLeuAspTrpTrpLeuAspAspIle 260

QY 1004 ATTGACTTATTTAATTTTGAACAATGTTTCTTCAATTTTCCCTGGAGTGTGACTAT 1063
    |||

```

```

Db 261 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280

QY 1064 GAAAGGGTAAAGAACTTTTCTTAAATTTGAGATGGCAACTTGAATGATTAAGTATGCT 1123
    |||
Db 281 GluArgValIlyAspPheSerTrpAsnPheGlyTrpGlnHisLeuGluLeuValAsnCys 300

QY 1124 AAAATTGACAGTTTCCCACTTGAACCTGAAATCTGAAATCTTCAAAAGCTTACTTCACTTC 1183
    |||
Db 301 LysPheGlyGlnPheProThrLeuGlyLeuGlySerLeuGlyAspGluThrPheThrSer 320

QY 1184 AACAAAGGTGGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAGTTTCTAGATCTC 1243
    |||
Db 321 AsnIlyGlyGlyAsnHisPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340

QY 1244 AGTAGAAATGCTTGAATTTCAAGGTGCTGTTCTCAAGTATGATTTTGGAGCAACGAGC 1303
    |||
Db 341 SerArgAsnGlyLeuSerPheLeuGlyGlyCysCysSerGlnSerAspPheGlyThrThrSer 360

QY 1304 CTAAAGTATTTAGATCTGAGCTTCAATGCTGTATTAACATGAGTTCAAACTTTGGGC 1363
    |||
Db 361 LeuIlyTrpLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380

QY 1364 TTGAAACAACCTAGAACATCTGATTTCCAGACTTCCAAATTTGAAACAATGAGTGAATT 1423
    |||
Db 381 LeuGluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuGlyGlnMetSerGluPhe 400

QY 1424 TCAGTATTCCTATCACTGAGCAAACTCAATTAATTAATTAATTAATTAATTAATTAATTA 1483
    |||
Db 401 SerValPheLeuSerLeuArgAsnLeuIleTrpLeuAspIleSerHisThrHisSerArg 420

QY 1484 GTTGCTTTCAATGAGCATCTTCAATGAGCTTGTCCAGTCTCGAAATCTTGAATGAGTGGC 1543
    |||
Db 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuGlyMetAlaGly 440

QY 1544 AATTCTTTCCAGGAAATCTTCTTCAAGATATCTTCAAGAGCTGAGAACTTGACCTTC 1603
    |||
Db 441 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 460

QY 1604 CTGAGCTCTCTCAGTGTCACCTGAGGAGCTTCTCCCAACACATTAATTAATCACTGCC 1663
    |||
Db 461 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 480

QY 1664 AGCTTTCAGGTAATAATATGAGCCCAACAACCTTCTTTCATTTGATGATGATGCTTCTTAT 1723
    |||
Db 481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTrp 500

QY 1724 AAGTGTCTGAATCTCCCTCCAGGTTCTTGATTTACAGTCTCAATACATATGACTTCCAA 1783
    |||
Db 501 LysCysLeuAsnSerLeuGlnValLeuAspTrpSerLeuAsnHisIleMetThrSerLys 520

QY 1784 AACACGAACCTACAGCATTTTCCAAATGATGCTTCTTAAATCTTACTCAGAAATGAC 1843
    |||
Db 521 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540

QY 1844 TTGCTTGTACTCTGTGAACACGAGATTTCTCAATGATGATCAAGGACGAGGACGCTC 1903
    |||
Db 541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnHisGlnLeu 560

QY 1904 TTGGTGAAGTTGAAGAAATGGAATGGAACCTTCAAGATGAGCAGGGCATGCTGTG 1963
    |||
Db 561 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 580

QY 1964 CTGAGTTTGAATATCACTGCTGACGATGATTAACAACATCATTTGGTGTGGTCTCAGT 2023
    |||
Db 581 LeuSerLeuAsnHisLeuThrCysGlnMetAsnLysThrIleIleGlyAlaSerValLeuSer 600

QY 2024 GTGCTGTGATGATCTGTGAGAGCTTGTGCTATTAAGTTCAATTTTCACTGAGCTT 2083
    |||
Db 601 ValLeuValValSerValValAlaValLeuValIlyLysPheTrpPheHisLeuMetLeu 620

QY 2084 CTGCTGCTGCTCAATAAGATGAGTGAAGTGAACATCTATGATGCTTTGTTATCTAC 2143
    |||
Db 621 LeuAlaGlyCysIleLeuSerTrpGlyArgGlyGluAsnIleTrpAspAlaPheValIleTrp 640

```

QY 2144 TCAGCCAGGATGAGGACTGGTAAAGGATGAGCTAGTAAAGATTAGAGAGAGGCTG 2203
| | | | |
Db 641 SerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlyVal 660
QY 2204 CCTCCATTTCAGCTGCTGCTTCACTACAGAGACTTTATTCGGGTGGCCATTGCTGCC 2263
| | | | |
Db 661 ProProPheGlnLeuLeuCysLeuHisArgAspPheLeuProGlyValAlaIleAla 680
QY 2264 AACATCATCCATGAGGTTTCCATTAAGCCGAAAGGATGTTGTGGTGGTCCGAC 2323
| | | | |
Db 681 AsnIleIleHisGlnGlnPheHisLysSerArgLysValIleValValIleSerGlnHis 700
QY 2324 TTCATCCAGAGCCGCTGCTGCTATCTTGAATATGAGATTGCTGAGACTGGCAGTTTCTG 2383
| | | | |
Db 701 PheIleGlnSerArgTrpCysIlePheGlnGlyTrpGlnIleGlnIleHisTrpGlnPheLeu 720
QY 2384 AGCAGTGTGCTGCTGATTCATCTTCATTTGCTTCGACAGAGGTGAGAAACCTGCTCAG 2443
| | | | |
Db 721 SerSerArgLysGlnGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg 740
QY 2444 CAGCAGGTGAGCTGTACCGCCTTCTCAGAGAGAACTTACCTGAGTGGAGAGACGT 2503
| | | | |
Db 741 GlnGlnValGlnLeuLeuTrpArgLeuLeuSerArgAsnThrLysLeuGlnTrpGlnAspSer 760
QY 2504 GTCCTGGGCGGACATCTTCTGAGAGCAGCTCAGAAAACCTGCTGATGGTAAATCA 2563
| | | | |
Db 761 ValLeuGlnArgHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlnLysSer 780
QY 2564 TGGAAATCCAGAGAAACAGTGGGTACAGATGCAATTTGGCAGAGAACACATCTTATC 2620
| | | | |
Db 781 TrpAsnProGlnGlnThrValGlnThrGlyCysAsnTrpGlnGlnAlaThrSerIle 799

RESULT 15

ABB83162
ID ABB83162 standard; protein; 799 AA.
AC ABB83162;
DT 09-AUG-2002 (first entry)
DE Human Toll-like receptor-4, Tlr4.
XX Human; virulence; antibacterial; fungicide; parasiticide; receptor;
XX cytotoxic; immunostimulatory; scavenger receptor; Toll receptor;
XX respiratory tract infection; Toll-like receptor; Tlr4.
OS Homo sapiens.
XX
XX MO200235236-A1.
XX
XX 02-MAY-2002.
XX
XX 26-OCT-2001; 2001WO-FR003352.
XX
XX 27-OCT-2000; 2000FR-00013883.
XX
XX (FABR) FABRE MEDICAMENT SA PIERRE.
XX
XX Jeanmin P, Magistrelli G, Herdault N, Bonnefoy J;
XX
XX MPI; 2002-383586/41.
XX
XX DR N-PSDB; ABB83318.
XX
XX
XX PT Identifying agent that binds to scavenger receptors and signals through a
XX Toll receptor, useful as carrier or adjuvant in vaccines, promotes a
XX cytotoxic T cell response.
XX
XX
XX PS Disclosure; Page 58-60; 71pp; French.
XX
XX
XX The present invention relates to a method for identifying new therapeutic
XX compounds (1) by selecting molecules that bind to scavenger receptors and
XX signal through a Toll receptor. The present sequence is the protein

CC sequence for human Toll-like receptor-4, Tlr4, which was used to
CC illustrate the method of the invention. (1) are useful as carriers and/or
CC adjuvants in prophylactic or therapeutic vaccines, particularly where the
CC antigen is derived from a virus, bacterium, yeast, fungus, parasite or
CC tumour cell, especially a pathogen that causes respiratory tract
CC infection, also more generally for inducing an immune response. (1) can
CC also be used for specific targeting of active agents (antigens etc.) to
CC antigen-presenting cells (especially immature dendritic cells), for
CC subsequent internalisation by these cells

SQ Sequence 799 AA;

Alignment Scores:

Pred. No.:	0	Length:	799
Score:	4141.00	Matches:	799
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	48.27%	Indels:	0
DB:	5	Gaps:	0

US-09-396-985B-1 (1-4868) x ABB83162 (1-799)

QY 224 ATGAGACTGAATTTCTACAAATCCCGACAACTTCCCTTCTCAACCAAGACTGGAC 283
| | | | |
Db 1 MetGlnLeuAsnPheTrpLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 20
QY 284 CTGAGCTTAAATCCCTGAGGACATTTAGGACGATTAAGCTTCTTCAAGTTTCCAGAACTG 343
| | | | |
Db 21 LeuSerPheAsnProLeuArgHisLysGlnLysSerLysSerPheSerPheProGlnLeu 40
QY 344 CAGGTCTGATTTATTCAGGTGTGAATTCAGACAAATTAAGATGGGCGATTCAGAGC 403
| | | | |
Db 41 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlnLysArgIleSer 60
QY 404 CTAGCCACCTGCTCTTCTTAATATTCAGAGAAACCCATCCAGAGTTTACGCCCTGGGA 463
| | | | |
Db 61 LeuSerHisLeuSerThrLeuIleLeuThrGlnLysAsnProIleGlnSerLeuAlaLeuGly 80
QY 464 GACCTTTCTGACTATCAAGTTTACAGAGCTGTGGTGGAGCAAAATCTAGACATCT 523
| | | | |
Db 81 AlaPheSerGlnLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSer 100
QY 524 CTAGAGACTTCCCATTTGAGACATCTCAAACTTTGAAAGACTTATGTGCTCAAT 583
| | | | |
Db 101 LeuGlnAsnPheProIleGlnHisLeuLysThrLeuLysGlnLeuAsnValAlaHisAsn 120
QY 584 CTATCCAACTTTCAATTTACCTGAGTATTTTCTTAATTCAGCAATCTAGAGCACTTG 643
| | | | |
Db 121 LeuIleGlnSerPheLysLeuProGlnLysPheSerAsnLeuThrAsnLeuGlnHisLeu 140
QY 644 GACCTTCCAGAACAAAGATTCAAGATTATTCAGACAGCTTGGGGGTTCTACATCAA 703
| | | | |
Db 141 AspLeuSerSerAsnLysIleGlnSerIleTrpCysThrAspLeuArgLysLeuHisGln 160
QY 704 ATGCCCTTACTCAATCTCTTTTGAACCTGTCCCTGAATCTATGAACTTTATCCAAACA 763
| | | | |
Db 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
QY 764 GGTGCAATTAAGAAATTTAGGCTTCTTAAGCTGACCTTTAAGAAATATTTGATAGTTTA 823
| | | | |
Db 181 GlyAlaPheLysGlnIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu 200
QY 824 AATGTAATGAAAACCTGTATTCAAGGCTGGGCTGTGAAGTGCATGGTTGGTCTTG 883
| | | | |
Db 201 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeu 220
QY 884 GGAGAAATTTAGAAATGAGAAACTTGAAAGTTTGACAAATCTGCTAGAGGCGCTG 943
| | | | |
Db 221 GlyGlnPheArgAsnGlnGlnLysLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 240
QY 944 TGCAAATTTGACATTTAAGAAATTCGATTTAGCATTTGACTACTTACCTCGATGATTT 1003
| | | | |
Db 241 CysAsnLeuThrIleGlnGlnPheArgLeuAlaTrpLeuAspTrpTrpLeuAspAspIle 260

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 14:31:58 ; Search time 42.7671 Seconds
(without alignments)
16993.973 Million cell updates/sec

Title: US-09-396-985B-1
Perfect score: 8579
Sequence: 1 aaatactcctctgcctca.....caaaaaaaaaaaaaaa 4868

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 segs, 7464904 residues
Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p model -DEV=xlh
-Q=/cgn2_3/USPTO_spool/US0939685/Runat_28032005_155744_21170/app_query.fasta.1.85098
-DB=Issued Patents_AA -OPT=faatan -SUFFIX=rai -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUT=nt-plot -NORM=ext -HEAPSIZE=500 -MTLEN=0 -MAXLEN=200000000
-USER=US0939685 @CNC 1.1.732 @runat_28032005_155744_21170 -NCPU=6 -ICPU=3
-NO MAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents_AA:*
1: /cgn2_6/prodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4197	48.9	844	4	US-09-949-016-9438
2	629.5	7.3	661	1	US-08-514-014-4
3	629.5	7.3	661	2	US-08-833-823-4
4	599.5	7.0	784	4	US-09-982-308B-23
5	539	6.3	775	4	US-09-949-016-8799
6	316	3.7	605	3	US-09-063-950-5
7	305	3.6	623	4	US-09-949-016-10995
8	303.5	3.5	907	4	US-09-170-496D-264
9	303.5	3.5	907	4	US-09-170-496D-278
10	303	3.5	605	1	US-08-190-802A-49
11	303	3.5	605	1	US-08-477-346-49
12	303	3.5	605	3	US-08-473-089-49

13	303	3.5	605	4	US-08-487-072A-49	Sequence 49, Appl
14	303	3.5	605	4	US-09-538-092-1087	Sequence 1087, Ap
15	299.5	3.5	662	4	US-09-538-092-1325	Sequence 1325, Ap
16	299.5	3.5	662	4	US-09-949-016-6619	Sequence 6619, Ap
17	299.5	3.5	665	4	US-09-949-016-10710	Sequence 10710, A
18	299	3.5	1525	3	US-09-191-647-2	Sequence 2, Appl1
19	299	3.5	1525	3	US-09-540-245A-2	Sequence 2, Appl1
20	299	3.5	1525	3	US-09-540-153-2	Sequence 2, Appl1
21	296	3.5	603	1	US-08-170-346A-50	Sequence 50, Appl
22	296	3.5	603	1	US-08-477-802B-50	Sequence 50, Appl
23	296	3.5	603	3	US-08-473-089-50	Sequence 50, Appl
24	296	3.5	603	4	US-08-487-072A-50	Sequence 50, Appl
25	289.5	3.4	1112	3	US-09-353-585-3	Sequence 3, Appl1
26	289	3.4	1529	4	US-09-312-283C-336	Sequence 396, App
27	286.5	3.3	1166	4	US-10-101-464A-900	Sequence 900, App
28	286	3.3	1112	3	US-09-353-585-2	Sequence 2, Appl1
29	285	3.3	1091	3	US-08-986-485-5	Sequence 5, Appl1
30	285	3.3	1523	3	US-09-182-024A-2	Sequence 2, Appl1
31	284	3.3	1101	3	US-08-986-485-2	Sequence 2, Appl1
32	275	3.2	620	4	US-09-907-794A-73	Sequence 73, Appl
33	275	3.2	620	4	US-09-905-125A-73	Sequence 73, Appl
34	275	3.2	620	4	US-09-902-775A-73	Sequence 73, Appl
35	275	3.2	620	4	US-09-906-700-73	Sequence 73, Appl
36	275	3.2	620	4	US-09-903-603A-73	Sequence 73, Appl
37	275	3.2	620	4	US-09-904-920A-73	Sequence 73, Appl
38	275	3.2	620	4	US-09-909-064-73	Sequence 73, Appl
39	275	3.2	620	4	US-09-905-381A-73	Sequence 73, Appl
40	275	3.2	620	4	US-09-906-618-73	Sequence 73, Appl
41	272	3.2	1480	3	US-09-191-647-7	Sequence 7, Appl1
42	272	3.2	1480	3	US-09-540-245A-7	Sequence 7, Appl1
43	272	3.2	1480	3	US-09-540-153-7	Sequence 2, Appl1
44	272	3.2	1480	5	PCT-US91-09055-2	Sequence 2, Appl1
45	271	3.2	1139	4	US-09-513-505-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C10010307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Alignment Scores:
Pred. No.: 0
Score: 4197.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 48.92%
DB: 4
Gaps: 0

US-09-396-985B-1 (1-4868) x US-09-949-016-9438 (1-844)
QY 194 GAGGTGGTTCCTAATATCTTACTTCAATGACGAGCTGAATTTCTCAAAATCCCGAC 253

|||||
Db 36 GluValAlaProAsnIleThrTyrGlnCysMetGlnLeuAsnPheTyrIleProAsp 55
254 AACCTCCCTTCACACCAAGAACCTGGACCTTAAATCCCTGAGGACCTTTAGC 313
Db 56 AsnLeuProPheSerThrIlyAsnLeuAspLeuSerPheAsnProLeuAlaGhIleuGly 75
314 AGCTATAGCTTCTTCAGTTTCCAGAACTGCAGGTGCTGATTATCCAGTGTGAATC 373
Db 76 SerTyrSerPhePheSerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIle 95
374 CAGACAAATGAAAGTGGGCAATACAGAGCTTAAGCCACTCTCTACCTTAATATTGACA 433
Db 96 GlnThrIleGlnAspGlyAlaTyrGlnSerLeuSerIleuSerThrLeuIleLeuThr 115
434 GGAACCCCATCCAGAGTTTAGCCCTGGAGCCCTTTTCTGAGATATCAATTTACAGAG 493
Db 116 GlyAsnProIleGlnSerIleuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys 135
494 CTGGTGGCTGTGAGACAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAA 553
Db 136 LeuValAlaValAlaGlnThrAsnLeuAlaSerLeuGlnAsnPheProIleGlyIleSleuLys 155
554 ACTTTGAAGACCTTAAATGTGGCTCACAAATCTTATCCAAATCTTTCAAAATTCCTGATAT 613
Db 156 ThrIleuSeglnLeuAsnValAlaIleAsnLeuIleGlnSerPheLysLeuProGlnLys 175
614 TTTTCAATCTGACCAATCTAGAGCACTTGAGCACTTTCAGCAAAAGATTCAAAGATT 673
Db 176 PheSerAsnLeuThrAsnLeuGlnIleSleuAspLeuSerSerAsnLysIleGlnSerIle 195
674 TATTGACAGACTTGCAGGTCTTACATCAATGCCCCCTACTCAATCTCTTTAGACTG 733
Db 196 TyrCysThrAspLeuAspValIleuHisGlnMetProLeuLeuAsnLeuSerIleuAspLeu 215
734 TCCCTGAATCTTATGAACTTTATCCAAACGAGTGCAATTTAAAGAAATTTAGCTTCATAG 793
Db 216 SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGlnIleArgLeuHisLys 235
794 CTGACTTAAAGAAATATTTGATAGTTTAAATGTAATGAAACTGTATTCAGAGCTG 853
Db 236 LeuThrIleuArgAsnAsnPheAspSerLeuAsnAlaMetLysThrCysIleGlnGlyLeu 255
854 GCTGTTTAGAAGTCCATCGTTGGTCTGAGAGAAATTTAGAAATGAAGAAACTTGGA 913
Db 256 AlaGlyLeuGlnIlyAlaHisArgLeuValLeuGlyGlnPheArgAsnGlnIlyAsnLeuGln 275
914 AAGTTGACAAATCTGCTTGAAGAGGCTGTGCAATTTGACATTTGAAGAAATTCGATTA 973
Db 276 LysPheAspLysSerAlaLeuGlnIlyLeuCysAsnLeuThrIleGlnIlyPheArgLeu 295
974 GCATCTTAGACTACTACCTCGATGATATATGACTTATTAATGTTGACAAATGTT 1033
Db 296 AlaTyrLeuAspLysTyrTyrLeuAspAspIleIleAspLeuPheAsnCysLeuThrIleAsnVal 315
1034 TCTTCATTTTCCCTGAGTGTGATGACTATGAAAGGCTTAAGACTTTCTTAATTTTC 1093
Db 316 SerSerPheSerIleuValSerValThrIleGlnArgAlaLysAspPheSerTyrAsnPhe 335
1094 GGAATGCAACATTTAGATTAGTTAACTGTAAATTTGACAGTTTCCACATTTGAAATC 1153
Db 336 GlyTyrGlnIleHisLeuGlnLeuValAsnCysLysPheGlyGlnPheProThrIleuLysLeu 355
1154 AAATCTCTCAAAAGGCTTACTTTCACTTCCAAACAAGTGGAAATGTTTTTCAGAGTT 1213
Db 356 LysSerIleuLysArgLeuThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGlnVal 375
1214 GATCTACCAAGCTTGAAGTTTATGATCTGATGAGAAATGGCTTGAAGTTTCAAGGTGC 1273
Db 376 AspLeuProSerIleuGlnIlyPheLeuAspLeuSerArgAsnGlyLeuSerPheIlyGlyCys 395
1274 TGTTCCAAAAGTGAATTTTGGACCAACAGCCTTAAAGATTATTAAGTCTGAGCTTCAATGCT 1333

Db 396 CysSerGlnSerAspPheGlyThrThrSerIleuLysTyrLeuAspLeuSerPheAsnGly 415
1334 GTTATATACATGATGTTCAAACTTCTTGAGCTTAGAAACAATCAATCTGATTTTCCAG 1393
Db 416 ValIleThrMetSerSerAsnPheLeuGlyLeuGlnGlnIleuGlnHisLeuAspPheGln 435
1394 CATTCCAAATTTGAAACAAATGAGTGAAGTTTCAATTTCTATCACTCAAGAAACCTGATT 1453
Db 436 HisSerAsnLeuSeglnMetSerGlnPheSerValPheLeuSerIleuArgAsnLeuIle 455
1454 TACCTTGACATTTTCTCATCTACACACCAAGTTGCTTTCAATGGCATCTTCAATGGCTTG 1513
Db 456 TyrLeuAspIleSerThrIleThrIleArgValAlaPheAsnGlyIlePheAsnGlyLeu 475
1514 TCCAGTCTGAAGTCTTGAATAATGGCTGGCAATCTTTCAGAGAAACTTCTCTCCAGAT 1573
Db 476 SerSerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAsp 495
1574 ATCTTCACAGAGCTGAGAAACTTGAACCTTCTGAGACTTCTCACTGATGTCACCTGAGCAG 1633
Db 496 IlePheThrGlnLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 515
1634 TTGTCTCCAAACAGCATTTAACTCACTCTCTCACTTTCAGGTACTAATAATGACCACAC 1693
Db 516 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 535
1694 AACTCTTTCAATGATGATGCTTCTTCAATAGTGTCTGAACCTCCCTCAGAGTTCTTGAT 1753
Db 536 AsnPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAsp 555
1754 TACAGTCTCAATCACATAATGACTTCAAAAAACAGAACTACAGACTTTTCCAACTAGT 1813
Db 556 TyrSerLeuAsnHisIleMetThrSerLysGlnGlnIleuGlnHisPheProSerSer 575
1814 CTAGCTTTCTTAAATCTTACTAGAAATGACTTGTGTGATCTTGTGAACACCAAGACTTC 1873
Db 576 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnIleSeglnSerPhe 595
1874 CTGCAATGATCAAGACCAAGAGGAGCTCTTGAGTGAAGTTGAACGAATGGAATGTGCA 1933
Db 596 LeuGlnThrIleLysAspGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAla 615
1934 ACACCTTCAGATTAAGCAGGAGCATGCTGTGCTGAGTTGAATATCACTGTCAAGATGAT 1993
Db 616 ThrProSerAspLysGlnIlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 635
1994 AAGACATCATTTGATGTGTGCTGCTCACTGATGCTTGTGATCTTGTGATGACATTTG 2053
Db 636 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaAlaValLeu 655
2054 GTCTATAGTTCTAATTTTCACTGATGCTTCTTGCTGGCTGCATAAAGTATGGTAGAGT 2113
Db 656 ValTyrLysPheThrPheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyAspGly 675
2114 GAAACATCTAGATGCTCTTGTATCTACACAGCAGATGAGACTGGCTTAAGAAAT 2173
Db 676 GluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspIlePheValArgAsn 695
2174 GAGCTGTAAAGAAATTTAGAAGAGGGGTGCTTCATTTGAGTCTGCTTCACTACAGA 2233
Db 696 GlnLeuValLysAsnLeuGlnIlyGlyValProProPheGlnLeuCysLeuHisTyrArg 715
2234 GACTTATTTCCGGGTGGCAGTGTGTCACATCATCATGATGATGAAAGTTTCCATAAAG 2293
Db 716 AspPheIleProGlyAlaAlaIleAlaAlaAsnIleIleHisGlnIlyPheHisLysSer 735
2294 CGAAAGTGAATTTGTGTGTGCTCCAGACCTTCATCCAGAGCCGTGATCTTTGAA 2353
Db 736 ArgLysValIleValAlaValSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 755
2354 TATGAGATTGCTCAAGCTTGAGCTTTCAGAGAGTGTGCTGTGATCATCTTCAATTTGC 2413
Db 756 TyrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 775

QY 2414 CTGAGAGGTGAGAGAGACCTGCTCAGCAGAGGTGAGTGTACCCCTTCTAGC 2473
 |||||
 Db 776 LeuGlnIysValIgluYsThrLeuLeuArgIlnValIgluLeuYrAsgLeuSer 795
 |||||
 QY 2474 AGAACAATTACCTGAGGTGAGAGACAGTGTCTGGGGCGGACATCTTCTGAGACGA 2533
 |||||
 Db 796 ArgAsnThrYrLeuGlnIurTpgIuAspSerValIeuGlyrghsIlePheTrpArg 815
 |||||
 QY 2534 CTGAGAAAGCCCTGCTGAGTGTGAATCATGTGAAACAGAGAGAGGTGATACGA 2593
 |||||
 Db 816 LeuArgYsAlaIeuLeuAspGlyYsSerTrpAsnProGlnIyThrValIglYThrGly 835
 |||||
 QY 2594 TGCAATTGCGAGAGACATCTATC 2620
 |||||
 Db 836 CysAsnTrpGlnIuAlaThrSerIle 844
 |||||
 RESULT 2
 US-08-514-014-4
 ; Sequence 4, Application US/08514014
 ; Patent No. 5,707,829
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John
 ; APPLICANT: Kelleher, Kerry
 ; APPLICANT: Carlin, McKeough
 ; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 ; TITLE OF INVENTION: ENCODED THEREBY
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
 ; STREET: 87 Cambridgepark Drive
 ; City: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/514,014
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; REFERENCE/DOCKET NUMBER: G16000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 661 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-514-014-4
 Alignment Scores:
 Pred. No.: 5,35e-59 length: 661
 Score: 629.50 Matches: 199
 Percent Similarity: 45.90% Conservative: 109
 Best Local Similarity: 29.66% Mismatches: 274
 Query Match: 7.34% Indels: 89
 DB: 1 Gaps: 24
 US-09-396-985b-1 (1-4868) x US-08-514-014-4 (1-661)
 QY 176 AGCTGGAGAGCC--TGCGTGAGGTGTTCTTAATATTATCTTATCATGTCATGAGCTG 232
 |||||
 Db 23 SerTrpAspIlnMetCysIleGlnYsGluAlaAsnIyThrYrAsnYsGluAsnIeu 42

QY 223 AATTTCAGAAATCCCGCACAACCTCCCTTCTCAACCAAGAACCTGACCTGATTT 292
 ::::|
 Db 43 GlyLeuSerGlnIleProAspThrLeuProAsnThrThrGluPheLeuGlnPheSerPhe 62
 |||||
 QY 293 AATCCCTGAGGATTTAGGACAGCTATTCATCTTCTTCCAGAACTGCAGGTGCTG 352
 ::::|
 Db 63 AsnPheLeuProThrIleHisAsnArgThrPheSerArgLeuMetAsnIeuThrPheLeu 82
 |||||
 QY 353 GATTTCACAGGTGTAATCCAGACATTTGAAGATGGGGCATATACAGGCCCTAAGCCAC 412
 ::::|
 Db 83 AspLeuThrArgYsGlnIleAsnTrpIleHisGluAspThrPheGlnSerHisGln 102
 |||||
 QY 413 CTCTACCTTAATATTTGACAGAAACCCCATCTCAGAGTTAGCCCTGGAGGCTTTTCT 472
 |||||
 Db 103 LeuSerThrLeuValIeuThrGlyAsnProLeuIlePheMetAlaGluThrSerLeuAsn 122
 |||||
 QY 473 GGAATATCAAGTTTACAGAGCTGTGGCTGTGAGACAAATCTACATCTTACAGAAC 532
 |||||
 Db 123 GlyProIySerLeuYsHisIeuPheLeuIleGlnThrGlyYleSerAsnIeuGlnPhe 142
 |||||
 QY 533 TTCCCATTTGACATCTCAAACTTTGAAGAATTAATGTGCTCACATCTTATCCAA 592
 |||||
 Db 143 IleProValHisAsnIeuGlnAsnIeuGlnSerLeuYrLeuGlySerAsnHisIleSer 162
 |||||
 QY 593 TCTTCAAAATTAAGCTGATTTTCTAATCTGACCACTAGACATCTGACCTTTCC 652
 |||||
 Db 163 SerIleIyPheProIyAspPhePro--AlaArgAsnIeuYsValIeuAspPheGln 181
 |||||
 QY 653 AGCAACAGATTCAAAGATTATTATTCACAGACATTCGGGGTCTTACATCAAAATGCCCTA 712
 ::::|
 Db 182 AsnAsnAlaIleHisIerYrIleSerArgGluAspMetArgSerIeuGln-----Ala 199
 |||||
 QY 713 CTCAATCTCTTTTACACCTGTCCTGAAATCTTATGAACTTATCCAACAGGTGATTT 772
 ::::|
 Db 200 IleAsnIeuSerIeuAsnPheAsnGlyAsnAsnValIyGlyIleGluIeuGlyAlaPhe 219
 |||||
 QY 773 AAGAATTAAGCTTCATAAGCTGATTTAAGAAATTAATTTGATGTTAAATGTAAAG 832
 |||||
 Db 220 AspSerThrValPheGlnSerIeu-----AspPheGlyIyThrProAsnIeu 235
 |||||
 QY 833 AAAACTTGTATTCAGGTCTGCTGCTTGAAGTCCATCTGTTGCTTGGAGAAATTT 892
 |||||
 Db 236 SerValIlePheAsnIyIeuGlnAsnSerThrThrGlnSerIeuTrpIeuGlyThrPhe 255
 |||||
 QY 893 AGAAATGAAGAACTTGAAAAAGTTGACAAATCTGCTTGAAGGCGCTGTGCATTTG 952
 ::::|
 Db 256 GluAspIleAspAsp---GluAspIleSerSerAlaMetLeuIyGlyIeuCysGluMet 274
 |||||
 QY 953 ACCATTGAAGAAATTCGATTAAGCATTAAGCTATACCTGATGATTTATTTGAC--- 1009
 ::::|
 Db 275 SerValGluSerIeuAsnIeuGln-----GluHisArgPheSerAspIleSerThr 292
 |||||
 QY 1010 TTAATTAATGTTTGAAGATGTTCTTCAATTTTCCCTGATGAGTGAATTTGAAGA 1069
 |||||
 Db 293 ThrPheGlnCysPheThrGlnIeuGlnIuIeuAspLeuThrAlaThrHisIeuIySgIy 312
 |||||
 QY 1070 GTAAAGACTTTTCTTAATATTTCGATGCGAACATTTGAATTTAGTTAAC----- 1120
 ::::|
 Db 313 LeuProSer-----GlyMetIySgIyLeuAsnIeuIySgIyLeuVal 327
 |||||
 QY 1121 -----TGTAATTT-----GACAGTTTCCCACTTG 1147
 |||||
 Db 328 LeuSerValAsnHisPheAspGlnIeuCysGlnIleSerAlaAlaAsnPheProSerIeu 347
 |||||
 QY 1148 -----AACTCAATCTCTCAAAAGCTTACTTTCACTTCACTTCAAC 1186
 ::::|
 Db 348 ThrHisLeuYrIleArgGlyAsnValIySgIyLeuHisIeuGlyValGlyCysIeuGln 367
 |||||
 QY 1187 AAAGTGGAAATGCTTTTCAAGATGTGATGTACCAAGCCTTGAGTTTCTAGATCTCAGT 1246
 |||||
 Db 368 IySgIyLeuGlyAsn-----LeuGlnThrIeuAspLeuSer 378


```

Db      163 SerIleYsbPheProLysAspPhePro--AlaArgAsnLeuValLeuAspPheGln 181
QY      653 AGCAACAAGATTCAAAATTTATTTATTCACAGACTCGGGTTTACATCAAAATGCCCTTA 712
      182 AAmserAlaIleHisrYrIleSerArgGluAspMetArgSerLeuGln-----Ala 199
QY      713 CTCATCTCTCTTTAGACCTGTCCTGATCTATGAACTTTATTCACACCGAGTCGATTT 772
      200 IleAsnLeuSerLeuAsnPheAsnGlyAsnAsnValIleGlyIleGluLeuGlyAlaPhe 219
QY      773 AAAGAAATTAGGCTTCAATAGCTGACTTTAAGAAATATTTCATAGTTAAATGAAG 832
      220 AspSerThrValPheGlnSerLeu-----AsnPheGlyGlyThrProAsnLeu 235
QY      833 AAAACTGTATTCAAGCTCGGCTGGTTTGAAGTCATCGATTGGTTCGGGAGAAATT 892
      236 SerValIlePheAsnGlyLeuGlnAsnSerThrThrGlnSerLeuThrPhe 255
QY      893 AGAAATGAAGAACTTGAAAGTTTGACAAATCTGCTTAGAGGCGCTGTCGAATTTG 952
      256 GluAspIleAspAsp---GluAspIleSerSerAlaMetLeuIysGlyLeuGlyMet 274
QY      953 ACCATTGAAGAATTCGATTAAGTACTTAACTACTGATGATGATTTATTGAC--- 1009
      275 SerValGluSerLeuAsnLeuGln-----GluHisArgPheSerAspIleSerSerThr 292
QY      1010 TTTATTAATGTTTGCAAAATGTTTCTCATTTTCCCTGGTGAAGTGAATGAAG 1069
      293 ThrPheGlnCysPheThrGlnLeuGlnGluLeuAspLeuThrAlaThrHisLeuIysGly 312
QY      1070 GTAAAGACTTTTCTTAATATTCGATGAGCAATTTAGATTAATTAAC----- 1120
      313 LeuProSer-----GlyMetIysGlyLeuAsnLeuLeuIysIysLeuVal 327
QY      1121 -----TGTAATTT-----GGACAGTTTCCCACTTG 1147
      328 LeuSerValAsnHisPheAspGlnLeuGlyGlnIleSerAlaIleAsnPheProSerLeu 347
QY      1148 -----AACTCAATCTCTCAAAAGCTTCACTTCACTTCCAC 1186
      348 ThrHisLeuTyrIleArgGlyAsnValIysIysLeuHisLeuGlyValGlyCysLeuGln 367
QY      1187 AAAGTGGGAATGCTTTTTCAGAAATGATCTACAAAGCTTGAGTTTCAATGATCTAGT 1246
      368 IysLeuGlyAsn-----LeuGlnThrLeuAspLeuSer 378
QY      1247 AATAATGCTTGAATTTCAAAAGTTCGTTCTCAAAAGTATTTGGACAAACACGCTTA 1306
      379 HisAsnAspIleGluIleSerAspCysCysSerLeuGlnLeuIysAsnLeuSerHisLeu 398
QY      1307 AAGTATTTAGATGATGCTTCAATGATGTTATTCATCAATGATTTCAAAAC---TTCTTGGGC 1363
      399 GlnThrLeuAsnLeuSerHisAsnGluProLeuGlyLeuGlnSerGlnAlaPheIysGln 418
QY      1364 TTAGAACAACACTAGACATCTGATTTCCAG-----CATTCGAATTTGAACA 1411
      419 CysProGlnLeuGlnLeuLeuAspLeuAlaPheThrArgLeuHisIleAsnAlaProGln 438
QY      1412 ATGAGTGAATTTCA-----GTATTCATATCACTGAAACCTCATTTAC-----CTT 1459
      439 ---SerProPheGlnAsnLeuHisPheLeuGlnValLeuAsnLeuThrGlyCysPheLeu 457
QY      1460 GACATTTCTCATATCAACACACGAGTGGTTTCAATGGCATCTTCAATGCTTGTCCACT 1519
      458 AspThrSerAsnGlnHis-----LeuLeuAlaGlyLeuProVal 470
QY      1520 CTCGAAGTCTTGAAATGCTGCAATTTCTTCCAGAAAACTCTCTT-----CCAGAT 1573
      471 LeuArgHisLeuAsnLeuIysGlyAsnHisPheGlnAspGlyThrIleThrIysThrAsn 490
QY      1574 ATCTTCACAGAGCTGAAGAACTTGACCTTCTGACCTCTCTGAGTGTCACTGAGACAG 1633
      491 LeuLeuGlnThrValGlySerLeuGlnValLeuIleLeuSerSerCysGlyLeuLeuSer 510

```

```

QY      1634 TTGTCTCAACAGACTTTAATCACTCTCCAGCTTTCAGATCTAATAATAGACCAAC 1693
      511 IleAspGlnAlaIlePheHisSerLeuGlyIysMetSerHisValAspLeuSerHisAsn 530
QY      1694 AACTTCTTT-----TCATTGATACGTTTCTTTAT-----AAG 1726
      531 SerLeuThrCysAspSerIleAspSerIleAspSerLeuSerHisLeuIysGlyIleTyrLeuAsnLeu 550
QY      1727 TGTCTGAATCCCTCCAGCTTCTGATTTACGTTCTCAATCAGATTAATGACTTCCAAA 1786
      551 AlaIleAsnSerIleAsnIleIleSerProArgLeuLeuProIleLeu----- 566
QY      1787 CAGAACTACAGACATTTTCCAGTACTGATGCTTCTTAATCTTCAATGACTTT 1846
      567 -----SerGlnGlnSerThrIleAsnLeuSerHisAsnProLeu 579
QY      1847 GCTTGTACTTGTGAACACCAAGATTCTGCAATGGATGACAGACAGGAGCTTTG 1906
      580 AspCysThrCysSerSerHisPheLeuThrIlePheGlyIysGlyAsnLeuHisIysLeu 599
QY      1907 GTGGAAGTTGAACGAATGGAATGTGACACCTTCAATAGACAGGAGCATGCTGCTG 1966
      600 GluGlySerGluGluThrThrCysAlaAsnProProSerLeuArgGlyValIysLeuSer 619
QY      1967 AGTTGAATATGACACCTGTCAGATGAATAGACCATCATGATGATGCTGCTGCTGCTG 2026
      620 AspValIysLeuSerCysGlyIle-----ThrAlaIleGlyIlePhePheLeuIleVal 637
QY      2027 CTTGATGATCTGTTGTAGACCTTGTGATCTAT 2059
      638 PheLeuLeu---LeuLeuAlaIleLeuLeuPhe 647

```

RESULT 4

```

US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
; APPLICANT: Dalié, Barbara
; APPLICANT: Fan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tan, Jimmy C.
; APPLICANT: Zavadny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: JB06010C
; CURRENT APPLICATION NUMBER: US/09/982,308B
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-308B-23

```

Alignment Scores:

```

Pred. No.: 1,166-55 Length: 784
Score: 599.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 6.99% Indels: 219
DB: 4 Gaps: 38

```

US-09-396-985B-1 (1-4868) x US-09-982-308B-23 (1-784)

QY 245 ATCCCGACAACTCCCTTTCACCAAGAACTGACCTGATTAATCCCTGAGG 304

```

Db      46  ILeProSerGlyLeuThrGluAlaValLysSerLeuAspLeuSerAsnAsnArgIleThr 65
      305  CATTAGGACGACTAGACTCTTCACTTCCAGAACTGCAGCTGCTGATTTATCCAG 364
      66  TyrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValLeuThrSer 85
      365  TGTGAATCCAGACATTGAAAGATGGGGCATATCAGACCTAGACCTCCTTACTCTTA 424
      86  AsnGlyIleAsnThrIleGlnGlnAspSerPheSerSerLeuGlySerLeuGlnIleu 105
      425  ATATGACAGAAACCCCATCCAGAGTTTAGCCCTGGAGCCTTTCTGACATATCAAGT 484
      106  AspLeuSerTyrAsnTyrIleuSerAsnLeuSerSerTyrPheLysProLeuSerSer 125
      485  TTRCAGAAAGCTG-----GTGGCTGTGGAG 508
      126  LeuThrPheLeuAsnLeuLeuGlyAsnProTyrLysThrLeuGlyGlnThrSerLeuPhe 145
      509  ACAAACTAGCATCTTAGAGAACTCCCATTTGGACATCTCAAACT----- 556
      146  SerHisLeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIle 165
      557  -----TTGAAAGAACTTATGTGGCTCACAATCTT 586
      166  GlnArgLysAspPheAlaGlyLeuThrPheLeuGlnGlnLeuGlnIleAspAlaSerAsp 185
      587  ATCCAACTCTTCAAAATTACTGAGTATTTTCTAATCTGACCAATCTAGACGACTTGAC 646
      186  LeuGlnSerTyrGln---ProLysSerLeuLysSerIleGlnAsnValSerHisLeuIle 204
      647  CTTTCAGAGAAAG-----ATTCAAGATAT 673
      205  LeuHisMetLysGlnHisIleLeuLeuLeuGlnIlePheValAspValThrSerSerVal 224
      674  TATTCAGACAGACTGGGGTTCTTACATCAAAATGCCCTACTCATCTCTTTAGACCTG 723
      225  GluCysLeuGlnLeuArg-----AspThr 232
      734  TCCCTGAATCTTATGAACCTT-----ATCCAAACAGGCTGCAATTTTAAAGAAATTAAGCTT 787
      233  AspLeuAspThrPheHisPheSerGlnLeuSerThrGlyLysThrAsnSerLeu---Ile 251
      788  CATTAAGCTGACTTAAAGAAAT-----AATTTGATAGTTTA---AATGTATGAAG 835
      252  LysLysPheThrPheArgAsnValLysIleThrAspGlnSerLeuPheGlnValMetLys 271
      836  ACTTGT-----ATTCAGGCTCTGGCTGTTTAGAATCCATCGTTTGTTCTG----- 883
      272  LeuLeuAsnGlnIleSerGlyLeuLeuGlnLeuGlnPheAspArgCysThrLeuAsnGly 291
      884  ---GGAGATTTTGAAATGAGAAACTTGAAAAAGTTTGACAAATCTGCTTAGAGGCG 940
      292  ValGlyAsnPheArgLysAspAsnAspArgValIleAspProGlyLysValGln--- 310
      941  CTGTGCAATTTGACATTGAAGAATCCGATTAGCA-----TACTTAGACTCTACTC 994
      311  -----ThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyr--- 326
      995  GATGATATTAATTAATTAATTAATTTGTTGACAAATTTTCTTCAATTTTCCCTGGTAGT 1054
      327  ---AspLeuSerThrLeuTyrSerLeuThrGlnArgValLys-----Arg 340
      1055  GTGACTATTTGAAGGGTAAAGAACTTTTCTTATTAATTTCCGATGGCAACTTTAGAAATTA 1114
      341  IleThrValGlnLysAsnSerLysValPhe-----Leu 350
      1115  GTTAACGTAAATTTTGGACAGTTTCCACATGTGAACTCAATCTCTCAAAAGGCTTACT 1174
      351  ValProCysLeuLeuSerGln----- 357
      1175  TTCACTTCCAAAGGCTGGAAATGCTTTTTCAGAAATGATCTACCAAGCTTGAGTTT 1234

```

```

Db      358  -----HisLeuLysSerLeuGlnTyr 364
      1235  CTAGATCTCAGTAGAAAT-----GGCTTAGATTTCAAAGGTTGCTGTCT 1279
      365  LeuAspLeuSerGlnAsnLeuMetValGlnGlyTyrLeuLysAsnSerAlaCys----- 382
      1280  CAAAGGATTTTGGGACAAACAGCTTAAAGTATTTAGATCTGAGCTTCAATGATGTATTT 1339
      383  -----GlnAspAlaTyrProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 397
      1340  ACCATGAGTTCAAACTCTTGGGCTTTAGAACACTAGAACATCTGATTTCCAGACTTCC 1399
      398  -----HisLeu-----Ala 400
      1400  AATTGAAACAAATGATGATGAGTTTCAATTCATATCTATCACTGACAACTTCAATTAACCTT 1459
      401  SerLeuGlnLysThrGlyGln-----ThrLeuLeuThrLeuLysAsnLeuThrAsnIle 418
      1460  GACATTTCTCATATCATCACACAGAGTGTCTTCAATGGCATCTTCAATGGCTTGCCAGT 1519
      419  AspIleSerLys----- 422
      1520  CTCGAAGTCTTGAATAATGGCTGGCAATTTCTTTCAGAAAACTTCTTCCAGATATCTTC 1579
      423  -----AsnSerPheHisSer-----MetProGlnThrCys 432
      1580  ACAGAGCTGAGAACTTGACCTTCCGTCGACCTCTCATGTCACATGTCAGTGAAGCTGTCT 1639
      433  GlnThrProGlnLysMetLysTyrLeuAsnLeuSerSerThrArgIleHisSerValThr 452
      1640  -----CCAACAGCATTTAACTCACTCTCCAGACTTCCAGTACTAATATGAGCCAC 1690
      453  GlyCysIlePro-----LysThrLeuGlnIleLeuAspAlaSerAsn 466
      1691  AAC-----AAGCTTTCTTCAATGAT----- 1711
      467  AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGlnLeuTyrIleSerArg 486
      1712  ---ACGTTTCT---TATAAGTGTGAACTCCCTCCAGGTTCTTGATTAAC 1756
      487  AsnLysLeuMetThrLeuProAspAlaSerLeuLeuPheMetLeuLeuValLeuLysIle 506
      1757  AGTCTCAATCACAATATGACTTCCAAAAACAGAACTCAGACATTTTCCAAAGTACTTA 1816
      507  SerArgAsnAlaIleThrThrPheSerLysGlnGlnLeuAspSerPhe---HisThrLeu 525
      1817  GCTTCTTAATCTTACTCAAGATGACTTGTCTGTTGATCTTGGAACACAGACTTCTCTG 1876
      526  LysThrLeuGlnAlaGlyLysAsnAsnPheIleCysSerCysGlnPheLeuSerPheThr 545
      1877  CAATGATCAAGGACGAGAGGAGCTGTGGTGAAGTT-----GAAAGCA 1921
      546  Gln-----GlnGlnGlnAlaLeuAlaLysValLeuIleAspTyrProAlaAsn 561
      1922  ATGGAATGTGCAACACTTCCAGATTAAGAGGCACTCTGTGCTGAGTTTGAATATCAC 1981
      562  TyrLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581
      1982  -----TGTCAAGTAAATGAACCAATCATTTGCTGTGTGGTCTCAGTGTCTTGTGA 2032
      582  ValSerGlnCysHisArgIleAlaLeuValSerGlyMetCysCysAlaLeuPheLeuLeu 601
      2033  GATCTGTGTGACAACTTCTGCTATTAAGTTCTAT-----TTTCACTGATGCTTCTT 2086
      602  IleLeuLeuThrGlyAlaLeuCysHisArgPheHisGlyLeuTyrTyrMetLysMetLys 621
      2087  GCTGCTGCAATAAGTATGCTAGA-----GCTGAAACATC---TAT 2125
      622  TyrAlaTyrPheGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTyr 641
      2126  GATGCTTTGTTATCTACTCAAGCCAGATGAGAGACTGGGTAAAGATGACTAGTAAG 2185
      642  AspAlaPheValSerTyrSerGlnArgAspAlaTyrTyrValGlnLysAsnLeuMetValGln 661

```

```

QY      2186  AATTGTAAGAAGAGGGGTGCTCCATTGTCAGTCTGCTTCACATGACAGAGCTTATTCCTC      2245
DB      6682  GGUUUGUUAASnpheasnProphoPhySleCySleuHhISlyArGAspHeillepro      681
QY      2246  GGTGTGGCCATTGCTGCCAATCATCATTCATGAAGTTTCCATTAAGCCGAAAGGTGATT      2305
DB      682  GilySTripIleilleAspSenillele---AspSerilleglulysSerHhISlyTrVal      700
QY      2306  GTTGTGGTGTCCCGACACTTCATCCAGACCCGCTGGTGTATCTTTGAATATGAGATTGCT      2365
DB      701  PheValLeuSerGluAsnPhenValIysSerGluTrpCySlySerIgluLeuAspPheSer      720
QY      2366  CAGACCTGGACATTTCTTGACAGCTCGCTGCTGTGATCATCTTCATTTGCTTCGACAGAGTG      2425
DB      721  HIsPheArGlyLeuPheAsnSpIuAsnAsnApeAlaIleleuIleuLeuGluProlle      740
QY      2426  GAGAAAGACCTTCCTCAGCAGCAG--GTGGAGCTGTACCGCCTTTCAGCAGAAACACT      2482
DB      741  GilySlyAlaIleProGlnArGlyPheCySlyLeuArGlyIleMetAsnThrIysTrn      760
QY      2483  TACCTGGAGTGGAGAGACAGTGTCCCGGGCGGCACTTCCTGGAGAGACATCAGAAAA      2542
DB      761  TyIleuGluTrpProMetAspGluAlaGlnArGlyGluIlyPheTrpValAsnLeuArGala      780
QY      2543  GCCCTG 2548
DB      781  AlaIle 782

RESULT 5
US-09-949-016-8799
; Sequence 8799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMERPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMANS DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRF
; ORGANISM: Human
US-09-949-016-8799

Alignment Scores:
Pred. No.: 4,72e-49 Length: 775
Score: 539.00 Matches: 218
Percent Similarity: 41.22% Conservative: 120
Best Local Similarity: 26.59% Mismatches: 264
Query Match: 6.28% Indels: 218
DB: 4 Gaps: 37

US-09-396-985B-1 (1-4868) x US-09-949-016-8799 (1-775)
QY      245  ATCCCGACAACTCCCTTCATCCACCAAGAACTGAGCTTATATCCCTGAGG 304
DB      81  HleProSerGlyLeuHrGluAlaValIysSerLeuAspLeuSerAsnSngIleThr 100
QY      305  CATTATGAGCAATATGCTTCTTCAGTTCCCGAAGCTGAGAGTGCTGATTAATCAGG 364
DB      101  TyIleSerAsnSerAspLeuGlnArGlyCySValAsnLeuGlnAlaLeuValIleuTrnSer 120
QY      365  TGTAAGATCCAGACAAATTAAGATGGGCAATACAGAGCCTTAAGCCACTCTTACCTTA 424

```

Db		121	AsnGlyIleAsnThrIleGlnGlnIleuSerPheSerSerLeuGlySerLeuGlnHisLeu	140
QY		425	ATATTTGACAGAAAACCCCATCCAGAGTTTACCCTGGAGGCTTTTCTGACATCAAGT	484
Db		141	AspLeuSerTyrAsnTyrLeuSerAsnLeuSerSerTyrPheLeuProLeuSerSer	160
QY		485	TTACAGAACTG-----GTGGCTCTGGAG	508
Db		161	LeuThrPheLeuAsnLeuLeuGlyAsnProTyrIleThrLeuGlyGlnThrSerLeuPhe	180
QY		509	ACAAATCTGACATCTCTAGAGACTTCCCATGTGGACATCTCAAAACT-----	556
Db		181	SerHisLeuThrIleuLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrIle	200
QY		557	-----TTGAAAGAACTTAAATGTGGCTCACAACTCTT	586
Db		201	GlnIleArgAspPheAlaGlyLeuThrPheLeuGlnGlnIleAspAlaSerAsp	220
QY		587	ATCCAAATTTTCAAAATTACTGAGTATTTTCTAATCTGACCAATCTTGAGACCTTGAC	646
Db		221	LeuGlnSerTyrGln-----ProlYserLeuYserIleGlnAsnValSerHisLeuIle	239
QY		647	CTTTCAGCAACAAG-----ATTCAAAAGTAT	673
Db		240	LeuHisMetIysGlnHisIleLeuLeuLeuGlnIlePheValAspValThrSerSerVal	259
QY		674	TATTGACACAGACTTCCGGGTTCTACATCAAAATGCCCTTACAACTCTTTAGACCTG	733
Db		260	GlnIysLeuGlnIleuLeuArg-----AspThr	267
QY		734	TCCCTGAATCCTATGAACTTT-----ATCCAACCGAGTGCAATTAAAGAAATTAGGCTT	787
Db		268	AspLeuAspThrPheHisPheSerGlnLeuSerThrGlyIleThrAsnSerLeu---Ile	286
QY		788	CATTAAGCTGACTTTAAGAAAT-----AATTGGATAGTTA--AAATGTAATGAA	835
Db		287	LysIysPheThrPheArgAsnValIleThrAspGlnSerLeuPheGlnValMetIys	306
QY		836	ACTGGT-----ATTCAAGGCTGGCTGGTTTAGAAGTCCATCGTTGGTCTG-----	883
Db		307	LeuLeuAsnGlnIleSerGlyLeuLeuGlnIleuGlnIlePheAspArgCysThrLeuAsnGly	326
QY		884	---GGAGAAATTAGAAATGAAGAAACTTGGAAAAATTGACAAATCTGCTTAGAGGCG	940
Db		327	ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyIleValGlu---	345
QY		941	CTGTGCAATTTGACCATTTGAAGAAATCCGATTAGCA-----TACTTAGACTATCACTC	994
Db		346	-----ThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyr-----	361
QY		995	GATGATATTAATGACTTATTAATGTTTGGCAAAATGTTCTTCATTTTCCCTGGTGAGT	105
Db		362	---AspLeuSerThrLeuTyrSerLeuThrGlnArgValIys-----Arg	375
QY		1055	GTGACTATTGAAAGGATAAAAGACTTTTCTTATATTTCGATGGAGCAATTTAGAAATTA	1114
Db		376	IleThrValGluAsnSerIysValPhe-----Leu	385
QY		1115	GTTACTGTATAATTGGACAGTTTCCACATTTGAAACTCAAACTCTCAAAAGCTTACT	1174
Db		386	ValProCysLeuLeuSerGln-----	392
QY		1175	TTCACTTCGCAACAAAGGTGGAGATGCTTTTCAAGAATGTGATCTTACCAAGCCTTGAGTTT	1233
Db		393	-----HisLeuIysSerLeuGlnIleTyr	399
QY		1235	CTAGATCTCAGTAGAAAT-----GGCTTGAGTTTCAAAAGTTGCTGCTTCT	1279
Db		400	LeuAspIleuSerGlnIleAsnLeuMetValGlnIleTyrIleuYAsnSerAlaCys-----	417
QY		1280	CAAAATGATTTTGGGACACCAAGCTTAAAGTATTTAGATCTGAGCTTCAATGCTGTATTT	1338

418 -----GluAspAlaIrrProSerLeuGlnThrLeuIleuArgGlnAsn----- 432
QY 1340 ACCATGAGTTCAAACTTTGGGCTTAGAACAACCTGATGATTTCCAGCATTC 1399
Db 433 -----HisLeu-----Ala 435
QY 1400 AATTGAAACAATGAGTGGTTTCAGTATTCCTACATCTGAGAACCTCATTTACCT 1459
Db 436 SerLeuGlnIlyThrLeuGln-----ThrLeuIleuThrLeuValAsnIle 453
QY 1460 GACATTTCTCATCTGACACAGAGTTGCTTCAATGGCATCTTCAATGGCTTGCAGT 1519
Db 454 AspIleSerIys----- 457
QY 1520 CTGGAAGTCTGAAAATGGCTGGCAATCTTTCCAGAAAACCTTCCAGATATCTTC 1579
Db 458 -----AsnSerPheHisSer-----MetProGluThrCys 467
QY 1580 ACAGAGCTGAGAACTTGACCTTCTGAGACCTCTCTCAGTGTGACAGAGCTTGTCT 1639
Db 468 GlnTrpGluIlySerLeuIlyThrLeuAsnLeuSerThrArgIleHisSerValThr 487
QY 1640 -----CCAAAGCATTTAACTCACTCTCCAGTCTTCCAGTACTTAATATAGCCAC 1690
Db 488 GlyCysIlePro-----LysThrLeuGlnIleLeuAspValSerAsn 501
QY 1691 AAC-----AAGCTTTTCATTTGAT----- 1711
Db 502 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuIlyGlnLeuTyrlleSerArg 521
QY 1712 -----ACGTTTCTCT--TATTAAGTGTCTGAACTCCCTCCAGGTTCTTGATTAAC 1756
Db 522 AsnIlyLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValLeuIlySile 541
QY 1757 AGTCTCAATCACTAATGACTCTCCAAAAACAGAACTACAGCATTTTCCAGTACTCTA 1816
Db 542 SerArgAsnAlaIleThrThrPheSerIyGlnIleuAspSerPhe--HisThrLeu 560
QY 1817 GCTTTCTTAATCTTACTGAGATGACTTGTGCTTGTATCTGTGAACACAGATTTTCCTG 1876
Db 561 LysThrLeuGlnIlyAlaGlyIlyAsnAsnPheIleCysSerCysGlnPheLeuSerPheThr 580
QY 1877 CAATGATCAAGAGCAGAGCAGCTCTGTGGAAGTT-----GAAACA 1921
Db 581 Gln-----GluGlnGlnAlaLeuAlaIlyValLeuIleAspTrpProAlaAsn 596
QY 1922 ATGGAATGCAACACCTTGATAGACAGGAGCTGTGCTGTGAGTTGAATATCAC 1981
Db 597 TyrLeuCysAspSerProSerHisValArgGlyGlnGlnIlyAlaAspValArgLeuSer 616
QY 1982 -----TGTCAAGATGAATAGACATCATTTGGTGTGCGGTCCCACTGTGCTGTA 2032
Db 617 ValSerGlnCysHisArgThrAlaLeuValSerIlyMetCysValAlaLeuPheLeuLeu 636
QY 2033 GATAGCTTTGTATCTCTCAAGCAGATGAGACTGGGTAAAGATGAGCTTATTAAG 2185
Db 637 IleuLeuIlyThrGlyValLeuCysHisArgPheHisIleIlyLeuTrpIlyMetIlySerMet 656
QY 2087 GCTGGCTGATTAAGTATGTA-----GGTAAAATC--TAT 2125
Db 657 TrpAlaIrrPheGlnAlaIlyAspGlyProArgIlyAspAlaProSerArgAsnIleCysTy 676
QY 2126 GATAGCTTTGTATCTCTCAAGCAGATGAGACTGGGTAAAGATGAGCTTATTAAG 2185
Db 677 AspAlaIleValSerIySerGlnArgAspAlaTyrrIlyValGlnAsnLeuMetValGln 696
QY 2186 AATTAGAAAGAGGGCTCCATCTTCAAGCTGTGCTTCACTACAGAGCTTATTAAGCT 2245
Db 697 GlnLeuGlnIlyAsnPheAsnProProPheIlyLeuIlySerIlyValArgPheIleIlePro 716
QY 2246 GGTGTGGCAATGTCTGCAACATCATCAGTAAGGTTTCCATAAAGCCGAAAGTGAT 2305
Db 717 GlyIlySerTrpIleIleAspAsnIleIle--AspSerIleGlnIlySerHisIlyThrVal 735

QY 2306 GTTGTGTGTCCAGACTTTCATCCAGACCGGTGTGATCTTGAATATGAGATTCCT 2365
Db 736 PheValIleuSerGlnAsnPheValIlySerGlnTyrrCysIlyGlnLeuAspPheSer 755
QY 2366 CAGACTGGCAGCTTCTGAGCAGTGTGCTGTATCATCTTCAATGCTCCGAGAGCTG 2425
Db 756 HisPheArgLeuPheAspGlnIlyAsnAsnAspAlaIleIleuIleLeuGlnIleProIle 775

RESULT 6
US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: HOLTSMAN, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: MEI-019
; CURRENT APPLICATION NUMBER: US/09/063,950C
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 605
; TYPE: PRF
; ORGANISM: Papio hamadryas
US-09-063-950-5

Alignment Scores:
Pred. No.: 9,46e-25 Length: 605
Score: 316.00 Matches: 157
Percent Similarity: 39.04% Conservative: 94
Best Local Similarity: 24.42% Mismatches: 242
Query Match: 3,688 Indels: 150
Gaps: 23

US-09-396-985B-1 (1-4868) x US-09-063-950-5 (1-605)

QY 200 GTTCCATATATTAATCATGATGAGCTGAAATTTCTAACAATCCCGACAACCTC 259
Db 53 ValAsnGlnLeuSerValPheCysSerSerArgAsnLeuThrArgLeuProAspGlyIle 72
QY 260 CCGTTCTCAACAAGAACCTTGACCTGACCTTAAATCCCTGAGGACTTATGAGCACTAT 319
Db 73 ProGlyIlyThrGlnAlaIleuThrPheLeuAspSerAsnAsnLeuSerIleProProAla 92
QY 320 AGCTTCTTCAAGTTCCAGACACTGCAAGTCTGTGATTTATCCAGGTGTAAATCCAGACA 379
Db 93 AlaPheArgAsnLeuSerSerIleuAlaPheLeuAsnLeuGlnGlyIlyGlnLeuGlySer 112
QY 380 ATTGAAGATGGGGCATATGACAGCCTTAAGCACCCTCTAACCCTTAATATTTGACAGGAAC 439
Db 113 LeuGlnIlyProGlnIlyAlaLeuLeuGlnIlyLeuGlnAsnLeuCysHisIleuHisIleuGlnIlyArgAsn 132
QY 440 CCCATCCAGAGTTTAACTCCCTGGAGCCTTTCT----- 472
Db 133 GlnLeuArgSerIleuAlaValGlnIlyThrPheAlaIlyThrProAlaLeuAlaLeuLeuGly 152
QY 473 -----GGACTATCAAGTTA 487
Db 153 LeuSerAsnAsnArgIleuSerArgIleuGlnIlyAspGlyLeuPheGlnIlyLeuGlnIlyAsnLeu 172
QY 488 CAGAACTGTGTGCTGTGAGACAAATCTAGACATCTCTAGAGACTTCCCAATGGACAT 547
Db 173 TrpAspLeuAsnLeuGlnIlyTrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGly 192
QY 548 CTCAAAACTTTGGAAGAAGCTTAATGTGCTCAATCTTATCCAACTTTCAATTAATTCCT 607
Db 193 LeuGlnIlyLeuArgIlyLeuValLeuAlaGlyIlyAsnArgLeu--AlaIlyThrLeuGlnPro 211
QY 608 GAGTATTTTCTTAATCTGACCAATCTTACAGCACTTGACCTTTCCAGCAACAAGATTCAA 667
Db 212 AlaLeuPheSerGlyLeuAlaGlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArg 231

QY	668	AGATTTATGTCAGACAGCTGGGGGTTCTACATCAAAAGGCCCTCAATCTCTTTA	727
Db	232	AlaIle-----LysAlaAsnValPheAlaGlnLeuProArgLeuGln---LysLeu	247
QY	728	GACCTGTCCTGAATCTATGAACTTTATCCAAACAGGTGCATTTTAAAGAAATTAGC---	784
Db	248	TyrLeuAspArgAsnLeuIleAlaValAlaProGlyAlaPheLeuGlyLysAla	267
QY	785	CTTCATAGCTGCATTTTAAGAAATTAATTTGATTAATTTAAATGTAAGAAACTGTAT	844
Db	268	LeuArgTyrPheLeuAspLeuSerHisAsn--ArgValAlaGlyLeuLeuGlnAspThrPhe	286
QY	845	CAAGCTCTGGCTGGTTTGAAGATCCATCGTTTGGTCTTGGAGAAATTTAGAATGAAGA	904
Db	287	ProGlyLeuLeuGlyLeuArgValLeuArgLeu-----	297
QY	905	AACTTGGAAAAGTTTGACAAATCTGCTCTAGAGGGCCCTGTCATTTGACCATGAAGA	964
Db	298	-----SerHisAsnAlaIleAlaSerLeuArgProArgThrPheGlnLys	312
QY	965	TTCCGATTAGACATCTTAGACATCACTCGATATATTTAGATTATTTAATTGTTTG	1022
Db	313	Leu-----HisPheLeuGlnGluLeu-----	319
QY	1025	ACAAATGTTTCTTCATTTTCCCTGGTGAGTGATCTTAAGAAAGGTAAAGACTTTTCT	1084
Db	320	-----GlnLeuGlyHisAsnArgIleArgGlnLeuAlaGlnArgSer	333
QY	1085	TATATATTTCCGATGGCAACATTTAGAATTAAGTTAACTGTAATTTGGACAGTTTCCACA	1144
Db	334	PheGlu---GlyLeuGlyGlnLeuGlyValLeuThrLeuAspHisAsnGlnLeuGlnLys	352
QY	1145	TTGAACATCAATCTCTCAAAAAGGCTTATCTTCACTTCC-----ACAAAGGTGGAGAT	1198
Db	353	ValLysValGlyAlaPheLeuGlyLeuThrHisValAlaValMetHisLeuSerGlyAsn	372
QY	1199	GCTTTTTCAGAACTTATCTACCAAGCCTTGAGTTTTCAGATCTCAGTAGA--AATGAC	1255
Db	373	CysLeuArg-----AsnLeuProGlnGlnValPheArgGlyLeuGlyLysLeuHisSer	390
QY	1256	TTGAGTTTCAAGGTTGCTGT-----TCTCAAGATATTTTGGGCAACAC	1300
Db	391	LeuHisLeuGlnGlySerCysLeuGlyAlaArgIleArgProHisPheAlaGlyLeuSer	410
QY	1301	AGCCTAAAGTATTTAGATCTAGCTTCATGAGTGTTATTCACATGATTCAAACTTCTG	1360
Db	411	GlyLeuArgArgPheLeuLysAspHisnGlyLeuValGlyIleGlnGlnGlnSerLeu	430
QY	1361	---GGCTTAGAACATTAACATCTGGATTTCCAGCATTCCTCAATTTTAAACAAATGAGT	1417
Db	431	TyrGlyLeuAlaGlnLeuLeuGlnLeuAspLeuThrSerAsnGlnLeu-----	446
QY	1418	GAGTTTTCAGATTTCTATCACTCAGAAACCTCATTTACCTTGAATTTTCATCTAC	1477
Db	447	-----ThrHis-----	448
QY	1478	ACCAGAGTTGCTTCATAGCATCTTCATGAGCTTTCAGCTTCGAACTTCGAAATG	1537
Db	449	LeuPro-----HisGlnLeuPheGlnGlyLeuGlyLysLeuGlnTyrLeuLeuLeu	465
QY	1538	GCTGGCAATTTCTTTCAGAGAAAATCTTCTCA--GATATCTTACAGAGCTGAGAAC	1594
Db	466	SerHisAsnArgLeuAlaGln-----LeuProAlaAspAlaLeuGlyProLeuGlnArg	483
QY	1595	TTGACCTTTCGAGACCTCTCAGTGTCACCTGAGAGAGTTGTCTCCACAGCAATTTAAC	1654
Db	484	AlaPheTyrPheLeuAspValSerHisAsnArgLeuGlnAlaLeuProGlySerLeuLeuAla	503
QY	1655	TCACCTTCCAGCTTTCAAGTACTAAATATGAGCCACAACAACTTTTTCATTTGATGATCG	1714
Db	504	SerLeuGlyArgLeuArgTyrLeuAsnLeuArgHisn-----SerLeuArgThr	520

Qy	1715	TTTCTTAAATGATGTGAACTCCCTCAGGTTCTTATTACAGTCTCAATCACATATG	1774
		:::	
Db	521	PheThrProGln-----	524
Qy	1775	ACTTCCAAAAAACAGAACTACAGACATTTTCCAAGTAGTCTAGCTTTCTTAATCTTACT	1834
Db	525	-----ProProGlyLeuGluArgLeuTyrPheGlu	534
Qy	1835	CAGAACTCTTGTCTTACTGTGAACACCAGAT-----	1870
		:::	
		:	
		:::::	
Db	535	GIyAnbProTyrPheCysSerCysProLeuIlyAlaLeuArgPheAlaLeuGlnAsn	554
Qy	1871	-----TTCTTCGCAATGATC-----AAGAGCCAGAGGCACTC	1903
Db	555	ProSerAlaValAlaProArgPheValGlnAlaIleCysGlnIlyAspAspCysGlnProPro	574
Qy	1904	TTTGTTGGAAGTTGAACAAATGGAATGTGCAAACCTTCAATATAGAAGGGCATGCTGTG	1963
		:::	
		:::	
Db	575	ValIlyrThrTyrAsnAsnIleThrCysAlaSerProGluValAlaGlyLeuAspLeu	594
Qy	1964	CTGAGTTTG	1972
Db	595	ArgAspLeu	597

```

RESULT 7
US-09-949-016-10995
: Sequence 10995, Application US/03949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01307
: CURRENT APPLICATION NUMBER: US/09/949,016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10995
: LENGTH: 623
: TYPE: PRT
: ORGANISM: Human
US-09-949-016-10995

```

Alignment Scores:	
Pred. No.:	1,54e-23
Score:	305.00
Percent Similarity:	37.87%
Best Local Similarity:	24.26%
Query Match:	3.56%
DB:	4
	Gaps: 28
	Length: 623
	Matches: 171
	Conservative: 96
	Mismatches: 260
	Indels: 178

US-09-396-985B-1 (1-4868) x US-09-949-016-10995 (1-623)

QY	113	GCCTCGCGCTGAGCT-----GGAGCTGTGATCCAGCCATGAGCTTCTCTCTCTGC	163
Db	16	AlAcGArGMeAlaLeuArGlyGlyLeuAlaLeuAlaLeuAlaLeuSerTyr	35
QY	164	GTGAGAG-----CCGAAAGCTGGAG-----	188
Db	36	ValAlaLeuGlyProArGSerLeuGluGlyAlaAspProGlyThrProGlyAlaGlu	55
QY	185	-----CCCTGCGCTG-----GAGGTGGTTCCTCAATATTACT	214
Db	56	GlyProAlaCyAspProAlaIaIaCySerValCySerTyrAspAspAlaIaAspGluLeuSer	75
QY	215	TATCATGATGATGAGGTGAATTCTTACAAAAATCCCCGACAACTCCCTTCTCAACGAG	274


```

; LENGTH: 907
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-264

Alignment Scores:
Pred. No.: 2,97e-23 Length: 907
Score: 303.50 Matches: 194
Percent Similarity: 36.00% Conservative: 116
Best Local Similarity: 22.53% Mismatches: 285
Query Match: 3.54% Indels: 266
DB: Gaps: 36

US-09-396-985b-1 (1-4868) x US-09-170-496D-264 (1-907)

QY 32 TCMAAGCGTATGCAACGACGCG-----ATTGACAGGCGCACTGCTGCACAAA 82
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 19 AlarhrlgllyserProargserglvalleuuarlglyCysProthrhisCys 38
QY 83 ACCAGTGAAGATGCGCAGAGATGTCGCTCGCGCTGGCGTGGAGCTGTGATCCA 142
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 39 HisCysgluProaspbglyArgmetleu----- 47
QY 143 GCCATGGCCTTCTCTCTCGTGAGACCAAGAACTGGAGCCCTGCGTGAAGTGTT 202
   47 ----- 47
Db 203 CCTAATATTACTTATCAATGCAATGAGCTGAATTTTCACAAAATCCCGCAAACTTCCC 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 48 -----LeuArgvalAspCysSerAspLeuglyLeuSerIleuProSerAsnLeuSer 65
QY 263 TTCTCAACCAAGAACCTGACCTGAGCTTAATCCCTGAGCATTTAGCAGCTATAGC 322
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 ValPheThrSerIyrleuAspLeuSerMetAsn----- 76
QY 323 TTCTCAGTTTCCCAAGCTGACAGTGCATTTATCCAGTGTGAATTCAGACAAATT 382
   77 ----- 77
Db 383 GAAGATGGGCAATATGACGCTTAAGCCTCTCTAATCTTATATTGACAGAAACCC 442
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 82 LeuProAsnProleuProSerIleuArgPheleuGlulLeuArgleuAlaGlyAspAla 101
QY 443 ATCCAGATTTAGCCCTGGAGGCTTTTGTGACTATCAAGTTTACAGAACTGGTGGCT 502
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 102 LeuThrIyrIleProIySglYalAlaPheThrIglYleuIyrSerleuIySvalleuMetleu 121
QY 503 GTGAGACAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAACTTTGAA 562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 GluAsnAsnIleuArgHisValProThrGluAlaIleuGlInAsnleuArgSerleuGlIn 141
QY 563 GAATTAATGTGGCTGACATCTTATTCATCTTTCAATTAACCTGATTTTTTCTAAT 622
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 142 SerleuArgleuAspAlaAsnHisIle-----SerIyrValProProSerCysPheSerGly 160
QY 623 CTGACCAATCTAGAGCACTTGACCTTTCCAGCAACAAGATTCAAAGTATTATTGACA 682
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 161 LeuHisSerleuArgHisleuThrPleuAspAspAsnAlaIleuThrGluIleProValGln 180
QY 683 GACTTGGGGTCTTATCAATCAATGCCCCCTACTCAATCTCTTTAGAAGCTGCTCAAT 742
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 AlaPheArgSerleuSerAlaIleuGlIn-----AlaMetThrleuAlaIleuAsn 196
QY 743 CCTATGAACCTTATCCACACAGGTGCATTTAAAGAAATT--AGCTTCATAAGCTGACT 799
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 LysIleHisIleIleProAspIyrAlaPheGlyAsnleuSerSerleuValIleuHis 216
QY 800 TTAGAAGATTAAT--TTTGAATGTTTAATGTATGAAGCTGTATTTCAAGGTGGCT 856
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 217 LeuHisAsnAsnArgIleHisSerleuGly-----LysIyScyPheAspGlyleuHis 234
QY 857 GGTTAGAAGTCCATCGTTGGTTCGGAGAAATTTAGAATGAAGAACTTGAAGAG 916
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db 235 SerleuGlulThrleuAspleu-----AsnIyrAsnAsnleuAspGlu 248
QY 917 TTGACAAATCTGCTCTAGAGGCTGTGCAATTGACATTGACAAATTCGATTAGCA 976
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 Phe--ProThrAlaIleArgThrleuSerAsn-----LeuIyS 260
QY 977 TACTTAAGTACTACTCTGATGATATATTATGACTTA-----TTTAATTGTTTG 1024
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 261 GluIleGlyPheHisSerAsnAsnIleArgSerIleProGluIyAlaPhe----- 277
QY 1025 ACAATGTTTCTTCATTTTCCCTGTGAGTGCATTAAT--GAAGGGTAAAAAGCTTT 1081
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 278 -----ValGlyAsnProSerleuIleThrIleHisPheIyrAspAsnProIleGlnPhe 295
QY 1082 TCTTATTAATTTGGAGGCAACATTTAGAATTAAGTTAACTGTAAATTTGGACGTTTCCC 1141
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 296 ValGlyArgSerAlaPheGlnHisleuPro-----GluLeuAsp 308
QY 1142 ACATTGAACCTCAAAATCTCTCAAAAGCTTACTTTCATCTTCCAAACAAAGTGGAAATGCT 1201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 ThrleuThrleuAsnIyAlaSerGlnIleThr----- 319
QY 1202 TTTTCAAGATTTGATCTACCAAGCCTTGAGTTTCTAGATCTCAGTGAATGCGTTGAGT 1261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 320 -----GluPheProAspLeuThr----- 325
QY 1262 TTCAAGGTTCGTCTTCAAGATGATTTTGGGACCAACGCTTAAGTATTAGATCTG 1321
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 326 -----GlyThrAlaAsnleuIleuSerleuThrleu 335
QY 1322 AGCTTCMAATGAGTGTATTCATAGATGATCAAACTTCTGAGC--TTAGAACAACTAGAA 1378
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 336 ThrGlyAlaGlnIleSerSerleuProGlnThrIyAlCysAsnGlnleuProAsnleuGlIn 355
QY 1379 CATCTGATTTCCAGATTCATTTGAACAAGATGAGTTCCTGATTTCTTATCTA 1438
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 356 ValIleuAspLeuSerIyrAsnleuIleuGluAspLeuProSerPheSerValCysGlnIyS 375
QY 1439 CTCAGAAACCTCATTTACCTGATTCATTTCTCATCTCACACAGATTCCTTCANTGGC 1498
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 376 LeuGlnIyS-----IleAspLeuArgHis----- 383
QY 1499 ATCTTCATAGGCTTGTCCAGATCTCGAAGCTTGAAGATGGCTGCAATTTCTTCCAGGAA 1558
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 384 -----AsnGlnIleIyrGluIleIySval----- 391
QY 1559 AACTCTCTTCCAGATATCTTCAACAGCTGAGAACTTGACCTTCTGACCTCTCTCAG 1618
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 392 -----AspThrPheGlnGlnleuIleuSerleuArgSerleuAsnleuAlaIyr 407
QY 1619 TGTCAACTGAGACAGTGTCTCCAAACAGATTTAACTCATCTCCAGTCTTCAAGTACTA 1678
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 408 AsnIySAlaIleIleHisProAsnAlaPheSerThrleuProSerleuIleIySleu 427
QY 1679 AATATGAGCACAACAACATTTTTCATAGATACCTTTCTTATTAAGTGTGAACTCC 1738
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 428 AspLeuSerSerAsn-----LeuIleuSerSerPheProIleThrGlyleuHisGly 444
QY 1739 CTCGAGTTCCTTGATTACGCTCATCATCAATATGACTTCCAAAAACAGAACTACAG 1798
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 445 LeuThrHisIleuIySleuThrGlyAsnHisAlaIleuGlnSerleuIleSerSer--Glu 463
QY 1799 CATTTTCCAGATGATCTTACTCTTAAATCTTACTCAAGAAAGACTTTCCTGTACTGCT 1858
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 464 AsnPheProGlu-----LeuIySValIleGluMetProIyrAlaIyrGlnCys 479
QY 1859 -----GAACACACAGATTTCTCTCAATGATCAAG----- 1888
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 480 CysAlaPheGlyValCysGluAsnAlaIyrIySIIeSerAsnGlnIyrAsnIySglYAsp 499
QY 1889 -----GACGAG 1894
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 500 AsnSerSerMetAspAspLeuHisIySylSAspAlaGlyMetPheGlnAlaGlnAspGlu 519
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY      1895 AGGCAGCTC-----TTGGTGAAGTTGAACGAATG 1924
           ||| |||
Db      520 hrgAspIeuGluaSpheLeuLAspPheGluGluAspLeuYsAlaLeuHisSerVal 539
QY      1925 GAATGTGCAACACCTTCAGATTAAGCAGGCGATCCCT----- 1960
           ||| |||
Db      540 GlncYs---SerProSerProGlyProPheLeuProCyseGluHisLeuLeuAerGlyTyr 558
QY      1961 -----GTGCTGAGTTGAATATCACTCTGTCAGATGAATTAAG 1996
           ||| |||
Db      559 LeuIleArgIleGlyValTyrPheTLeuAlaValLeuAlaLeuThrCys-----AsnAla 576
QY      1997 ACCATCATTTGTTGTCGCTCCTCAGTGTCTTGATGATCTTTGATGAGCATTTGATGTC 2056
           ||| |||
Db      577 LeuValThrSerThrValPheArgSerProLeuTyrIleSerProIleuYsLeuLeuIle 596
QY      2057 TATTAAGTTCTAATTTTCACTGATGCTT-----CTTGCTGCTGCTGC 2095
           ||| |||
Db      597 GlyValIleAlaAlaValAsnMetLeuThrGlyValSerSerAlaValLeuAlaGlyVal 616
QY      2096 ATTAAGAT-----GTTAAGAT 2113
           ||| |||
Db      617 AspAlaPheThrPheGlySerPheAlaArgHisGlyAlaTyrTrpGluAsnGlyValGly 636
QY      2114 GAAACATCTATGATGCTTTGTTATCTACTCAAGCAGCATGAGCATGGATTAAGGAAT 2173
           ||| |||
Db      637 CysHisValIleGlyPheLeuSerIlePheAlaSerGluSerValPheLeuLeuThr 656
QY      2174 GACCTAGTAAAGATTAGAGAAGGGG--TGCTTCATTTGAGCTGCTGCTTCACTAC 2230
           ||| |||
Db      657 -----LeuAlaIleLeuGluArgGlyPheSerValTyrSerAlaYsPheGluThr 674
QY      2231 AGAGACTTATTTCCCGGTGGCCATTGCTGCCAATCATCCATGAAGTTTCCATTA 2290
           ||| |||
Db      674 rLySAla-----ProPheSerSerLeuYsValIleIle-- 685
QY      2291 AGCCGAAAGGTGATGTTGTGTGTCGCCAGACTTCATCCAGACCGCTGATCTT 2350
           ||| |||
Db      686 -----LeuLeuYsAlaLeuAlaLeuThrMetAlaAlaValProle 700
QY      2351 G 2351
Db      700 u 700

RESULT 9
US-09-170-496D-278
; Sequence 278, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170, 496D
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 278
; LENGTH: 907
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-278

Alignment Scores:
Pred. No.: 2,97e-23 Length: 907
Score: 303.50 Matches: 194
Percent Similarity: 36.00% Conservative: 116
Best Local Similarity: 22.53% Mismatches: 285
Query Match: 3.54% Indels: 266
DB: 4 Gaps: 36

```

```

US-09-396-985B-1 (1-4868) x US-09-170-496D-278 (1-907)
QY      32 TCMAAGCGTGATAGCAACACGACG-----ATTCAACAGGCGCACATGCTGTCACAAA 82
           ||| |||
Db      19 AlaTrpGlyGlySerSerProArgSerGlyValLeuLeuAlaGlyCysProThrHisCys 38
QY      83 ACCAGTGAAGATGATGCGCAGATGATGTCGCTGCGCGCTGCGGACCTGTGATCCCA 142
           ||| |||
Db      39 HisCysGluProAspGlyArgMetLeu----- 47
QY      143 GCGATGCGCTTCTCTCTGCTGAGACCAAGAAAGCTGGAGCCCTGCTGAGGTGTT 202
           ||| |||
Db      47 ----- 47
QY      203 CCTAATATTACTTATCATGATGAGCTGATTTTCTACAAATGCCGACAACTCCGCC 262
           ||| |||
Db      48 -----LeuArgValAspCysSerAspLeuGlyLeuSerGluLeuProSerAsnLeuSer 65
QY      263 TTCTCAACCAAGAACCTGGACCTGAGCTTAAATCCCTGAGGCAATTGAGCAGTATAGC 322
           ||| |||
Db      66 ValPheThrSerTyrLeuAspLeuSerMetAsn----- 76
QY      323 TTCTTCAAGTTCCAGAACTGCAAGCTGCTGATTTATCCAGGTGGAATTCAGACAAAT 382
           ||| |||
Db      77 -----AsnIleSerGluLeu 81
QY      383 GAAAGATGGGCGCATATCAGACGCTTAAGCCACTCTCTACTTATATATGACAGAAACCCC 442
           ||| |||
Db      82 LeuProAsnProLeuProSerLeuArgPheLeuGluGluLeuArgLeuAlaGlyAsnAla 101
QY      443 ATCCAGAGTTTGAAGCCCTGGAGACCTTTTGTGACTATCAAGTTTACAGAAAGCTGGTGCST 502
           ||| |||
Db      102 LeuThrTyrIleProIySelYalAlaPheThrGlyLeuTyrSerLeuYsValLeuMetLeu 121
QY      503 GTGGAGACAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAAA 562
           ||| |||
Db      122 GluAsnAsnGluLeuAsnArgHisValProThrGluAlaLeuGluAsnLeuArgSerLeuGlu 141
QY      563 GAATTAATGTGGCTCAACAATCTTATCCAAATCTTCAAAATTCAGAGATTTTCTAAT 622
           ||| |||
Db      142 SerLeuArgLeuAspAlaAsnHisIle--SerTyrValProProSerCysPheSerGly 160
QY      623 CTGACCAATCTAGAGACTTGGACTTTCACAGAACAGATTCMAAGTATTATTATTCACA 682
           ||| |||
Db      161 LeuHisSerLeuArgHisLeuThrPheAspAspAlaLeuThrGluIleProValGlu 180
QY      683 GACTTGGGGTTCTATCATCAAAATGCCCTACTCAATCTCTTTAGACTGTGCCGTAAT 742
           ||| |||
Db      181 AlaPheArgSerLeuSerAlaLeuGlu-----AlaMetThrLeuAlaLeuAsn 196
QY      743 CCTATGAATCTTATCCAAACAGGTGATTTAAAGAAAT--AGCTTCATAAGCTGAGCT 799
           ||| |||
Db      197 LysIleHisHisIleProAspTyrAlaPheGlyAsnLeuSerSerLeuValIleuHis 216
QY      800 TTAAGAAATTAAT--TTGATAGTTTAAATGTAATGAAGAACTTGATTAAGCTGTGCTGCT 856
           ||| |||
Db      217 LeuHisAsnAsnArgIleHisSerLeuGly-----LysLysCysPheAspGlyLeuHis 234
QY      857 GGTTTGAAGATCCATGTTGGTTGCTTGGAGAAATTGAAGATGAAGAACTTTGAAAAG 916
           ||| |||
Db      235 SerLeuGluThrLeuAspLeu-----AsnTyrAsnAsnLeuAspGlu 248
QY      917 TTGACAAATTCGCTTATAGAGGCGCTGTGCAATTTGACATTTGAAGAAATTCGATTAAGCA 976
           ||| |||
Db      249 Phe--ProThrAlaIleArgThrLeuSerAsn-----LeuLys 260
QY      977 TACTTACATCACTGATGATGATATATTATGACTTA-----TTAATGTGTTG 1024
           ||| |||
Db      261 GluLeuGlyPheHisSerAsnAsnIleArgSerIleProGluLysAlaPhe----- 277
QY      1025 ACAAAATGTTCTTCAATTTTCCCTGCTGAGTGTGACTAAT--GAAAGGGTAAAGAACTTT 1081
           ||| |||

```

Db 278 -----ValGlyAsnProSerLeuIleThrIleHisPheTyraAsnProIleGlnPhe 295
 QY 1082 TCTTAATTAATTCGGATGACATTTAGATTAAGTAAATTTGGACAGTTTCCC 1141
 Db 296 ValGlyArgSerAlaPheGlnHisLeuPro-----GluLeuArg 308
 QY 1142 ACATGAAATCAAAATCTCTCAAAAGGCTTCTTCACTTCAACAAAGGTGGAAATGCT 1201
 Db 309 ThrIleuThrLeuAsnGlyAlaSerGlnIleThr----- 319
 QY 1202 TTTTCAGAACTGATCTACCAAGCCTTGACTTCTAGATCTCAGTAGAAATGGCTTGAGT 1261
 Db 320 -----GluPheProAspLeuThr----- 325
 QY 1262 TTCAAAAGTTGCTGTTCTCAAAAGATTTGGACAACAGCTTAAAGTATTAGATCTG 1321
 Db 326 -----GlyThrAlaAsnLeuGlnSerLeuThrLeu 335
 QY 1322 AGCTCAATGTTGTTATTACATGAGTTCAAACTTTTGGGC---TTAGAACAACTAGAA 1378
 Db 336 ThrGlyAlaGlnIleSerSerLeuProGlnThrValCysAsnGlnLeuProAsnLeuGln 355
 QY 1379 CATCTGATTTCCAGCATTTCCAAATTTGAAACAAATGAGTGGATTTTCAGTATTCCTATCA 1438
 Db 356 ValLeuAspLeuSerTyraAsnLeuGlnAspLeuProSerPheSerValCysGlnIys 375
 QY 1439 CTCAGAACTCTATTACCTTCGATTTCTCATACCTACACCAAGAGTTGCTTCAATGGC 1498
 Db 376 LeuGlnIys-----IleAspLeuArgHis----- 383
 QY 1499 ATCTTCATGCTGTTGCCAGCTCTCGAAGTCTTGAAATGCTGGCAATTTCTTCCAGGAA 1558
 Db 384 -----AsnGlnIleTyraGlnIleVal----- 391
 QY 1559 AACTCTCTTCCAGATATCTTCACAGAGCTGAGAACTTGAACCTTCTGACCTCTCTCAG 1618
 Db 392 -----AspThrPheGlnGlnIleLeuSerLeuArgSerLeuAsnLeuAlaTrp 407
 QY 1619 TGTCACTGGAGAGATGTCTCCAAAGCATTTTAACCTGCTCCAGTCTTCAGTAACTA 1678
 Db 408 AsnIleIleAlaIleIleHisProAsnAlaPheSerThrLeuProSerLeuIleValLeu 427
 QY 1679 AATATGAGCCACCAACTCTTTTCAATGATAGATCTTCTTAAATGATCTGAACTCC 1738
 Db 428 AspLeuSerSerAsn-----LeuLeuSerSerPheThrIleThrGlyLeuHisGly 444
 QY 1739 CTCAGAGTTCTTGAATTAACGTCGATCACAATATGACTTCCAAAACAGAACTACAG 1798
 Db 445 LeuThrHisLeuIysLeuThrGlyAsnHisAlaLeuGlnSerLeuIleSerSer---Glu 463
 QY 1799 CATTTCCAGTAGTGTAGCTTCTTAAATCTTACAGAAATGACTTGTGTTACTGTG 1858
 Db 464 AsnPheProGln-----LeuIysValIleGlnLeuProTyraIleTyraIys 479
 QY 1859 -----GAACACCAAGATTTCTCGCAATGATCAAG----- 1888
 Db 480 CysAlaPheGlyValCysGlnAsnAlaTyraIysIleSerAsnGlnIleTrpAsnIysGlyAsp 499
 QY 1889 -----GACCAG 1894
 Db 500 AsnSerSerMetAspAspLeuHisIlyIysAspAlaGlyMetPheGlnAlaGlnAspGln 519
 QY 1895 AGGCAGCTC-----TTGGTGAAGTTGAACGAATG 1924
 Db 520 ArgAspLeuGlnAspPheLeuLeuAspPheGlnGlnAspLeuIysAlaLeuHisSerVal 539
 QY 1925 GAATGTCACACACTTCAGATAAGCAGGAGCATGCT----- 1960
 Db 540 GlnCys---SerProSerProGlyProPheIysProCysGlnHisLeuLeuAspGlyTrp 558
 QY 1961 -----GTGCTGAGTTTGAATATCACTGTCAGATGAATTAAG 1996
 Db 559 LeuIleArgIleGlyValTrpThrIleAlaValLeuAlaLeuThrCys-----AsnAla 576

QY 1997 ACCATCATTTGTTGTCGGTCCCTCACTGTCCTTGTAGTATCTGTGTAGACAGTTCTGTC 2056
 Db 577 LeuValThrSerThrValPheArgSerProLeuTyrlleSerProIleIysLeuLeuIle 596
 QY 2057 TATACTTCTATTTCACCTGATGCTT-----CTTGCTGCTGC 2095
 Db 597 GlyValIleAlaValAsnMetLeuThrGlyValSerSerAlaValLeuAlaGlyVal 616
 QY 2096 ATTAAGTAT-----GGTAGAGGT 2113
 Db 617 AspAlaPheThrPheGlySerPheAlaArgHisGlyAlaTrpTrpGlnAsnGlyValGly 636
 QY 2114 GAAACATCTATGATGCTTTGTTATCTACTCAAGCCAGATGAGATGAGTGGTAGAAT 2173
 Db 637 CysHisValIleGlyPheLeuSerIlePheAlaSerGlnSerSerValPheLeuLeuThr 656
 QY 2174 GAGCTAGTAAAGATTTAGAAGAGGG---TGCCTTCATTTGACCTGCTTCACTAC 2230
 Db 657 -----LeuAlaAlaLeuGln-ArgGlyPheSerValIysTyraSerAlaIysPheGln 674
 QY 2231 AGAGACTTATTCCTCGGTGGCCATTGCTGCCAATCATCATGAGAGTTTCCATTA 2290
 Db 674 IlyVala-----ProPheSerSerLeuIysValIleIle-- 685
 QY 2291 AGCCGAAAGTGAATGTTGTGTCGTCAGCACTTATCATCAGACCCGCTGCTATCTTT 2350
 Db 686 -----LeuLeuCysAlaLeuLeuAlaLeuThrMetAlaValProle 700
 QY 2351 G 2351
 Db 700 u 700

RESULT 10
 US-08-190-802A-49
 ; Sequence 49, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; TITLE OF INVENTION: Theoreof
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSSEE: Dehlinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/190,802A
 ; FILING DATE: 01-FEB-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 8600-0139
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 49:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 605 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO

```

; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Ineu1n-like growth factor binding
; INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

Alignment Scores:
Pred. No.: 2,5e-23 Length: 605
Score: 303.00 Matches: 157
Percent Similarity: 38.57% Conservative: 91
Best Local Similarity: 24.42% Mismatches: 243
Query Match: 3.53% Indels: 152
DB: 1 Gaps: 24

US-09-396-985B-1 (1-4868) x US-08-190-802A-49 (1-605)

QY 221 TGCATGAGAGCTGAATTTCTAACAATATCCCGACACCTCCCTTCTCAACAAGAACTTG 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 60 CysSerSerArgSerLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAlaLeu 79

QY 281 GACCTGAGCTTTAAATCCCTGAGGACATTTAGGACGATATAGCTTTCAGTTTCCAGAA 340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 80 TrpLeuAspGlyAsnAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSerSer 99

QY 341 CTGCAGATGCTGATTTATTCAGAGTGTGAATCCAGACATTTGAAGATGGAGCATATCAG 400
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 100 LeuGlyPheLeuAsnLeuGlnGlyGlyLeuGlySerLeuGlnProGlnAlaLeu 119

QY 401 AGCCTAAGCCACTCTCTACCTTAATATTGACAGAAACCCATCCAGATTGACCTTG 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 120 GlyLeuGlnAsnLeuGlySerHisLeuHisLeuGlnArgAsnGlnLeuArgSerLeuAlaLeu 139

QY 461 GGAGCCTTTCT----- 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 140 GlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeuSer 159

QY 473 -----GACATATCAAGTTTACAGAGCTGTGCTGTGAG 508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 160 ArgLeuGlnAspGlyLeuPheGlnGlyLeuGlySerLeuThrAspLeuAsnLeuGlyTrp 179

QY 509 ACAATATCAATCTCTAGAGAACTTCCCATTTGACATTCAAAATTGAAAGAACTT 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 180 AsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuArgGlnLeu 199

QY 569 AATGTGCTCACATCTTATCCATCTTCAATTCCTGAGATTTTATTTATCTGAGC 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 200 ValLeuAlaGlyAsnArgLeu---AlaTrpLeuGlnProAlaLeuPheSerGlyLeuAla 218

QY 629 AATCTAGAGCAGCTTGACCTTTCAGACACAAATTCAGATTTATTTATTCACAGACTTG 688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 219 GlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArgAlaLeu-----LysAla 235

QY 689 CGGGTTCTACATAAATGCCCTACTCAATCTCTTTAGACCTGTCCCTGAATCTCATG 748
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 236 AsnValPheValGlnLeuProArgLeuGln---LysLeuTrpLeuAspArgAsnLeuLe 254

QY 749 AACTTTATCCAAACAGGTGATTTAAAGAAATTAG---CTTCATAAGCTGACCTTAAAGA 805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 255 AlaAlaValAlaProGlyAlaPheLeuGlyLeuAlaLeuArgTrpLeuAspLeuSer 274

QY 806 AATAATTTTGATGATTTAAATGTATGAAAACCTTGATTCAGAGTCTGCTGGTTTGAAG 865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 275 HisAsn---ArgAlaAlaGlyLeuLeuGlnAspThrPheProGlyLeuLeuGlyLeuArg 293

QY 866 GTTCATCGTTTGTGTTCTGGAGAAATTTAGAAATGAAGAAACTTGAAAAGTTTGACAA 925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 294 ValLeuArgLeu-----SerHis 299

QY 926 TCTGCTCTAGAGGCGCTGTGCAATTTGACATTTGAAGAAATCCGATTAGCATATTAGAC 985
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 300 AsnAlaIleLeuAsnLeuArgProArgThrPheLysAspLeu----- 313

QY 986 TACTACTCGATGATATTATGACTTATTTAATTTGTTGACAAATGTTTCTCATTTTCC 1045

```

```

DB 314 HisPheLeuGlnGlnLeu-----Gln 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1046 CTGGCAGATGTACTATTGAAAAGGTAAGAACTTTCTTATATTTTGGATGGCAACAT 1105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 321 LeuGlyHisAsnArgGlyLeuArgGlnLeuAlaGlnArgSerPheGln---GlyLeuGlyGln 339

QY 1106 TTGAATTTGATTAATCTGTAATTTTGGACAGTTTCCACATTTGAATCAATCTCTCAAA 1165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 340 LeuGlnValLeuThrLeuAspHisAsnGlnLeuGlnGlnValLysAlaGlyAlaPheLeu 359

QY 1166 AGCCTTACTTCACTTCC-----AACAAAGGTGGAAATGCTTTTTCAGAGTTGATCTA 1219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 360 GlyLeuThrAsnValAlaValMetAsnLeuSerGlyAsnGlyLeuArg-----AsnLeu 377

QY 1220 CCAAGCCTTGAATTTCTAGATTCAGATGAGA---AATGGTTGAGTTTCAAGATTCCTGT 1276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 378 ProGlnGlnValPheArgGlyLeuGlyLysLeuHisSerLeuHisLeuGlnGlySerCys 397

QY 1277 -----TCTCAAGTGAATTTTGGACACACAGCCTTAAGATTTAGATCTG 1321
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 398 LeuGlyArgGlyLeuArgProHisThrThrPheThrGlyLeuSerGlyLeuArgArgLeuPheLeu 417

QY 1322 AGCTTCATATGTTGTTATTTACATGATGATTCAACTTCTTG---GGCTTAGACATAGAA 1378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 418 LysAspAsnGlyLeuValGlyLeuGlnGlnSerLeuThrGlyLeuAlaGlnLeuLeu 437

QY 1379 CATCTGGAATTTCCAGATTCCTCAATTTGAAACAAATGACGATTTTCAGATTTCCATCA 1438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 438 GlnLeuAspLeuThrSerAsnGlnLeu----- 446

QY 1439 CTCAGAAACCTGATTTACTTGACATTTCTCATACTCACACAGAGTTGCTTTCATATGC 1498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 447 -----ThrHisLeuPro-----HisArg 452

QY 1499 ATCTTCATATGCTTGTCCAGTCTCGAAGTCTTGAAGATGCTGGCAATTTCTTCAGAA 1558
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 453 LeuPheGlnGlyLeuGlyLysLeuGlnGlyTrpLeuLeuLeuSerArgAsnArgLeuAlaGln 472

QY 1559 AACTTCCTTCCA---GATATCTTCACAGAGCTGAGAAACTTGAACCTCTGACCTCTCT 1615
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 473 -----LeuProAlaAspAlaLeuGlyProLeuGlnArgAlaPheThrLeuAspValSer 490

QY 1616 CAGTGTCACTGAGAGCATGTTGTCTCCACAGCATTTTACTCACTCTCCAGTCTTCAGAT 1675
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 491 HisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuAlaGlyTrp 510

QY 1676 CTAAATATGAGCCACAACTTCTTTTCATTTGATACGTTTCTTATTAAGTGTCTGAAC 1735
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 511 LeuSerLeuArgAsnAsn-----SerLeuArgThrPheThrProGln----- 524

QY 1736 TCCCTTCAGTCTTGATTAACAGTCTCAATCACTATATATGATTTCCAAAAACAGAACTA 1795
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 524 ----- 524

QY 1796 CAGCATTTTCCAAGTACTAGCTTTCTTAATCTTACTCAGAAATGACTTTGGTTGTACT 1855
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 525 -----ProProGlyLeuGlnArgLeuTrpLeuGlnGlyAsnProTrpAspCysGly 541

QY 1856 TGTGAACACCAAGTTTCTGCAATGATCAAGAC----- 1891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 542 CysPro-----LeuLysAlaLeuArgAspPheAlaLeuGlnAsnProSerAla 557

QY 1892 ---CAGAGCAGCTCTTGGTGAAGTGAACGAATGGAATGTGCAACACCTTCAGATTAAG 1948
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 558 ValProArgPheValGlnAlaIleCysGlnGlyAspAspCysGlnProProAlaTrpThr 577

QY 1949 CAGGCAATGCTGTGCTGATTTGAATATCACTGTCAATGAATAAGACATCATTTGT 2008
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 578 TyrAsn-----AsnIleHisCysAlaSerProProGlnValValGly 591

QY 2009 GTGTCCGATC 2017
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Db 592 LeuaspLeu 594

RESULT 11
US-08-477-346-49

Sequence 49, Application US/08477346
Patent No. 6262023

GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thee of
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32

US-08-477-346-49

Alignment Scores:
Pred. No.: 2.5e-23 Length: 605
Score: 303.00 Matches: 157
Percent Similarity: 38.57% Conservative: 91
Best Local Similarity: 24.42% Mismatches: 243
Query Match: 3.53% Indels: 152
DB: 3 Gaps: 24

US-09-396-985b-1 (1-4868) x US-08-477-346-49 (1-605)

QY 221 TGCATGAGCTGATTTCTCAAAATCCCGACAACCTCCCTTCACACCAAGACCTG 280
Db 60 CysSerSerArgSerLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAlaLeu 79
QY 281 GACCTGAGCTTTATCCCTGAGGACATTTAGGACGCTATGCTTCTTCAGTTTCCCGAGA 340
Db 80 TrpLeuAspGlyAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSerSer 99
QY 341 CTGCAAGTGTGATTTATCCAGGTGTGAATTCACGACATTTGAAGATGGGGCATATCAG 400
Db 100 LeuGlyPheLeuAsnLeuGlnGlyGlyGlnLeuGlySerLeuGlnProGlnAlaLeuLeu 119

QY 401 AGCCTAAGCACCCTCTCTACCTTAATATTTGACAGAAACCCCATCCAGATTAGCCCTG 460
Db 120 GlyLeuGlyAsnLeuCyshisLeuHisLeuGlyArgAsnGlnLeuArgSerLeuAlaLeu 139
QY 461 GGAAGCTTTTCT----- 472
Db 140 GlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeuSer 159
QY 473 -----GGACTATCAAGTTTACAGAAAGCTGGTGGCTGGAG 508
Db 160 ArgLeuGlyAspGlyLeuPheGlnGlyLeuGlySerLeuThrAspLeuAsnLeuGlyTrp 179
QY 509 ACAAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAAGAACTT 568
Db 180 AsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuArgGlyLeu 199
QY 569 AATGGGCTCAACATCTTATCCAAATTTTCAAAATTACTAGATTTTCTAATCTGACC 628
Db 200 ValLeuAlaGlyAsnArgLeu--AlaTrpLeuGlnProAlaLeuPheSerGlyLeuAla 218
QY 629 AATCTAGACACTTGGACCTTTCAGCAACAAGATTCAAAGTATTATTGACACAGACTTG 688
Db 219 GlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArgAlaLe-----LysAla 235
QY 689 CGGGTTCTACATCAATGCCCCCTACTCAATCTCTTTAGACCTGTCCTGAATCTTAG 748
Db 236 AsnValPheValGlnLeuProArgLeuGln--LysLeuTrpLeuAspArgLeuLeu 254
QY 749 AACTTATCCAAACAGGTGATTTAAAGAAATTAGG--CTTCATTAAGTGACTTTAAGA 805
Db 255 AlaAlaValAlaProGlyAlaPheLeuGlyLeuValaLeuArgTrpLeuAspLeuSer 274
QY 806 AATATTTTGAATGTTTAATTAATGAAGAACTTGATTCAGGCTGGCTGTTAGAA 865
Db 275 HisAsn--ArgValaAlaGlyLeuLeuGlyAspTrpPheProGlyLeuGlyLeuArg 293
QY 866 GTCCATCGTTGGTGTTCGGAGAAATTAGAAATGAAGAAACTTGAAAAATTGACAAA 925
Db 294 ValLeuArgLeu-----SerHis 229
QY 926 TTGCTCTAGAGGGCCTGTGCAATTTGACCAATGAAGAAATTCGATTAGCATTTAGAC 985
Db 300 AsnAlaIleAlaSerLeuArgProArgTrpPheLysAspLeu----- 313
QY 986 TACTACCTCGAGATTTATTTAGCTATTATTTAATGTTTGAACAATGTTCTTATTTC 1045
Db 314 HisPheLeuGlnLeu-----Gln 320
QY 1046 CTGGTGAAGTGTGACTATTGAAGAGTAAAGACTTTTCTTAATTTGAGATGGCAACAT 1105
Db 321 LeuGlyHisAsnArgIleArgGlnLeuAlaGlyArgSerPheGlu--GlyLeuGlyGln 339
QY 1106 TTGAAATTAAGTAACTGTAATTTGAGACAGTTTCCACATTTGAACATACTTCACAA 1165
Db 340 LeuGlnValaLeuThrLeuAspHisAsnGlnLeuGlnGlnValaLysAlaPheLeu 359
QY 1166 AGGCTTACTTCACTTCC-----AACAAAGGTGGGAAGCTTTTCAGAGTTGATCTA 1219
Db 360 GlyLeuThrAsnValaAlaValaIleAsnLeuSerGlyAsnCyLeuArg-----AsnLeu 377
QY 1220 CCNAGCCTTGAAGTTTCTAGATCTCAGTAGA--AAATGGCTTGAAGTTTCAAGGCTCTGT 1276
Db 378 ProGlnGlnValaPheArgGlyLeuGlyLysLeuHisSerLeuHisLeuGlnGlySerCy 397
QY 1277 -----TTCAAAGTGAATTTTGGACAAACCAAGCTTAAGATTTAGATCTG 1321
Db 398 LeuGlyArgIleArgProHisThrPheThrGlyLeuSerGlyLeuArgArgLeuPheLeu 417
QY 1322 AGCTTCAATGCTTATTTACAGATTCAGACTTCTG--GGCTTAAGAACATAGAA 1378
Db 418 LysAspAsnGlyLeuValaGlyIleGlnGlnGlnSerLeuTrpGlyLeuAlaGlyLeuLeu 437
QY 1379 CATCTGATTTCCAGCATTCCAATTTGAACAACAAATGAGTGAATTTCAATTTCTATCA 1438

Db	438	GIUleuApLeuThrSerAsnGlnLeu-----	446
QY	1439	CTCAGAAACCTCATTTTACCTTGACATTTCTCATCTCACACCAGATTGCTTTCATGGC	1498
Db	447	-----	452
QY	1499	ATCTTCATGGCTTGTCCAGTCTCGAAGTCTTGAATAATGCTGGCAATCTTTCAGAGAA	1558
Db	453	LeuPheGlnGlyLeuGlyLysLeuGlnLysIleuLeuLeuSerArgAsnArgLeuAlaGln	472
QY	1559	AACCTTCCTTCCA---GATATCTTCACAGAGCGAGAAACTTGACCTTCCTGACCTGCT	1615
Db	473	-----LeuProAlaAspAlaLeuGlyProLeuGlnAlaAlaPheTrpLeuAspAlaSer	490
QY	1616	CAGTGTCAACTGAGACAGTGTCTTCCAAACAGCATTTTAACTCATCTCCAGTCTTCAGACTA	1675
Db	491	HisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuArgTyr	510
QY	1676	CTAAATATGAGCCACACAACTCTCTTTCATGTGATACGTTTCTTAAAGTGTCTGAAC	1735
Db	511	LeuSerLeuArgAsnAsn-----SerLeuArgTrpPheThrProGln-----	524
QY	1736	TCCCTCCACAGTTCCTTGATTACAGTCTCATCATCAATAGATCTTCCAAAAACAGGAATA	1795
Db	524	-----	524
QY	1796	CAGCATTTTCCAGAGTGTAGTCTTCTTAAATCTTACTCAGAAATGACTTGTGTTACT	1855
Db	525	-----ProProGlyLeuGlnArgLeuTrpLeuGlnArgLeuProTrpAspCysGly	541
QY	1856	TGTGACACACAGAGATTCTCTGCATGATCAAGAC-----	1891
Db	542	CysPro-----LeuIysAlaLeuArgPheAlaLeuGlnAsnProSerAla	557
QY	1892	---CAGAGCAGCTCTGTGTGGAAATGTAAGCAATGATGGCAACCTTCAGATAAG	1948
Db	558	ValProAlaGlyPheValGlnAlaIleCysGlnGlyAspAspCysGlnProProAlaTyrThr	577
QY	1949	CAGGCGCATCGCTGTGCTGATGTTTGAATATCACTGTCAAGATGAATAGACCATATTGGT	2008
Db	578	TyrAsn-----AsnIleThrCysAlaSerProProGlnValValGly	591
QY	2009	GTGTCGGTC 2017	
Db	592	LeuApLeu 594	
RESULT 12			
US-08-473-089-49			
; Sequence 49, Application US/08473089			
; Patent No. 6342368			
; GENERAL INFORMATION:			
; APPLICANT: Mochly-Rosen, Daria			
; APPLICANT: Ron, Dorit			
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses			
; NUMBER OF SEQUENCES: 265			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: Morrison & Foerster			
; STREET: 2000 Pennsylvania Avenue, NW			
; CITY: Washington			
; STATE: DC			
; COUNTRY: USA			
; ZIP: 20006-1812			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; COMPUTER: IBM PC compatible			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: PatentIn Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/473,089			
; FILING DATE: 07-JUN-1995			
; CLASSIFICATION: 435			

```

QY 806 AATAATTTGATGATTAAATGATGAAAACTTGATTCAGAGCTGCGGTGTTAGAA 865
   |||
   |||
   |||
Db 275 Hisasn---ArgvalalaglLeuLeuGlnAspThrProGlyLeuLeuGlyLeuArg 293
QY 866 GTCCATCGTTTGGTCTCGGAGAAATTGAAATGAAGAAAATTGAAAAATTGACAAA 925
   |||
   |||
   |||
Db 294 ValLeuArgLeu-----SerHis 299
QY 926 TCGCTCTAGAGGCGCTGTCGCAATTGACCATGGAAGAAATTCGATTAGCATCTTAGAC 985
   |||
   |||
   |||
Db 300 AsnAlaIleAlaSerLeuArgProAlaGlyThrPheLeuAspLeu----- 313
QY 986 TACTACCTCGATGATATTATGACTTATTAATTGTTGACAAATGTTCTCATTTTCC 1045
   |||
   |||
   |||
Db 314 HisPheLeuGlnGluLeu-----Gln 320
QY 1046 CTGGTGAGTGTGACTATGTAAGAGGTAAGAACTTTCTTAATAATTCGATGCAACAT 1105
   |||
   |||
   |||
Db 321 LeuGlyHisAsnArgIleArgGlnLeuAlaGluArgSerPheGlu---GlyLeuGlyGln 339
QY 1106 TTGGAATTAGTTAACTGAAATTTGGACAGTTTCCCATTTGAAACTCAAACTCTCAAA 1165
   |||
   |||
   |||
Db 340 LeuGlyValLeuThrLeuAspHisAsnGlnLeuGlnGlyValIleAspLeu 359
QY 1166 AGGCTTACTTCACTTCC-----AACAAAGTGCGGAATGCTTTTCAGAAAGTTGATCTA 1219
   |||
   |||
   |||
Db 360 GlyLeuThrAsnValAlaValMetAsnLeuSerGlyAsnGlyLeuArg-----AsnLeu 377
QY 1220 CCAAGCTTGAGTTTCTAGATCTCAGTAGA---AATGGCTTGAGTTTCAAGAGTGTCTG 1276
   |||
   |||
   |||
Db 378 ProGluGlnValPheArgGlyLeuGlyLeuLeuHisSerLeuHisLeuGlnGlySerCys 397
QY 1277 -----TCTCAAAGTGAATTGGGACCAACCGCTTAAGTATTTAGATCTG 1321
   |||
   |||
   |||
Db 398 LeuGlyArgIleArgProHisIleThrPheThrGlyLeuSerGlyLeuArgLeuPheLeu 417
QY 1322 AGCTCAATGGTGTATTATTCATGATGAGTTCAAACTTCTT---GAGCTTAGAACATAGAA 1378
   |||
   |||
   |||
Db 418 LysAspAsnGlyLeuValGlyIleGluGlnSerLeuThrProIleValIleGluLeu 437
QY 1379 CATCTGATTTCCAGCATTCCAATTTGAAAACAAATGAGTGTTCAGTATTCCTATCA 1438
   |||
   |||
   |||
Db 438 GluLeuAspLeuThrSerAsnGlnLeu----- 446
QY 1439 CTGAGAACTCATTTACCTTGACATTTCTCATACTCACCAAGAGTTGCTTCAATGCG 1498
   |||
   |||
   |||
Db 447 -----ThrHisLeuPro-----HisArg 452
QY 1499 ATCTCAATGGCTTTCGACGTCGAAAGTCTTGAATAAGCTGCGCAATTTCTTCAGGAA 1558
   |||
   |||
   |||
Db 453 LeuPheGlnIleLeuGlyLysLeuGlyLysLeuLeuSerArgAsnArgLeuAlaGlu 472
QY 1559 AACTCTCTTCCA---GATATCTTCACAGAGCTGAGAACTTGACCTTCTCGACCTCTCT 1615
   |||
   |||
   |||
Db 473 -----LeuProAlaAspAlaLeuGlyProLeuGlnArgAlaPheThrLeuAspValSer 490
QY 1616 CAGTGTCACTGAGACAGATTCTCCAAACAGCAATTTAACTCACTTCCAGCTTCAGAGTA 1675
   |||
   |||
   |||
Db 491 HisAsnArgLeuGlnIleLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuAspGly 510
QY 1676 CTAAATATGAGCAACAACAACCTTTTTCATGATAGACGTTTCTTAATAAGTCTGAAAC 1735
   |||
   |||
   |||
Db 511 LeuSerLeuArgAsnAsn-----SerLeuArgThrPheThrProGln----- 524
QY 1736 TCCTCCAGGTTCTTGATTACAGTCTCAATCACATATGACTTCCAAAAACAGAACTA 1795
   |||
   |||
   |||
Db 524 ----- 524
QY 1796 CAGCATTTTCAAGTACTAGCTTTCTTAATCTTACTCAGATGACTTTGCTTGTACT 1855
   |||
   |||
   |||
Db 525 -----ProProGlyLeuGlnArgLeuThrIleLeuGlnIleGlyAsnProIlePheProIlePhe 541

```

```

QY 1856 TGTGAACACAGAGTTTCTCGAATGATCAAGAC----- 1891
   |||
   |||
   |||
Db 542 CysPro-----LeuIleValAlaLeuArgAspPheAlaLeuGlnAsnProSerAla 557
QY 1892 ---CAGAGCAGCTCTTGTGTGAAGTGAACAAATGAATGTGCAACACCTTCAGATAAG 1948
   |||
   |||
   |||
Db 558 ValProArgPheValGlnAlaIleLeuCysGluGlyAspAspCysGlnProProAlaTyrThr 577
QY 1949 CAGGCGATCGCTGTGTGATGTTGAATATACCTGTGCAATGAAATGAACCATCATTTG 2008
   |||
   |||
   |||
Db 578 TyrAsn-----AsnIleThrCysAlaSerProGluValValGly 591
QY 2009 GTGTGCGTC 2017
   |||
   |||
   |||
Db 592 LeuAspLeu 594

RESULT 13
US-08-487-072A-49
/ Sequence 49, Application US/08487072A
/ Patent No. 6423684
/ GENERAL INFORMATION:
/ APPLICANT: Mochly-Rosen, Daria
/ APPLICANT: Ron, Dorit
/ TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
/ TITLE OF INVENTION: Thereof
/ NUMBER OF SEQUENCES: 265
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Morrison & Foerster
/ STREET: 2000 Pennsylvania Avenue, NW
/ CITY: Washington
/ STATE: DC
/ COUNTRY: USA
/ ZIP: 20006-1812
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/487,072A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: MURASHIGE, KATE H.
/ REGISTRATION NUMBER: 29,959
/ REFERENCE/DOCKET NUMBER: 2550-0025.20
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-1500
/ TELEFAX: (202) 887-0763
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 605 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ HYPOTHEetical: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: Insulin-like growth factor binding
/ INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-487-072A-49

Alignment Scores:
Pred. No.: 2,5e-23
Score: 303.00
Percent Similarity: 38.57%
Best Local Similarity: 24.42%
Query Match: 3.53%
DB: 4
Gaps: 24

US-09-396-985B-1 (1-4868) x US-08-487-072A-49 (1-605)
QY 221 TGCATGAGCTGAATTTCTACAAATCCCGACAACTCCCTCTCAACGAAGACTG 280

```



```

; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: curatseqformatter Version 0.9
; SEQ ID NO: 1087
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

Alignment Scores:
Pred. No.: 2,56-23      Length: 605
Score: 303.00          Matches: 157
Percent Similarity: 38.57%      Conservative: 91
Best Local Similarity: 24.42%    Mismatches: 243
Query Match: 3.53%             Indels: 152
DB: 4                    Gaps: 24

US-09-396-985b-1 (1-4868) x US-09-538-092-1087 (1-605)

QY 221 TGCATGAGCTGAATTTCTACAAATCCCGACAACCTCCCTTTCACACCAAGACCTG 280
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 60 CysSerSerArgAsnLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAlaLeu 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 281 GACCTGAGCTTTATCCCTGAGGACATTGAGCAGCTATAGCTTTCAGTTCCCGAA 340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 80 TrpLeuAspGlyAsnAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSerSer 99
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 341 CTGCAGGCTGCTGATTTATCCAGGTGGAATCCAGACAATGGAATGGGGCATATCAG 400
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 100 LeuGlyPheLeuAsnLeuGlnGlyGlyGlnLeuGlySerLeuGlnProGlnAlaLeu 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 401 AGCCTAAGCACTCTCTACCTTAATATGACAGAAACCCCATCCAGAGTTAGCCCTG 460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 120 GlyLeuGlnAsnLeuCysHisLeuHisLeuGlnArgAsnGlnLeuArgSerLeuAlaLeu 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 461 GGAGCCTTTCT 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 140 GlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeuSer 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 473 -----GACATATCAAGTTTACAGAACTGCTGCTGAG 508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 160 ArgLeuGlnAspGlyLeuPheGlnGlyLeuGlySerLeuThrAspLeuAsnLeuGlyTrp 179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 509 ACAAAATGACATCTTAGAGAACTTCCCATGAGCATCTCAAACTTGGAAAGACTT 568
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 180 AsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuArgGlnLeu 199
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 569 AATGTGCTCACAATCTTATCCAACTCTTCAATATCCTGAGTATTTTCTAATCTGACC 628
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 200 ValLeuAlaGlyAsnArgLeu---AlaTrpLeuGlnProAlaLeuPheSerGlyLeuAla 218
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 629 AATTAAGACACTGACCTTCCAGCAACAAGATCAAGATATTTATTCACAGACTTG 688
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 219 GlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArgAlaLeu-----LysAla 235
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 689 CGGGTTTACATCAATGCCCCCTACTCAATCTCTTTAGACCTGCTCCGTAATCTCATG 748
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 236 AsnValPheValGlnLeuProArgLeuGln---LysLeuTrpLeuAspArgAsnLeuIle 254
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 749 AACTTATCCACAGAGCTTTAAGAAATTAGG---CTTCAATAGCTGACCTTTAAGA 805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 255 AlaAlaValAlaProGlyAlaPheLeuGlyLeuLysAlaLeuArgTrpLeuAspLeuSer 274
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 806 AATAATTTGATAGTTAAATGTAATGAATCTGTATTCAGAGCTGCTGGCTGTTTGAAG 865
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 275 HisAsn---ArgValAlaGlyLeuLeuGlnAspThrPheProGlyLeuGlnGlyLeuArg 293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 866 GTCCATCGTTGGTCTCGGAGAAATTTAGAAATGAAGAAACCTTGAAAGTTTGACAA 925
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 294 ValLeuArgLeu-----SerHis 299
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY 926 TCTGCTTAGAGGGCCCTGTGCAATTTGACCATTTGAAGAAATTCGATTAGCATATTAGAC 985
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 300 AsnAlaIleAlaSerLeuArgProArgThrPheLysAspLeu----- 313
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 986 TACTACCTCGATGATATTTATGACTTATTTAATTTGTCAGAAATGTTCTTCATTTTCC 1045
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 314 HisPheLeuGlnGlnLeu-----Gln 320
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1046 CTGTGAGTGTGACTATTTGAAGAGTAAAGACTTTTCTTATATTTTCGATGCAACAT 1105
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 321 LeuGlyHisAsnArgGlyLeuArgGlnLeuAlaGlyArgSerPheGln---GlyLeuGlyGln 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1106 TTGAATTTGATACGTAAATTTGACAGCTTCCACATTTGAACTCAATCTCTCAAA 1165
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 340 LeuGlnValLeuThrLeuAspHisAsnGlnLeuGlnGlnValLysAlaGlyAlaPheLeu 359
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1166 AGGCTTACTTTCATCTCC-----AACAAAGGTGGGAATGCTTTTTCAGAAATGATCTTA 1219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 360 GlyLeuThrAsnValAlaValMetAsnLeuSerGlyAsnGlyLeuArg-----AsnLeu 377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1220 CCAAGCTTGAAGTTTCTAGATCTCAGTAGA---AATGCTTGAAGTTCAAGTTCCTGT 1276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 378 ProGlnGlnValPheArgGlyLeuGlyLysLeuHisSerLeuHisLeuGlnGlySerCys 397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1277 -----TCTCAAGTGATTTTGGGCAACACGCTTAAGTATTAGATCTG 1321
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 398 LeuGlyArgGlyLeuArgProHisThrPheThrGlyLeuSerGlyLeuArgArgLeuPheLeu 417
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1322 AGCTTCATGTGTGTTTATTCATGATGATCAAACTTCTTG---GGCTTAGAACACTAGAA 1378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 418 LysAspAsnGlyLeuValGlyGlyGlnGlnGlnSerLeuThrGlyLeuAlaGlyLeuLeu 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1379 CATCTGGAATTTCCAGATTCCAATTTGAAACAAATGATGAGTTTTCAGTATTTCTATCA 1438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 438 GlnLeuAspLeuThrSerAsnGlnLeu----- 446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1439 CTCAGAAACCTCATTTACCTTGACATTTCTCACTCACACCGAGTTGCTTCATGAGC 1498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 447 -----ThrHisLeuPro-----HisArg 452
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1499 ATCTTCATGTGCTTGTTCAGATCTCGAAGCTTGGAAATGAGCTGGCAATCTTTCAGAA 1558
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 453 LeuPheGlnGlyLeuGlyLysLeuGlnLysTrpLeuLeuLeuSerArgAsnArgLeuAlaGly 472
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1559 AACTTCTTCCA---GATATCTTCACAGAGCTGAGAACTTGACCTTCTGACCTCTCT 1615
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 473 -----LeuProAlaAspAlaLeuGlyProLeuGlnArgAlaPheTrpLeuAspValSer 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1616 CAGTGTCACTGGAGAGCTGTCTCCACAGACATTTAACTCACTCCAGCTCCAGCTGA 1675
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 491 HisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuArgTrp 510
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1676 CTAAATATAGGCACACAACACTTCTTTCATTGATGATACCTTCTTATAGTGTCTGAAC 1735
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 511 LeuSerLeuArgAsnAsn-----SerLeuArgThrPheThrProGln----- 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1736 TCCCTTCAGGTTCTTGATTACAGTCTCAATCAATATGACTTCCAAAAACAGAACTTA 1795
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 524 ----- 524
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1796 CAGCATTTTCCAAAGTATGCTAGCTTCTTAAATCTTAACTCAGAAATGACTTGTCTACT 1855
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 525 -----ProProGlyLeuGlnArgLeuTrpLeuGlnGlyAsnProTrpAspCysGly 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1856 TGTGAACACCAAGATTTCTGCAATGATCAAGAC----- 1891
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 542 CysPro-----LeuLysAlaLeuAspArgPheAlaLeuGlnAsnProSerAla 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1892 ---CAGAGCAGCTCTTGTGTGAAGTGAAGTAAGTAAGTGTGAACACCTTTCAGATTAAG 1948
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 558 ValProArgPheValGlnAlaIleCysGlnGlyAspAspCysGlnProProAlaTrpThr 577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

QY 1949 CAGGCGATGCTGTGATGATTGAATATCATCTGTCAGATGATATGACCATCATTTGAT 2008
Db 578 TyrAsn-----AsnIleThrCysAlaSerProProGluValValGly 591
QY 2009 GTGTGGTC 2017
Db 592 LeuAspLeu 594

RESULT 15
US-09-538-092-1325
; Sequence 1325, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Gluc, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538, 092
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraparseFormatter Version 0.9
; SEQ ID NO 1325
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14392
US-09-538-092-1325

Alignment Scores:
Pred. No.: 6,44e-23 Length: 662
Score: 299.50 Matches: 187
Percent Similarity: 38.97% Conservative: 94
Best Local Similarity: 25.94% Mismatches: 259
Query Match: 3.49% Indels: 181
Gaps: 35
DB: 4

US-09-396-985b-1 (1-4868) x US-09-538-092-1325 (1-662)

QY 185 CCCGCGTGAAGTGTCTTAATATTAATTAATGAGCTGAGCTGAATTTCTACAA 244
Db 25 ProCysIysMetValAspLysValSer-----CysGlnValLeuGlyLeuGln 42
QY 245 ATCCCGACAACTCCCTTCTCAACCAAGAACTGAGCTGATTAATCCCTGAG 304
Db 43 ValProSerValLeuProProSerThrGlnThrLeuAspSerGlyAsnGlnLeuArg 62
QY 305 CATTAGCAGCTATAGCTTCTTCAGTTCCAGAACTGAGCTGATTAATCCAG 364
Db 63 SerIleuAlaSerProLeuGlyPheTyrThrAlaLeuArgHisLeuAspLeuSerThr 82
QY 365 TGTGAATCCAGCAATTTGAAGATGGGCAATATAGAGCTTAAGCCACTCTACTTA 424
Db 83 AsnGlnIleSerPheLeuGlnProGlyAlaPheGlnAlaLeuThrHisLeuGlnHisLeu 102
QY 425 ATATTGACAGGAACCCCATCCAGATCCAGATTGAGCTGGAGGCTTTCTGGACTATCAAGT 484
Db 103 SerIleuAlaHisAsnAlaGlyLeuAlaMetAlaThrAlaLeuSerAlaGlyGlyLeuGlyPro 122
QY 485 TTACAGAGCTGTGCTGTGAGAGCAATCTAGCATCT-----CTAGAG 529
Db 123 LeuProArgValThrSerLeuAspLeuSerGlyAsnSerLeuTyrSerGlyLeuLeuGln 142
QY 530 AACTTCCCATTTGACATCTCAAAACTTTGAAAGAACTTAATGTGGCTCAATCTTATC 589
Db 143 ArgLeu---LeuGlyGlnAlaProSerLeuHisThrLeuSerLeuAlaGlnAsnSerLeu 161

QY 590 CAATCTTTCAAAATTAACCTAGATAT---TTTCTAAATCTGACCAATCTAGAGCACTTGAC 646
Db 162 Thr-----ArgLeuThrArgHisThrPheArgAspMetProAlaLeuGlnIleLeuAsp 179
QY 647 CTTTCCAGACAAAGATTTCAAAATTTTATTGTCACAGACTTCGGGTTCTATACAAATG 706
Db 180 LeuHisSerAsnValLeuMetAspArgIleGluAspGlyAlaPheGlnGlyLeuProArgLeu 199
QY 707 CCCCTACTCAATCTCTCT----- 724
Db 200 ThrHisLeuAsnIleSerArgAsnSerLeuThrCysIleSerAspPheSerLeuGlnGln 219
QY 725 -----TTAGACCTGTCCCTGAATCCTATGAATTTATC-----CAACCA 763
Db 220 LeuArgValLeuAspLeuSerCysAsnSerIleGluAlaPheGlnThrAlaSerGlnPro 239
QY 764 GGTGCAATTTAAAGAAATTTAGGCTTCAAGCTGACTTATTAAGAAATAT----- 811
Db 240 GlnAla-----GluPheGlnLeuThrTyrLeuAspLeuArgGluAsnLysLeuLeuHis 257
QY 812 TTTGATAGTTTAATGTATATGAAGAACTGTATCAAGCTGCGCTTTAGAGTCAT 871
Db 258 PheProAspLeuAlaAlaLeuProArgLeuIleTyrLeuAsnLeuSerAsnAsnLeuIle 277
QY 872 CGTTTGGTTCTGGGAGAAATTTAGAAAT----- 898
Db 278 ArgLeuProThrGlyProProGlnAspSerLysGlyIleHisAlaProSerGlnGlyTyr 297
QY 899 -----GAGGAAACTTGAGAAAGTTTGACAAATCTGCTCTA 934
Db 298 SerAlaLeuProLeuSerAlaProSerGlyAsnAlaSerGlyArgProLeuSerGlnLeu 317
QY 935 GAGGCGCTGTGCAATTTGACATTTGAGAAATCCGATTTGACATCTAGACTACTCTC 994
Db 318 LeuAsnLeu---AspLeuSerTyrAsnGlnIleGlnLeu---IleProAspSerPheLeu 335
QY 995 GATGATATTAATTTGACTTATTT-----AATTGTTGACAAATGTTTCT 1036
Db 336 GlnHisLeuThrSerLeuCysPheLeuAsnLeuSerArgAsnCysLeuArgThrPheGln 355
QY 1037 TCATTTTCCCTGGTGAAGTGTGACTATTTGAAGGATTAAGACTTTTCTTATATTTGGA 1096
Db 356 AlaArgArgLeuGlySerLeuProCysLeuMetLeuLeuAspLeuSerHisAsn---Ala 374
QY 1097 TGGCAACATTTGAATTAATTAAGTAAATTTGACAGATTTCCCACTTGAAGTCAAA 1156
Db 375 LeuGlnThrLeuGlnLeuGlyAlaArgAlaLeuGlySerLeuArgThrLeuLeuGln 394
QY 1157 TCTCTCAAAAGGCTTACTTTCATCTTCCAAAGAGTGGAGATGCTTTTTCAGAAATGTT-- 1213
Db 395 -----GlyAsnAlaLeuArgAspLeuPro 402
QY 1214 -----GATTTACCAAGCTTTGAGATTTCTAGATCTCAGTGAAGATGGCTTG 1258
Db 403 ProTyrThrPheAlaAsnLeuAlaSerLeuGlnArgLeuAsnLeuGlnIleYAsnAlaGlyVal 422
QY 1259 AGT-----TTCAAAAGTTTGCTGCTTCAAAAGTATTT 1291
Db 423 SerProCysGlyGlyProAspArgLeuProGlyProSerGlyCysValAlaPheSer----- 440
QY 1292 GGGACAAACAGCCTTAAGATTTAGATCTGAGCTTCAAGTGGTGTATTATTCAGATGATCA 1351
Db 441 GlyIleThrSerLeuArgSerLeuSerLeuValAspAsnGlnIle----- 455
QY 1352 AACTTCTTGGCTTTAGACAACTAGAAACTGTGATTTCCAGATTTCCAAATTTGAAACA 1411
Db 456 -----GluLeuLeuArgAlaGlyAlaPheLeuHisThrProLeuThrGln 470
QY 1412 ATAGATGAGTTTCAATATTCATATTCATCAGAAACCTGATTTACCTTCAATTTCTCAT 1471
Db 471 -----LeuAspLeuSerSer 475
QY 1472 ACTCACACAGAGTGTCTTCAATGAGCATCTTCAATGAGCTTG---TCCAGTCTCGAAGTC 1528

```
Db      476 AsnProGlyLeuGluValAlaThrGlyAlaLeuGlyGlyLeuGluAlaSerLeuGluVal 495
QY      1529 TTGAAATGGCTGGCAATTTCTTCCAG-----GAAACCTTCTTCAGATATCTTCACA 1582
Db      496 LeuAlaLeuGlnGlyAsnGlyLeuMetValLeuGlnValAspLeuProCysPheIleCys 515
QY      1583 GAGCTGAGAAACTTGACCTTCTGACCTCTCTCAGTGCACCTGAGAGAGTGTCTCCA 1642
Db      516 -----LeuYsArgLeuAsnLeuAlaGluAsnArgLeuSerHisLeu----- 529
QY      1643 ACAGCATTTAACTCACTCTCCAGTCTTCAGGTAATAATATAGCCACAACAACTTCTTT 1702
Db      530 ProAlaIlePheThrGlnAlaValSerLeuGluValLeuAspLeu--ArgAsnAsnSerPhe 548
QY      1703 TCATTGGATACGTTTCTTCTTAAGTCTCTGAACCTCCCTCAGGTTCTTGATTACAGCTTC 1762
Db      549 SerLeu-----LeuProGlySerAlaMetGlyGlyLeuGlu----- 560
QY      1763 AATCACAATATGACTTCCAAAAACAGAACTACAGCATTTTCCAAGTAGTACGCTTTC 1822
Db      561 -----ThrsLeuArgArg 565
QY      1823 TTAAATCTTACTCAGAAATGACTTGTCTTGTACTGTGAACACAGAGTTTCTGCAATGG 1882
Db      566 LeuTyrLeuGlnGlyAsnProLeuSerCys--CysGlyAsn-----GlyTyr 580
QY      1883 ATCAGAGACCGAG--AGGCGAGCTCTGTGTGAAGTTGAACGAATGCA-----TGT 1930
Db      581 LeuAlaAlaGlnLeuHisGlnGlyArgValAspValAspAlaThrGlnAspLeuIleCys 600
QY      1931 GCAACACCTTCAGATTAAGCAGGGCAGTGCCTGTGCTGATTTGAATATCACCC----- 1981
Db      601 ArgPheSerSerGlnGlnGlu-----ValSerLeuSerHisValArgProGlu 616
QY      1982 ---TGTCAATGAAT-----AAGACCATCATTTGTGTGTGCGTCCCTCAGTGTGCTGTA 2032
Db      617 AspCysGlnIleGlyGlyLeuYsAsnIleAsnLeuIleIleLeuThrPheIleLeu 636
QY      2033 GTATCTGTTGTACGAGTTCGTGCTATTAAGTTCTATTTTCACTGATGCTTCTTGCTGGC 2092
Db      637 ValSerAlaIleLeu-----LeuThrThrLeuAlaAla 647
QY      2093 TGC 2095
Db      648 Cys 648
```

Search completed: March 29, 2005, 17:36:27
Job time : 100.767 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:51:33 ; Search time 50.705 Seconds

(without alignments)
18474.848 Million cell updates/sec

Title: US-09-396-985B-1

Perfect score: 8579
Sequence: 1 aaatactacctgcctcaaa.....caaaaaaaaaaaaaaa 4868

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 segs, 9621673 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ n2p.model -DEV=xlh
-Q=cg2_1/USFTO_epool/US0396985/runat_28032005_155743_21159/app.query.fasta_1.85098
-DB=PIR_79 -QMT=faiban -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bl0sum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0396985 @CCN 1.1 1364 @runat_28032005_155743_21159 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: PIR_79:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	663	7.7	661	2	156258 RPI05 - mouse
2	474	5.5	786	2	T08654 Toll protein-like
3	454	5.3	1097	2	A29943 Toll protein precu
4	433	5.0	1389	2	T13852 gene wheeler prote
5	421	4.9	1385	2	T13887 clr protein - fru1
6	396	4.6	1166	2	T15864 hypotheical prote
7	333.5	3.9	1134	1	A29944 chaoptin precursor
8	328.5	3.8	1280	2	B34087 hypotheical prote
9	326.5	3.8	712	2	S23650 retrovirus-related
10	320.5	3.7	1275	2	T38588 reverse transcript
11	319.5	3.7	1275	2	B28096 line-1 protein ORF
12	319.5	3.7	1275	2	S65824 reverse transcript
13	316	3.7	605	2	UC5239 insulin-like growt
14	307.5	3.6	1531	2	T42218 slt-1 protein hom

15	305	3.6	853	2	T17461 disease resistance
16	303.5	3.5	907	2	JB0176 orphan G protein-c
17	303	3.5	605	2	A41915 insulin-like growt
18	302	3.5	603	2	T24315 hypothetical prote
19	299.5	3.5	662	2	S42799 garp precursor - h
20	297	3.5	994	2	H96510 probable disease r
21	296.5	3.5	845	2	T07039 Hcr9-0 protein - t
22	296	3.5	603	2	UC1282 insulin-like growt
23	295	3.4	907	2	UG0193 G protein-coupled
24	290	3.4	603	2	JC6128 insulin-like growt
25	290	3.4	855	2	T07015 Cf-4a protein - to
26	289.5	3.4	1112	2	T10504 disease resistance
27	289	3.4	855	2	T17460 disease resistance
28	285.5	3.3	1134	2	T04587 hypothetical prote
29	285	3.3	632	2	JC7973 synleurtin - human
30	285	3.3	1091	2	A58532 glial cell membran
31	284	3.3	1259	4	GNH011 retrovirus-related
32	282.5	3.3	1027	2	B85089 receptor protein k
33	280	3.3	890	2	T00800 disease resistance
34	278.5	3.2	1019	2	C96519 probable disease r
35	276.5	3.2	768	2	T17462 disease resistance
36	276	3.2	983	2	G84524 probable disease r
37	275.5	3.2	1523	2	T13953 MEGF3 protein - ra
38	272	3.2	1469	2	B36665 slit protein 2 pre
39	272	3.2	1480	2	A36665 slit protein 1 pre
40	271	3.2	1143	2	T10636 hypothetical prote
41	270.5	3.2	1109	2	T19536 receptor-like prot
42	269.5	3.1	275	2	S21348 probable pol polyp
43	268	3.1	910	2	G84648 probable disease r
44	267	3.1	766	2	T01817 hypothetical prote
45	267	3.1	1784	2	C96615 hypothetical prote

ALIGNMENTS

RESULT 1
156258
RPI05 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #ext_change 09-Jul-2004
R:Accession: I56258
C:Accession: I56258
R:Make, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kinoto, M.
J. Immunol. 154, 3333-3340, 1995
A>Title: RPI05, a novel B cell surface molecule implicated in B cell activation, is a m
A:Reference number: I56258; NCBI:95204928; PMID:7897216
A:Accession: I56258
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-661 <RES>
A:Cross-references: UNIPROT:Q62192; GB:D37797; NID:g761711; PIDN:BA07043.1; PID:g761711

US-09-396-985B-1 (1-4868) x I56258 (1-661)

QY	143	GCATGCGCTTCCTCCTCGC---	GTGAGACCAAGAGCTGGAGCCCTGGAGAGT	199
DB	12	AlaLeuPheLeuAlaSerCysArgAlaThrThrSerSerAspGlnCysAlaGluLys	31	
QY	200	GTTCCTAATATTAATCATCATGAGCTGAATTTTCACAAATCCCGACCACTC	259	
DB	32	GluValAsnIleThrLysCysGluAsnLeuGlyLeuAsnGlnIleProGlyThrLeu	51	
QY	260	CCCTTTCACCAAGAACTGAGCTTGAATCCCTGAGGACATTAGGACACTT	319	
DB	52	ProAsnSerThrGluCysLeuGluIlePheSerPheAsnValLeuProThrIleGlnAsnThr	71	

QY	320	AGCTTCTTCAGTTTCCAGAACTGCAGGTCTGGATTATATCCAGGTGGAATTCAGAACTCAGACA	379
Db	72	ThrPheSerArgLeuIleAsnLeuThrPheLeuAspLeuThrArgCysGlnIleTryrTrp	91
QY	380	ATTGAAGAAGGGGCAATTATCAGAGCTCAGAGCCACCTCTCTACCTTAATATTTAGACAGGAAC	439
Db	92	IleHisGluAspThrPheGlnSerGlnHisArgLeuAspThrLeuValLeuThrAlaAsn	111
QY	440	CCCATCCAGAGTTTAGCCCTGGGAGCCCTTTTCTGGACATATCAAGTTCACAGACCTGGTG	499
Db	112	ProLeuIlePheMetAlaGluThrAlaLeuSerGlyProValAlaLeuYenHsEleuPhe	131
QY	500	GCTGTGGAGACAAATCTAGCATCTCTACAGAACTCCCATTTGGACATCTCAAAACTTTG	559
Db	132	PheIleGlnThrGlyIleSerSerIleAspPheIleProLeuHisAsnGlnYsThrLeu	151
QY	560	AAAGAAGCTTAATAGTGGCTCACAACTCTTATCCAACTCTTCAAAATTACCGAGATATTTTCT	619
Db	152	GluSerLeuTryrLeuGlySerAsnHisIleSerSerIleYsLeuProYsGlyPhePro	171
QY	620	AATCGACCAATCTAGACACTTGGACCTTTCCAGCAACAAGATCTCAAGATATTTATGC	679
Db	172	Thr---GluYsLeuIleValLeuAspPheGlnAsnAsnAlaIleHisTryLeuSerYs	190
QY	680	ACAGACTTGGGGTTCTACATCAAAATGCCCTCAATCTCTCTTTAGACTGTCCCTG	739
Db	191	GluAspMetSerSerLeuGlnGln---AlaThrAsnLeuSerLeuAsnLeuAsnGly	208
QY	740	AATCTTAAGAACTTATCAACCGAGCTGCATTTAAAGAAATTAGCGTTCAATACAGTACT	799
Db	209	AsnAspIleAlaGlyIleGluProGlyAlaPheAspSerAlaValPheGlnSerLeu---	227
QY	800	TTAAGAAATTAATTTGATAGATTAAATTAATTAAGAAACTTGATTAACAGTCTGGCTGT	859
Db	228	-----AsnPheGlyIleYrThrGlnAsnLeuValIlePheYsGlyLeuYsAsn	244
QY	860	TTAGAAGTCCATCGTTGGTCTGGGAGAAATTTAGAAATGAAGAACTTGAAAAGTTT	919
Db	245	SerThrIleGlnSerLeuTrpLeuGlyThrPheGluAspMetAspAsp---GluAspIle	263
QY	920	GACAAATCGCTCTAGAGGGCGCTGGCAATTGGACATTTGAAGAAATTCGATTTAGCATAC	979
Db	264	SerProAlaValPheGlnGlyLeuSerGluMetSerValGluSerIleAsnLeu---Gln	282
QY	980	TTAGACTACTACCTGATGATATTTATGATTAATTTATTTGGACAAATGTTCTTCA	1039
Db	283	LysHisTryrPhePheAsnHisIleSerSerAsnThrPheHisCysPheSer---	298
QY	1040	TTTTCCCTGGTAGTGTAATAATTGAAGGCTAAAGACTTTTCTTAATATTTCCGATCG	1099
Db	299	-----GlyLeu	300
QY	1100	CAACATTTAGATTACTTAACCTGTAAATTTTGACAGCTTCCACAC-----TTGAAATC	1153
Db	301	GlnGluLeuAspLeuThrAlaThrHisLeuSerGlnLeuProSerGlyLeuValGlyLeu	320
QY	1154	AAATCTCTCAAAAGCTTACTTTCATCTCCCAAGAGGTGGGAAT-----GCTTTTCA	1207
Db	321	SerThrLeuYsGlyLeuValLeuSerAlaAsnYsPheGluAsnLeuCysGlnIleSer	340
QY	1208	GAAGTGATCTACCAAGCCCTTGAGTTT-----	1234
Db	341	AlaSerAsnPheProSerLeuThrHisLeuSerIleYsGlyAsnThrYsArgGluGlu	360
QY	1235	-----CTAGATCTCAGTGAAGAAAT	1252
Db	361	IeuGlyThrGlyCysLeuGluAsnLeuGluAsnLeuArgGluLeuAspLeuSerHisAsp	380
QY	1253	GGCTTGAGTTGCAAAAGGTGCTGTTCTCAAAAGTGATTTTGGGACAAACAGAGCTTAAAGAT	1312
Db	381	AspIleGluThrSerAspCysAsnLeuGlnLeuAspAsnLeuSerHisLeuGlnSer	400
QY	1313	TTAGATCTGAGCTTCAATGCTGTATTATCCATGATGTTCAAACT---TTCCTGGGCTTAGAA	1369

[illegible]

RESULT 2
T08664
Toll protein-like receptor DKFZps4710610.1 - human
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T08664
R./Postka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A./Reference number: Z16466
A./Accession: T08664
A./Molecule type: mRNA
A./Residues: 1-786 <POU>
A./Cross-references: UNIPROT:Q15399; EMBL:AL050262
A./Experimental source: fetal brain; clone DKFZps4710610
C./Genetics:
A./Note: DKFZps4710610.1
Alignment Scores:

Alignment Scores:

Pred. No.: 1.06e-27 Length: 786
 Score: 474.00 Matches: 204
 Percent Similarity: 41.80% Conservative: 130
 Best Local Similarity: 25.53% Mismatches: 303
 Query Match: 5.53% Indels: 162
 DB: 2 Gaps: 32

US-09-396-985b-1 (1-4868) x T08664 (1-786)

QY 470 TCTGACTATCAAGTTTACAGAGCTGTGTGAGACAAATCTAGCATCTTAGAG 529
 DB 34 AenGlyLeuLleHisValProLysAspLeuSerGlnLysThrThrLleLeuAenLleSer 53
 QY 530 AACTTCCCATTTGACATCTCAAAACT-----TTGAAAGA 565
 DB 54 GlnAsnTrpLleSerGlnLeuTrpThrSerAspLleLeuSerLysLysLysGlyLe 73
 QY 566 CTTAATGTGGCTGACAACTTTATCCAACTTTCAATTAACCTGAGTATTTTCTAATCTG 625
 DB 74 LeuLleLleSerHisAsnArgLleGlnTrpLeuAspLleSerValPheLysPheAsn--- 92
 QY 626 ACCAATCTAGAGCACTTGACCTTTCCAGACAAAGATTCAAGATTTATTTCACACAG 665
 DB 93 GlnGlnLeuGlnLysLeuAspLeuSerHisAsnLysLeuValLysLleSerCys----- 110
 QY 686 TTGCGGGTTCTACATCAATGCCCCCTACTCATCTCTCT-----TTAGACCTGTCCCTGAAT 742
 DB 111 -----HisProThrValAsnLeuLysHisLleLeuAspLeuSerPheAsn 124
 QY 743 CCTATGAACTTATTC-----CAACAGCTGCATTTAAAGAAATTAAGCTTCAT 790
 DB 125 AlaPheAspLalaLeuProLleCysLysGluPheGlyAsnMetSerGlnLeuLysPheLeu 144
 QY 791 AAGCTGACTTAAAGAAATATTGATAGTTTAAATGAAATGAAATCTTATTAAGCT 850
 DB 145 GlyLeuSer-----ThrThrHisLeuGlnLysSerSerValLeuPro 158
 QY 851 CTGGCTGGTTTGAAGTCATCGTTGGTCTG-----GGAGAAATT 892
 DB 159 IleAlaHisLeuAsnLleSerLysValLeuLeuValLeuGlnLysGlnLysLys 178
 QY 893 AGAAATGAAGAACTTGAAAGATTGACAAATCTGCTAGAGCGCTGTGCAATTG 952
 DB 179 GluAspProGlyLysLeuGlnAspPheAsnThrGlnSerLysLleValPheProThr 198
 QY 953 ACCATTGAAGAAATTCGATTGACATTAAGTACTACTGCTGATGATATTATTGACTTA 1012
 DB 199 AsnLysGlu----- 201
 QY 1013 TTTAATGTTTGAACAATGTTTCTTCATTTCCCTGTGTGAGTGAATTAAGAGTA 1072
 DB 202 PheHisPheLleLeuAspValSerValLysThrValAlaAsnLeuGlnLeuSerAsnLle 221
 QY 1073 AAAGACTTTCTTAATATTTCGATGACCAACATTTAGAAATTAGTAACTGTAATTGGA 1132
 DB 222 LysCysValLeuGlnLysSerLysCysSerTrpPheLeuSerLleLeuAlaLysLeuGln 241
 QY 1133 CAGTTTCCCACTTGAACCTCAATCTCTCAAAAGCTTACTTTCACCTTCAACAAA--- 1189
 DB 242 ThrAspProLysLeuSerSerLysThrLleAsnAsnLleGlnThrThrTrpAsnSerPhe 261
 QY 1190 -----GTGGGAATGCTTTTTCAGAAATT 1213
 DB 262 IleArgLleLeuGlnLeuValLysPheLysThrValLysTrpLysSerLleSerAsnVal 281
 QY 1214 GATCTACCA---AGCCTTAGTTCTAGATCTCAGTAAAGTGGCTTGAATTCAAAGT 1270
 DB 282 LysLeuGlnGlnLysLeuAspPheArgAspPheAspTrpSerGlyThrSerLleLysAla 301
 QY 1271 TGTCTTTTCA-----AGTGAT----- 1288
 DB 302 LeuSerLleHisGlnValLysSerAspValPheGlyPheProGlnSerTrpLleLysGln 321

QY 1289 ---TTTGGGCAACAGCCTTAAG----- 1309
 DB 322 IlePheSerAsnMetAsnLleLysAsnPheThrValSerGlyThrArgMetValHisMet 341
 QY 1310 -----TATTAGATCTGAGCTTCAATGGTGTATT----- 1339
 DB 342 LeuCysProSerLysLleSerProPheLysLleLeuAspPheSerAsnLeuLeuThr 361
 QY 1340 ---ACCATGAGTTCAACCTTTGGGCTTGAACAACCTGAACATCTGATTTCCAGCAT 1396
 DB 362 AspThrValPheGlnLysCysGlyHisLleThrGlnLeuGlnThrLleLleGlnMet 381
 QY 1397 TCCAAATTTGAACAATGATGATGAGTTTGA---GTAATCTTATCACTGACAAATCTATT 1453
 DB 382 AenGlnLeuLysGlnLeuSerLysLleAlaGlnMetThrThrGlnLysSerLeuGln 401
 QY 1454 TACCTTGACATTTTGCATATCTACACACAGATGTTCTTCAAT-----GGCATCTTC 1504
 DB 402 GlnLeuAspLleSer-----GlnAsnSerValSerTrpAspGlnLysGlyAspCys 419
 QY 1505 AATGGCTTGCCAGTCTGAGATCTGAAATGCGGCAATCTTTCCAGAAATCTTC 1564
 DB 420 SerTrpThrLysSerLeuSerLysLeuAsnMetSerSerAsnLleLeuThrAspThrLle 439
 QY 1565 -----CTTCCAGATATCTTACAGAGCTGAGAAACTTGACCTTCTGACCTCTCT 1615
 DB 440 PheArgCysLeuProPro-----ArgLleLysValLeuAspLeuHis 453
 QY 1616 CAGTGTCAACTGAGAGATGTTGTCTCAACAGCATTTAACTACTCTCCAGTCTTCAAGTA 1675
 DB 454 SerAsnLysLleLysSerLle---ProLysGlnValValLysLeuGlnLysGln 472
 QY 1676 CTAAATATGAGCCACCAACACTTTTCAATGATGATGATGATGATGATGATGATGATGAT 1723
 DB 473 LeuAsnValAlaPheAsn-----SerLysThrAspLeuProGlyCysGlySerPhe 489
 QY 1724 AAGTGTCTGAACCTCCAGGTTCTTGATTAACGTCAATGATGATGATGATGATGATGATGAT 1783
 DB 490 SerSerLeuSerValLeuLleLleAspHisAsnSerValSerHisProSerAlaAspPhe 509
 QY 1784 AAACAGAACTACAGCATTTTCCAAATGATCTTAATCTTAAATCTTAACTGAAATGAC 1843
 DB 510 PheGlnSerCysGlnLysMetArgSer-----LleLysAlaGlyAspAsnPro 525
 QY 1844 TTTGCTTGAATCTTGAACACAGAGATTCTGCAATGATGATGATGATGATGATGATGATGAT 1903
 DB 526 PheGlnCysThrCysGlnLeuGlnLysLys-----ValLysAsnLleAspGlnVal 542
 QY 1904 TTGCTGGAAGTT-----GAACGAATGAATGTCACACACCTTCAAGATTAAG 1948
 DB 543 SerSerGlnValLeuGlnLysLysTrpProAspSerTrpLysCysAspTrpProGlnSerTrp 562
 QY 1949 CAGGCG-----ATGCTGTGCTGAGTTTGAATATCACTGCTGAC 1987
 DB 563 ArgGlyThrLeuLeuLysAspPheHisMetSerGlnLeuSerCysAsnLleThrLeuLeu 582
 QY 1988 ATGAATTAACACATCATTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2047
 DB 583 IleValThrLleValAlaThrMetLeuValLleAlaValThrValThrSerLeuCysLle 602
 QY 2048 GTTCTGTCTAATGAATTTTCACTGAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2107
 DB 603 TyrLeuAspLeuProTrpTrpLysLys---MetValCysGlnTrpThrGlnThrArgArg 621
 QY 2108 AGAGTGAAACATC-----TATGATGCTTTGTT 2137
 DB 622 ArgAlaLysAsnLleProLeuGlnLysLeuGlnArgAsnLeuGlnPheHisAlaPheLle 641
 QY 2138 ATCTACTCAGCAGATGAGACTGGTGAAGATGAAGATGATGATGATGATGATGATGATGATGAT 2194
 DB 642 SerTrpSerGlyHisAspSerPheTrpValLysAsnGlnLeuLeuProAsnLeuGlnLys 661
 QY 2195 GAAGGGGTGCTTCATTTCAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2254

```

Db      662  GLUGlymet-----GlnIleCybLeuHISgluHArgsbPheValProGlyLysSer 678
QY      2255  ATTCGTCGCAACATCATCATGAAAGTTTCCATPAAAAAGCGAAAGGATGTTGGTG 2314
Db      679  ILevalGluAsnIlelle---ThrcyVilegluLysSerTyxLysSerIlePheValLeu 697
QY      2315  TCCACAGACTTCATCCAGAGCCGCTGATCTTCATTCATGATATGATGATTCGTCAGACTGG 2374
Db      698  SerProAsnPheValGlnSerGluTrpCyshIstygGluLeuTyrrheAlaHshIsAsn 717
QY      2375  CAGTTTCGAGCAGCTGCTGCTGATCATCTTCATTCATTCCTGAGAGGTG---GAGAG 2431
Db      718  LeuPheHISgluLysSerAsnSerLeuIleLeuIleLeuLugluProIleProGlnTy 737
QY      2432  ACCCTGCTCAGGAGCAGGCTGAGCTGTACCCCTTCACGACGAAACACTTCCTGAG 2491
Db      738  SerIleProSerSerTyrrHISLysLysLysSerLeuMetAlaArgTrpThryrLysGlu 757
QY      2492  TGGAGAGCAGCTGCTCTGGGCGCACATCTTCGAGACGACTCGAAGAAAGCCCTG 2548
Db      758  TrpProLysgluLysSerLysArgGlyLeuPheTrpAlaAsnLeuArgAlaIle 776

RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A29943
R:Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A:Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, an
A:Reference number: A29943; MUID:88135760; PMID:2449285
A:Accession: A29943
A:Molecule type: DNA
A:Residues: 1-1097 <HAS>
A:Cross-references: UNIPROT:P08953; GB:M1969; GB:J02682; NID:G158640; PIDN:AAA28941.1;
C:Gene: FLYBase:TL
A:Cross-references: FLYBase:FBgn003717
C:Keywords: Transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-1097/Product: Toll protein #status predicted <MAT>

Alignment Scores:
Pred. No.: 3.78e-26 Length: 1097
Score: 454.00 Matches: 219
Percent Similarity: 38.97% Conservative: 129
Best Local Similarity: 24.52% Mismatches: 291
Query Match: 5.29% Indels: 254
DB: Gaps: 43

US-09-396-985b-1 (1-4868) x A29943 (1-1097)
QY      206  AATATTACTTATCATGATGAGCTGAATTTCTACAA--ATCCCGCAACCTCC 262
Db      270  AsnValThrAspIleAsnLeuSerAlaAsnLeuPheArgSerLeuProGlnGlyLeuPhe 289
QY      263  TTCTCAACCAAGAACTGGAC-----CTGAGCTTTAAT-----CCCCTGAGGCAT 307
Db      290  AspHisAsnLysHISLeuAsnGluValArgLeuMetAsnAsnArgValProLeuAlaThr 309
QY      308  TTAGGAGCTATAGCTTCTTCAGTTTCCAGAGCTGAGAGGCTGAGATTATCCAGGTG 367
Db      310  LeuProSerArgLeuPheAlaAsnGlnProGluLeuGlnIleLeuArgLeu---ArgAla 328
QY      368  GAATCCAGCAATGAGATGAGGAGCATATCAGAGCTTAAGCCACTCTCTACCTTATA 427
Db      329  GluLeuGlnSerLeuProGlyAspLeuPheGluHISerThrGlnIleThrAsnIleSer 348
QY      428  TTGACAGGAAACCCCATCCAGAGATTAGCCCTGGAGCCCTTTCTGAGATCAAGTTTA 487
Db      349  LeuGlyAspAsnLeuLeuLysThrLeuProAlaThrLeuGluHISGlnValAsnLeu 368

```

```

QY      488  CAGAGCTGATGCTGTGAGACAAATCTAGCATCTTAGAGAACTTCCCATTTGACAT 547
Db      369  LeuSerLeuAspLeuSerAsnAsnArgLeuThrHISLeuProAspSerLeuPheAlaHIS 388
QY      548  CTCMAAATCTTGAAGAACTTAATGTGCTCAATCTTATCCMAATCTTCAAAATTACCT 607
Db      389  ThrThrAsnLeuThrAspLeuArgLeuGluAspAsnLeuLeuThrGlyLysSer---Gly 407
QY      608  GAGTATTTTCTTAATGACCAATCTAGAGCACTTGAGACTTTCACGACAAAGATTCA 667
Db      408  AspIlePheSerAsnLeuGlyAsnLeuValThrLeuValMetSerArgAsnArgLeuArg 427
QY      668  AGTAT-----TATTCACAGACTTGGGCTTCAAT----- 700
Db      428  ThrIleAspSerArgAlaPheValSerThrAsnGlyLeuArgHISLeuHISLeuAspHis 447
QY      701  -----CAATGCCCTTACTCAATCTCTTTAGACCTGCTCCGTAAT--- 742
Db      448  AsnAspIleAspLeuGlnGlnProLeuLeuAspIleMetLeuGlnThrGlnIleAsnSer 467
QY      743  CCTATGAACTTATCCACACAGTGATTTAAAGAAATTAGCTTCATATAGCTGATT 802
Db      468  ProPheGlyTrpMetHIS-----GlyLeuLeuThrLeuAsnLeu 480
QY      803  AGAATATATTTGATGATTAAATGTAATGAAAACTTGATTCAGAGCTGCTGGCTTTA 862
Db      481  ArgAsnAsn-----SerIlelle----- 486
QY      863  GAAATCCATCGTTGGTCTGAGAGATTTAGAAATGAAAGAAACTTGAAAGTTTGAC 922
Db      487  -----PheValTyrrAsnAspTrpLysAsn----- 494
QY      923  AATCTGCTTAGAGGCGCTGTGCCAATTGACATGAAATTCGATAGCATCTTA 982
Db      495  -----ThrcMetLeuGlnLeuArgGluLeuAspLeuSerTyx--- 506
QY      983  GACTACCTGATGATGATTATTCATTTAATTGTTGCAAAATTTGCTTCATTT 1042
Db      507  -----AsnAsnIleSerSerLeu 512
QY      1043  TCCCTG-----GTGAGTGATCAATTGAA 1066
Db      513  GlyTyrrGluAspLeuAlaPheLeuSerGlnAsnArgLeuHISValAlaAsnMetThrHISAsn 532
QY      1067  AGGCTAAAGACTTTCT-----TATAATTCGGA 1096
Db      533  LysIleArgArgIleAlaLeuProGluAspValHISLeuGlyGlyTyrrAsnAsnAsn 552
QY      1097  TGGCAACATTTAGATT-----GTTAACTGTAAATTTTGACAGATT 1138
Db      553  LeuValHISValAspLeuAsnAsnAsnProLeuValCysAspCysThrIleLeuTrpPhe 572
QY      1139  CCCACATG-----AACTCAAAATCT 1159
Db      573  ILeGlnLeuValArgGlyValHISLysProGlnTyrrSerArgGlnPheLysLeuArgThr 592
QY      1160  CTCMAAAGCTTACTTCACTTCCAA---AAAGTGGGAATCTTTTCAAGAGTTGAT 1216
Db      593  AspArgLeuValCysSerGlnProAsnValLeuGluGlyThrProValArgGlnIleGlu 612
QY      1217  -----CTACCAAGCTTGTAGTTTCTGATCTCGATGCAATGAGCTGAGTTTC 1264
Db      613  ProGlnThrLeuIleCysProLeuAspPheSerAspProArgGluArgLysCysPro 632
QY      1265  AAGAGTTC---TGTTCTCAAGATGATTTTGGACAAACCAAGCTTAAGATTAGCTTG 1321
Db      633  ArgGlyCysAsnCyshISValArgThrTyrrAsp-----LysAlaLeuValIle 648
QY      1322  AGCTTCAATGAGTGTATTATCATGATTCAAACTTTTGGGCTTAAAGAACTAGAACT 1381
Db      649  AsnCyshIS-----SerGlyAsnLeuThrHISValProArgLeuProAsn 663

```

OY		1382	CTGGATTTCCAGCATTTCCAAATTGAAACAAATGAAGTGATTTTCAGTATTCCTTAACCTC	1441
Db		664	Leu-----HisLysAsnMetGlnLeuMetGlu-----LeuHisIleu	675
OY		1442	AGAAACSTCAATTTACTGTGCATATTTCTCATCTACACCACAGATTTCTTTCATGGCAGTC	1501
Db		676	GluAenAntlrInLeuLeuArgLeuProSerAlaAenThr-----	688
OY		1502	TTCATATGGCTGTGCCAGTCTCGAAGTCTTGAATAATGGCTGGCAATCTTTCCAGGAAGAAC	1561
Db		689	--ProGlyTyrgLusSerValThrSeuLeuHisIleuAlaGlyAsn-----	702
OY		1562	TTCTCTTCAGATATCTTCACAGAGCTGAGAAATCTGACCTTCGGACCTTCAGAGT	1621
Db		703	-----AbnLeuThrSerTlleAspValAspDlnLeu	712
OY		1622	CAACTGAGCAGATTGTCTCCAACAGACATTTAACTCATCTCCAGTCTTCAGGTACTAAAT	1681
Db		713	-----ProThr-----Asn	715
OY		1682	ATGAGCCCAACAACCTCTTTTCATGTGATACGTTTTCTTAATAGTGTGAACTCCCTC	1741
Db		716	LeuThirHis-----	718
OY		1742	CAGGTCTTTGATTCACAGTCTCAATPCACATATAGACTTCCAAAAACAGAAATCACAGAT	1801
Db		719	-----LeuAspDlnLeuSerTlrrAsnHisIleu-----GlnMetLeuasn---	730
OY		1802	TTTCCAACTAGCTCTGACTTTTCTTAAAT-----CTTAACT	1834
Db		731	---AlathrValIleuGlyPheLeuAsnArgThrMetLysTrpArgSerValLysLeuSer	749
OY		1835	CAGATGACTTGTCTTGTACTTGTGAACACACAGATTTCTTGCAATGGATCAAGGACCAAG	1894
Db		750	GlyAsnProTlrrPmeCyAspCyserThrAlaLysProLeuLeuLeuPheThrGlnAspAsn	769
OY		1895	AGGCAAGCTTTGTGGGAAGTTGAACGAATGGAATGTGCACACCTTCAGATTAAGCAGGCG	1954
Db		770	PheGlnArgIleGlyAspArgAsnGlnMetCysValAsnAlaGlnMetProThrArg	789
OY		1955	ATGCCCTGTGCTAGTTGAATATATCACTGTGCAGATGAATAGAACCATC--ATTGGATGTG	2011
Db		790	MetValGlnLeuSerThrAsnAspDlnLeuCyProAlaGlnLysGlyValPheIleAlaLeu	809
OY		2012	TCGGTCT-----CTCAGTGTGCTGTGAATCTGTGTGAGCAGTTCTGTGCTATTAAG	2062
Db		810	AlaValValIleAlaLeuThrGlyLeuLeuAlaGlyPheThrAlaAlaLeuTyrlTyrLys	829
OY		2063	TTC-----TATTTTCACTGATGCTTTCTTGCGTGCAGTA	2098
Db		830	PheGlnThrGlnIleLysIleTlrrLeuTyrlAlaHisAsnLeuLeuLeu-----	845
OY		2099	AAGTATGGTAAAGGTGAAGAATC-----TATGATGCTTTGTATATCTAC	2143
Db		846	TrpPheValThrGlnGlnAspLeuAspLysAspLysLysPheAspAlaPheIleSerTyr	865
OY		2144	TCAAAGCAGAGTAGAGACTGGGTGAAGAGATAGACTAGATTAAGAAATTTAGAGAAAGGGGTG	2203
Db		866	SerHisLysAspArgGlnSerPheIleGlnAspTyrLeuValProGlnLeuGlnHisGlyPro	885
OY		2204	CTTCCATTTACGCTCTGCTGCTTCACTACAGAGATTTATTTCCCGGTGGCATTTGCTGCC	2263
Db		886	GlnLysPheGlnLeuCysValHisGlnLysArgTlrrLeuValGlnGlnHisIleProGln	905
OY		2264	AACATTCATCCATGAAGTTTCCATPAAGGCGGAAGAAGTGATTTGTGTGTGTGTCCAGAC	2323
Db		906	AsnIleMet---ArgSerValAlaAspSerArgThrLleIleValLeuSerGlnAsn	924
OY		2324	TTTCATCCAGACCGGTGTGTATCTTTGAAATGAAGATTTGCTGCAGACCTGCAGCATTTCTG	2383
Db		925	PheIleLysSerArgLutPrpAlaArgLeuCluIurHeArgAlaAlaHisArgSerAlaLeuAsn	944
OY		2384	AGCAGTGTGCTGTATCATCTTCAATGTCT-----CTGCAGAAAGTGAAGAAGAC	2434

Db 945 GUGUGAAGSERRAGLLEILEVALLIELELYRserapllleGlyAspValGlnlys--- 963

Qy 2435 CTGCTCAGCAGCAGGTGGACCTGTACCGCTTTCAGACAGAACTTACCTGGAGTGG 2494

Db 964 ---LeuAaprglUGlnLeuLYaLAtyr-----LeuYswetAanThrTYLeuLYstrp 980

Qy 2495 GAGGACAGTGTCTCGGGGGCCACATCTTCTGGAGACGACATCCAGAAAAAGCCCTGTGGAT 2554

Db 981 GlyAspPro-----TrrPheTrrAspLYLeuAArgPheAlaLeuProHis 995

Qy 2555 GGTAAATCATGAAATCCAGAGAAAGTGGTGCAGCA 2593

Db 996 ArgArg-----ProValGlyAsnIleGlyAsnGly 1005

RESULT 4

T13852

gene wheeler protein - fruit fly (Drosophila melanogaster)

CtSpecies: Drosophila melanogaster

CtDate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

CtAccession: T13852

RtElidon, E.; Kooyer, S.; D'aveyln, D.; Duman, M.; Lawinger, P.; Botas, J.; Bellen, H.

development 120, 885-899, 1994

A.titile: The Drosophila 18 wheeler is required for morphogenesis and has striking simil

A.Reference number: Z17796; MUID:95324375; PMID:7600965

A.Accession: T13852

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-1389 <EUD>

A.Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAA792

A.Gene: wheeler

A.Cross-references: FlyBase:FBgn0004364

Alignment Scores:

Pred. No.: 1.57e-24 Length: 1389

Score: 433.00 Matches: 217

Percent Similarity: 39.93% Conservative: 138

Best Local Similarity: 24.41% Mismatches: 356

Query Match: 5.05% Indels: 178

DB: 2 Gaps: 34

US-09-396-985B-1 (1-4868) x T13852 (1-1389)

Qy 278 CTGACCTGACCTTAAATCCCTGAGGACATTTAGACGACTATAGCTTTCAGTTTCCA 337

Db 338 LeuAsnLeuSerAsnAsnAlaLeuThrArgIleGlySerLYstrPhelyGlnLeuYtr 357

Qy 338 GAACCTGACGCTGCGATTATTCAGGCTGCAATTCAGACATTTGAAGATGGGCATAT 397

Db 358 PheLeuGlnIleLeuApmetArgAsnAsnSerIleGlyHisIleGlnGlnLYAlaPhe 377

Qy 398 CAGAGCTTAAGCCACCTCTCACTTAATATGACAGAAACCCCATCCAGATTAGCC 457

Db 378 LeuProLeuLYrAsnLeuHisIsthLeuAsnLeuAlaGlnAsnArgLeuHisIsthLeuAsp 397

Qy 458 CTGGAGACCTTTTCTGACGATATCAAGTTTACAGAGCTGTGCTGTGGAGACAAATCTA 517

Db 398 AsnArgIlePheAsnGlyLeuYrValLeuThrIrysLeu---ThrLeuAsnAsnAsnLeu 416

Qy 518 GCATCTCTA---GAGAATTCCCATGACATCTCAAAACTTTGAAGAACTTAATGTG 574

Db 417 ValSerIleValGlnSerGlnAlaPheArgAsnCyserAerPLeuLYGlnLeuAspLeu 436

Qy 575 GCTCAATCTTAATCCAACTTTCAAAATTCAGAGATATTTTCTTAATTCAGCAATCTA 634

Db 437 SerSerAsn-----GlnLeuThrGlnValProGlnAlaValGlnAspLeuSerMetLeu 454

Qy 635 GAGACATTTGACCTTTCCAGCAACAAGATTTCAAGATTTATTCACAGACTTCCGGGTT 694

Db 455 LysThrLeuAspLeuGlyGlnAsnGlnIleSerGlnLeuLYsAsnAanThrPheArgAsn 474

Qy 695 CTACATCAAAATGCCCTACTCAATCTC----- 721

Db 475 LeuAsnGlnIleuThrGlyLeuArgLeuIleAspAsnArgIleGlyAsnIleThrValGly 494
QY 722 -----TCTTGAAGCTGTCCTGAACTCTTAAGAACTTT 754
Db 495 MetPheGlnAspLeuProArgLeuSerValLeuAsnIleValAsnArgIleGlnSer 514
QY 755 ATCCAACTGAGTGCATTT---AAAGAAATTAAGGCTTCATGAAGCTTATAGAAATTAAT 811
Db 515 IleGluArgGlyAlaPheSerPylAsnThrGluIleGluAlaIleArgLeuAspPylAsn 534
QY 812 TTTCATAGATTAAATGTAATGAATACTGTATTCAGAGCTGAGCTGGTTTGAAGTCCAT 871
Db 535 Phe-----LeuThrAspIleAsnGlyIlePheAlaThrLeuAlaSer 548
QY 872 CGTTGGTTCTGGAGAAATTTAGAAATGAA----- 901
Db 549 LeuLeuThrLeuAsnLeuSerGluAsnIleLeuValIlePheAspTyrAlaPheIlePro 568
QY 902 GGAAGCTTGAAAGATTGAC-----AAATCTGCTAGAGGGCTGTGCAATTTG--- 952
Db 569 SerAsnLeuPylStrLeuAspIleHisGlyAsnTyrIleGluAlaLeuGlyAsnTyrTyr 588
QY 953 ---ACCAATGAGAATTCGATTAGACATTAAGACTTAACCTCGATGATATTAATTGAC 1009
Db 589 LysLeuGlnGluGluIleArgValIleThrThrLeuAspAlaSerHisAsnArgIleThrGlu 608
QY 1010 TTATTTAATGTTTGACAAATGTTTCTCATTTTCCCTGGTAGCTGAGCTATTTGAAGG 1069
Db 609 Ile---GlyAlaMetSerValProAsnSerIleGluLeuLeuPheIleAsnAsnIle 627
QY 1070 GTAAAGACTTTTCTTTAAT-----TTCGATGCGCAATTTAGATTAAGTATTAATGCT 1123
Db 628 IleGlyGlnIleGlnAlaAsnThrPheValAspPylSerThrArgLeuAlaArgValAspLeu 647
QY 1124 AAATTTGACAGATTTCACCAATGAATGAATCTCAAAAGCTTACTTTCACTTCC 1183
Db 648 TyrAlaAsnValLeuSerPylSerLeuAsnAlaLeuArgValAlaProValSerAla 667
QY 1184 AACAAA-----GTCGGGAATGCTTTTCA----- 1207
Db 668 GluIleProValProGluPheTyrLeuGlyGlyAsnProPheGluCysAspCysSerMet 687
QY 1208 -----GAAGTTGATCTA 1219
Db 688 GluThrLeuGlnArgIleAsnAsnLeuThrThrArgGlnHisProHisValValAspLeu 707
QY 1220 CCAAGCTTGAGTTCTA----- 1240
Db 708 GlyAsnIleGluCysLeuMetProHisSerArgSerAlaProLeuArgProLeuAlaSer 727
QY 1241 CTCAGTATGAATGCTTGAAGTTTCA----- 1273
Db 728 LeuSerAlaSerThrPheValCysValTyrGluSerHisCysProProThrCysHisCys 747
QY 1274 TGTTCCTCAAGGTATTTGGGACAAACAGCTTAAAGATTAGATTCAGCTTCAATGCT 1333
Db 748 CysGluTyrGluGlnCysGluCysGluValIleCysProGluAsnCysSerCysPheHis 767
QY 1334 GTTATTAACATGATTCAAATCTTCTG---GGCTTAAGAACTAAGAACTTGGAT 1387
Db 768 AspAlaThrThrAlaThrAsnIleValAspCysGlyArgGlnAspLeuAlaIleLeu--- 786
QY 1388 TTCCAGATTCCAATTTGAAACAAATAGAGAGTTTTCAGTATTCCTATTCATCAGAAAC 1447
Db 787 -----ProAsnArgIleProGlnAspValSerAspLeuTyrLeuAspGlyAsnAsn 803
QY 1448 CTCATTAACCTGCAATTCCTCAATCTCACACCCAGAGTGTCTTCAATGGATGCTTCAAT 1507
Db 804 MetProGluLeuGluValGlyHisLeuThrGlyArgArgAsnLeuArgAlaLeuTyrLeu 823
QY 1508 GCGTTGTCAGTCTGAAAGCTTTGAAATGAGCTGGCAATTCCTTCCAGAAACTTCTCT 1567

Db 824 AsnAlaSerAsnLeuMetThrLeuGlnAsnGlySer----- 835
QY 1568 CCAAGATATCTTCACAGAGCTGAGAACTTGAAGCTTCTGGAGCTCTCAAGTGTCAAGT 1627
Db 836 -----LeuAlaGlnLeuValAlaAsnLeuArgValIleHisLeuGluAsnAsnValSer 852
QY 1628 GAGCAGTTGCTTCCAAACAGATTTTAAGTCACTTCCAGTCTTCAAGTACTTAATAGAC 1687
Db 853 ThrAlaLeuGlnGlyThrGluPheArgSerLeuGlyLeuLeuArgGluLeuTyrLeuHis 872
QY 1688 CACACAACTTCTTTTCATTCAGATACGTTTCTTATAGTGTCTGAACCTCCCTCCAGTT 1747
Db 873 AsnAsnMetLeuThrHisIleSerAsnAlaThrPheGluProLeuValSerLeuGluVal 892
QY 1748 CTGTATTAACATGTCATACATTAATGACTTCCAAAACAGAACTACAGCAATTTTCCA 1807
Db 893 LeuArgLeuAspAsnAsnArgLeuSerSerLeuProHisLeuGlnTyrArgHis----- 910
QY 1808 AGTACTGAGCTTTCTTAAATCTTACTCAGAAATGACTTGTGTGATCTTGTGAAAC--- 1864
Db 911 ---SerLeuGlnGlyLeuThrLeuGluArgAsnAlaIlePylSerCysArgCysGlnGlnLeu 929
QY 1865 CAGAGTTCTCTGCATGATGATCAAAGCACAGAGCAAGCTTGTGTGAAGTTGAACGAATG 1924
Db 930 ArgGluLeuAlaGlnPheValSerAspAsnAlaMetValValArgAspAlaHisAspIle 949
QY 1925 GAATGTGCAACACCTTCAGATTAAGCAGGAGCATGCGTGTCTG--- 1966
Db 950 TyrCysLeuAspAlaGlyIleLeuArgGluLeuGluLeuIleGlyAsnLeuAlaAsnGly 969
QY 1967 -----AATTGAATATGACCTGTGCAATGAATAAG 1996
Db 970 ProAspCysSerAspLeuAspLeuAspAlaSerAlaSerAlaSerSerSerGlnAspLeu 989
QY 1997 ACC---ATCATTTGCT-----GTCCGCTCTCAAGTGTGCTTGTAGTA 2035
Db 990 AlaGlyAlaIleGlyCysProCysTyrProAlaValLeuValLeuIlePheLeuValAla 1009
QY 2036 TCTGTTGTAAGCAGTTGCTGATTAAGTCTATTTTCACTGATGCTTCTGTGCTGCTG 2095
Db 1010 ValLeuIleIleValaPheValPheArgGluSerValaArgMetThrLeuPheAla----- 1027
QY 2096 ATAAAGTATGCT-----AGAGTGAAC---ATCTATGAT 2128
Db 1028 ---HisTyrGlyValaArgValCysGluProArgPheGluAspAlaGlyLysLeuTyrAsp 1046
QY 2129 GCGTTGTATTAATCTCAAGCCAGATGAGAGTGGGTAAAGAAATGAGTATGAAGAAAT 2188
Db 1047 AlaIleIleLeuHisSerGluLysAspTyrGluPheValCysArgAsnIleAlaIleGlu 1066
QY 2189 TTAGAAGAGGGGTGCTCCATTTCAAGTGTGCTGCTCAGTACAGACATTTATTCGCGGT 2248
Db 1067 LeuGlnHisGlyArgProPheArgLeuCysIleGlnGlnArgAsp---LeuProPro 1085
QY 2249 GTGCGCATTTGCTGCCAAATCATTCATGAAGTTTCCATTAAGGCCGAAGTGAATTTGT 2308
Db 1086 GlnAlaSerHisLeuGlnLeuVal---GluGlyAlaArgAlaSerArgLysIleIleLeu 1104
QY 2309 GTGCTGCCAGCACTTCAATCCAGAGCCGCTGTGATCTTTGAATATAGATGCTCAG 2368
Db 1105 ValLeuThrArgAsnLeuLeuAlaThrGluTyrAsnArgIleGluPheArgAsnAla--- 1123
QY 2369 ACCTGCGAGTTTGTGACAGTGTGCTGGATATCATTTCAATGCTCTGCAAG--- 2422
Db 1124 -----PheHisGluSerLeuArgGlyLeu-----AlaGlnLysLeuVal 1136
QY 2423 ---GTGAAGAAGACCTGTCAAGGCAAGAGTGAAGCTGATCCGCTTCCAGAGAAC 2479
Db 1137 IleIleGlnGluThrSerValSerAlaGluAlaGluAspValaIleGluLeuSer----- 1154
QY 2480 ACTTAACCTGAGTGGAGAGCAAGTGTCTGGGGCGGCACATC----- 2521
Db 1155 ProTyrLeuLys-----SerValProSerAsnArgLeuLeuThrCysAspArgTyr 1171

Oy	2522	TTCTGAGACGACTCAGAAAAAGCCCTG	2548
		:::	:::
Db	1172	PhETpGluysleuArGTYrAlaile	1180

RESULT 5

c1r protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: F13887
 R:Chiang, C.; Beachy, P. A.
 Mech. Dev. 47, 225-239, 1994
 A:Title: Expression of a novel Toll-like gene spans the parasegment boundary and contrib
 A:Reference number: Z17805; MUID:95151581; PMID:7848870
 A:Accession: F13887
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-1385 <CHI>
 A:Cross-references: UNIPROT:Q24591, EMBL:S76155, NID:g913247, PID:g913248, PIDN:AA833383
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0004364
 A:Note: c1r

Alignment Scores:

Pred. No.:	1,28-23	Length:	1,385
Score:	421.00	Matches:	213
Percent Similarity:	33.60%	Conservative:	139
Best Local Similarity:	23.96%	Mismatches:	359
Query Match:	4.91%	Indels:	178
DB:	2	Gaps:	33

US-09-396-985B-1 (1-4868) X T13887 (1-1385)

QY 278 CTGACGCTGACCTTAAATCCCTTGAGGACTTATGAGCTTACGTTCCAA 337
 |||:::||||| ||| |||:::||||| |||:::|||||
 Db 338 LeuasnleuSerAsnAenAlaLeuThrArgIleGlySerIysTrpPheIysGluLeuTyr 357
 QY 338 GAACGTGACGAGTGTGATTTATCCAGGTGTGAAATCCAGCAAAATTGAAGATGGGCGATAT 397
 |||:::||||| |||:::||||| |||:::||||| |||:::||||| |||:::|||||
 Db 358 PheLeuGlnIleLeuApmMetArgAsnAsnSerIleGlyHisIleGluGluGlyAlaPhe 377
 QY 398 CAGAGCCTTAAGCCCACTCTTACCTTAATATTAACAGAGAAACCCCACTCAGAGTTTACC 457
 |||:::||||| |||:::||||| |||:::||||| |||:::||||| |||:::|||||
 Db 378 LeuProLeuTyrAraenLeuHisThrLeuAsnLeuAlaGluAsnArgLeuHisThrLeuAsp 397
 QY 458 CTGGAGAGCCTTTCTTGACGTATCAAGTTTACAGAGTGGGTGGGTGGAGACAATTTA 517
 |||:::||||| |||:::||||| |||:::||||| |||:::||||| |||:::|||||
 Db 398 AsnArgIlePheAsnGlyLeuTyrValLeuThrIysLeu--ThrLeuAsnAsnLeu 416
 QY 518 GCATCTCTA---GGAACCTTCCCATGACATCTCAAACTTTGAAAGAATTAAAGTG 574
 |||:::||||| |||:::||||| |||:::||||| |||:::||||| |||:::|||||
 Db 417 ValSerIleValGluSerGlnAlaPheArgAsnIysSerAspLeuIysGluLeuAspLeu 436
 QY 575 GCTCAACAATCTTATTCAAATCTTTCAAAATTACCTGAGTATTTTCTTAATCTGACCAATCTA 634
 ::::||| |||:::||||| |||:::||||| |||:::||||| |||:::|||||
 Db 437 SerSerAsn-----GlnLeuThrGluValProGluAlaAlaGlnAspLeuSerMetLeu 454
 QY 635 GAGACACTTGACCTTCCAGCAACAAGATTCAAAGTATTATTTCACAGACTCCGGGCTT 694
 ::::||| |||:::||||| |||:::||||| |||:::||||| |||:::|||||
 Db 455 LysThrLeuAspLeuGlyGluAsnGlnIleSerGluPheIysAsnAsnThrPheArgAsn 474
 QY 695 CTACATCAAAATGCCCTTACTCAATCTC----- 721
 |||:::||||| |||:::||||| |||:::||||| |||:::||||| |||:::|||||
 Db 475 LeuAsnGlnIleuThrGlyLeuArgLeuIleAspAsnArgIleGlyAsnIleThrValGly 494
 QY 722 -----TCTTGAACCTGTCCCTGAATCCTATGAACTTT 754
 |||:::||||| |||:::||||| |||:::||||| |||:::||||| |||:::|||||
 Db 495 MetPheGlnAspLeuProArgLeuSerValLeuAsnLeuAlaIysAsnArgIleGlnSer 514
 QY 755 ATCAACACGATGCAATTT---AAGAATTAAGGCTTCATTAAGCTGACTTTAAGAAATAT 811
 |||:::||||| |||:::||||| |||:::||||| |||:::||||| |||:::|||||
 Db 515 IleGluArgGlyAlaPheAspIysAsnThrGlnIleGluAlaIleAspLeuAspIys 534

QY	812	TTTGAAGATTAAATGTAATGAAAACCTGTAATTCAGAGTCGGGCTGGTTTAAAGATCCAT	871
DB	535	Phe-----LeuThrAspIleAsnGlyIlePheAlaThrLeuAlaSer	548
QY	872	CGTTTGGCTCGGGAGAAATTAGAAATGAA-----	901
DB	549	LeuLeuThrLeuAsnLeuSerGluAsnHisLeuValIlePheAspTyrAlaPheIlePro	568
QY	902	GAAAACCTTGAAAAATTGAC-----AAATCTGCTCTAGAGGGCTGTGCAATTTCG---	952
DB	569	SerAsnLeuLeuSerPheLeuAspIleHisGlyAsnTyrIleGluAlaLeuGlyAsnTyrTyr	588
QY	953	---ACCAATTGAAGAATTCGCAATTGACACTTACTTAACTACTACTCCGATGATATTATTCAC	1009
DB	589	LeuLeuGlnGluGluIleArgValIleThrThrLeuAspAlaSerHisAsnArgIleThrGlu	608
QY	1010	TTATTTAATGTTTGAACAAATGTTCTCTCAATTTTCCGCGGAGCTGGACATTTGAAAG	1065
DB	609	Ile---GlyAlaMetSerValProHisSerIleGluLeuLeuPheIleAsnAsnIle	627
QY	1070	GTAAAGAAGCTTTTCTTAATAT-----TTGCGATGGCAACATTTGAATTAGTTAACTGT	1123
DB	628	IleGlyGlnIleGlnAlaAsnThrPheValAspTyrThrArgGluAlaArgValAspLeu	647
QY	1124	AAATTTGACACGTTTCCGACATTTGAAAACSTCAATCTCTCAAAAGGCTTACTTTCATCTCC	1183
DB	648	TyrAlaAsnValLeuSerTyrIleSerLeuAsnAlaArgValAlaProValSerAla	667
QY	1184	AACAA-----GGGGGAATGCTTTTCA-----	1207
DB	668	GluLeuSerProValProGluPheTyrGluGlyGlyAsnProPheGluCysAspCysSerMet	687
QY	1208	-----GAAGTTGATCTA	1219
DB	688	GluTyrLeuGlnArgIleAsnAsnLeuThrThrArgGlnHisProHisValAlaAspLeu	707
QY	1220	CCAAAGCTTGAAGTTCTA-----GAT	1240
DB	708	GlyAsnIleGluCysLeuMetProHisSerArgSerAlaProLeuArgProLeuAlaSer	727
QY	1241	CTCAATGAAAATGGCTTGAAGTTCAAA-----GGTTCC	1273
DB	728	LeuSerAlaSerAspPheValCysLeuTyrGluSerHisCysProProThrCysHisCys	747
QY	1274	TGTTCTCAAGATGATTTGGGACAAACAGACGCTAAAGATTTAGACTGAGCTTCAATGCT	1333
DB	748	CysGluTyrGlnGlnCysGluCysGluValIleLeuSerProGluAsnCysSerCysPheHis	767
QY	1334	GTTATTTACATGAGTTCAACTTCTTG-----GGCTTGAACAACATAGAACATCTGAT	1387
DB	768	AspAlaThrThrPheAlaThrAsnIleValAspCysGlyArgGlnSerLeuAlaAlaLeu---	786
QY	1388	TTCCAGACATTCCAATTGAAAACAAATGAGTGGATTTCCAGTATTCCTATGATCAACAAC	1447
DB	787	-----ProAsnArgIleProGlnAspValSerAspLeuTyrLeuAspGluAsnValn	803
QY	1448	CTCATTTACCTTGACATTTCTCATCTACACACAGACATCTGCTTCAATGAGATCTGCAT	1507
DB	804	MetSerGlnLeuGlnValGlyHisLeuThrGlyArgTyrAsnLeuArgAlaLeuTyrLeu	823
QY	1508	GGCTTGTCCAGTCTCCGAAGCTTTGAAAATGGCTGGCAATCTTTCCAGAAAACCTTCTT	1567
DB	824	AsnAlaSerAsnMetThrLeuGlnAsnGlySer-----	835
QY	1568	CCAGATATCTTCCACAGACSTGGAATATGACCTTCTGAGCTCTCTCACTGTCAACTG	1627
DB	836	-----LeuAlaGlnLeuValAsnLeuArgValLeuHisLeuGlnAsnAsnLeuLeu	852
QY	1628	GAGCAGTGTCTCCACAGACATTTAACTACTCTCCAGTCTTCAAGATCAAGATATAGAC	1687
DB	853	ThrAlaLeuGlnGlyThrGluPheArgSerLeuGlyLeuLeuArgGluLeuTyrGluHis	872

Oy	1688	CACAAACAACCTTTTCATTGGAATACGTTTCTCTTAATAAGTCTCGAACTCCCTCCAGATT	1747
Db	873	AsnMetLeuThrHisIleSerAsnAlaThrPheGluProLeuValSerLeuGluVal	892
Oy	1748	CTTGATTAACGTCCATCATCATATATAGCTTCCAAAACAGAACTACAGCATTTTCCCA	1807
Db	893	LeuArgLeuAspAsnAsnArgLeuSerSerLeuProHisLeuGlnTyrArgHis-----	910
Oy	1808	AGTAGCTAGCTTTCTTAAATCTTAACGAGAATGACTTTGGTGTGTACTTGAAAC--	1864
Db	911	--SerLeuGlnGlyLeuThrLeuGlnTyrArgAsnAlaTrpSerCysArgCysGlnGlnLeu	929
Oy	1865	CAGAGTTTCTCGCAATGAGATCAAGGACCAAGAGGAGCTCTTGGTGGAAAGTTGAACGAATG	1924
		:::	:::
Db	930	ArgGluLeuAlaGlnPheValSerAspAsnAlaMetValAlaArgAspAlaHisAspIle	949
Oy	1925	GAATGTGCAACACCTTTCAGATAGAGGAGGACGCTGGTGGCG--	1966
Db	950	TyrCysLeuAspAlaGlyIleLeuArgGluLeuGlnLeuIleGlyAsnLeuAlaMetGly	969
Oy	1967	-----AGTTGAATATCACCTGTGACATGAAT--	1993
Db	970	ProAspCysSerAspLeuLeuAspAlaSerAlaSerAsnIleSerSerSerGlnAspLeu	989
Oy	1994	-----AAGACATCATTTGGTGTGTGGTGCTTCAAGTGTCTGTAGTA	2035
Db	990	AlaGlyGlyTyrArgLeuProLeuLeuAlaValLeuValLeuIlePheLeuAspVal	1009
Oy	2036	TCTGTGTGAGACGTTCTGTCTCATATAGTTCATATTTCACGTGATGCTTCTTGCTGGCTGC	2095
Db	1010	ValLeuIleIleValAlaPheValPheArgGluSerValaTrpMetTrpLeuPheAla-----	1027
Oy	2096	ATAAAGTAGTGT-----AGAGGTGAAC-----ATCATGAT	2128
Db	1028	--HisTyrGlyValAlaArgValCysGluTrpProArgPheGluAspAlaGlyLeuTyrAsp	1046
Oy	2129	GCCTTGTATTACTCAACCCAGAGATGAGACTGGGTAGAGATAGACTAGTAAAGAT	2188
Db	1047	AlaIleIleLeuHisSerGlnLysAspTyrGluPheValCysArgAsnIleAlaIaGlu	1066
Oy	2189	TTAGAAGAAAGGGGTGCTCCATTTGAGCTGGCTGCTCACTACAGAGACTTTATTCGCCGT	2248
Db	1067	LeuGlnHisGlyArgProProPheArgLeuCysIleGlnGlnArgAsp--LeuPro	1085
Oy	2249	GTGGCCATGTGCTGCCAATCATTCATGAAGGTTTCCATAAAAGCCGAAGGTGATTGT	2308
Db	1086	GlnAlaSerHisLeuGlnLeuVal--GluGlyAlaArgAlaSerArgLysIleIleLeu	1104
Oy	2309	GTGGTGTCCCAACCTTATCCACAGACCGGTGTATCTTGATATAGATTGCTCAG	2368
Db	1105	ValLeuThrArgAsnLeuLeuAlaThrGluTrpAsnArgIleGluPheArgAsnAla-	1123
Oy	2369	ACCTGGCAGTTTCTGAGCAGTGTGCTGTGATTCATTTGATTCCTGACAGAG-----	2422
Db	1124	-----PheHisGluSerLeuArgGlyLeu-----AlaGlnLysLeuVal	1136
Oy	2423	--GTGAGAAACCCCTGCTCAGCAGCAGAGGTGAGCTGTACCGCTTCTCAGCAGAAC	2479
		:::	:::
		:::	:::
Db	1137	IleIleGlnGluThrSerValSerAlaGluAlaGluAspValAlaGluLeuSer-----	1155
Oy	2480	ACTTACCTGGAAGTGGAGAGCAGTGTCTCTGGGGCGGACATC-----	2521
Db	1155	ProTyrLeuLys-----SerValProSerAsnArgLeuLeuThrCysAspArgTyr	1177
Oy	2522	TTCTGAGACGACTCAAGAAAGCCCTG	2548
Db	1172	PheTrpGluLysLeuArgTyrAlaIle	1180

C/Accession: T15864
R/Fulton, L. submitted to the EMBL Data Library, November 1995
A/Description: The sequence of C. elegans cosmid C56B6.
A/Reference number: S69019
A/Accession: T15864
A/Status: preliminary; translated from GB/EMBL/DBD/J
A/Molecule type: DNA
A/Residues: 1-1066 <FULL>
C/Genetics:
A/Gene: CESP:C56B6.6
A/Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 5

Alignment Scores:
Pred. No.: 9.54e-22 Length: 1066
Score: 396.00 Matches: 156
Percent Similarity: 44.06% Conservative: 100
Best Local Similarity: 26.85% Mismatches: 227
Query Match: 4.62% Indels: 98
DB: 2 Gaps: 24

US-09-396-985B-1 (1-4868) x T15864 (1-1066)

QY 206 AATATTACTTATCATGATGATGAGACTGAATTTCTACAAAATCCCCGAAACCTCCCTTC 265
DB 131 Aa||l||t||h||r||h||s---L||e||u||M||e||C||A||S||p||h||r||A||s||h||u||V||a||l||h||r||P||h||e||G||u||S||e||r||G||u||M||e||L||y||S||e||V||a||l|| 149
QY 266 TCAACCAAGAACTGAGACCTGAGCTTTAAATCCCTGAGGACATTTAGGACAGCTATAGCTTC 325
DB 150 I||l||e||u||a||r||g||a||n||-----A||s||h||y||S||a||l||h||r||g||a||r||g||e||u||a||r||b||y||h||i||S||e||r||P||h||e|| 164
QY 326 TTCAAGTTTCCAGAACTGACAGCTGCTGATTTATCCAGTGTGAAATCCAGACATTTGAA 385
DB 165 A||r||g||S||e||r||P||h||e||a||r||g||y||l||e||a||r||g||l||u||d||e||u||a||S||p||l||e||S||e||r||T||y||r||a||n||g||i||n||l||e||g||i||n||t||h||r||V||a||l||g||l||u|| 184
QY 386 GATGGGGCATATCAGAGCTGAGCCACTCTCTACCTTAATATGACAGAAACCCATC 445
DB 185 A||S||p||S||e||r||S||e||r||P||h||e||g||l||u||t||h||r||V||a||l||g||l||y||h||i||M||e||t||C||i||n||S||e||r||L||e||u||S||e||r||T||y||r||A||s||h||y||l||e|| 204
QY 446 CAGAGTTAAGCCCTGGGAGACCTTTCTGAACTATCAAGTTTACAGAAAGCTGTGCTGTG 505
DB 205 A||a||t||y||r||l||e||u||P||r||o||a||r||g||l||y||----- 210
QY 506 GAGACMAATCTAGACATCTTAGAGAACTTCCCATGAGACATCTCAAAACTTTGAAGAA 565
DB 211 -----M||e||t||L||e||u||y||S||a||n||P||h||e||-----A||a||l||y||S||h||r||L||e||u||y||e||t||h||r|| 221
QY 566 CTTAATGCTGCTCACAATCTTATCCAACTTTTCAAAATTAAGCTGATATTTTCTAATCTG 625
DB 222 L||e||u||y||S||e||u||l||a||g||l||u||a||S||h||M||e||t||l||e||h||i||S||a||l||-----T||h||r||P||r||o||g||l||u||a||l||e||u||a||r||g||S||p||l||e||u|| 239
QY 626 ACCAATCTAGAGCACTTGAGCCTTCCAGCAAGAAATTCAAAGATTT----- 673
DB 240 A||r||g||a||n||S||e||u||t||h||r||h||i||S||e||u||a||S||h||e||u||a||S||h||e||l||y||a||S||h||i||S||e||u||a||n||a||r||g||l||e||a||S||p||l||a||S||p||a||l|| 259
QY 674 -----T||A||T||T||C||A||C||A||G||A||C||T||T||G||G||G||T||T||C||A||T||C||A||A||A||T||C||C||C||T||C||A||A||T||C||T||C||T||T||A|| 727
DB 260 L||e||u||y||S||g||l||y||C||y||e||t||h||A||S||p||h||r||L||e||u||a||l||-----G||l||u||d||e||u|| 270
QY 728 GACCTGTCCCTGATCCTATGAACTTTATCCAAACGATGATTTAAAGAAATTAAGCTT 787
DB 271 P||h||e||l||e||a||l||a||a||S||e||n||T||y||l||e||u||g||l||u||h||i||S||l||e||P||r||o||h||i||S||g||l||V||a||l||e||u||S||e||r||G||l||y||M||e||t||y||S||--- 289
QY 788 CATAAGCGACTTTAAGAAATTAATTTTGATGTGTTTAATGAATGAAGAAACTTGATGCA 847
DB 290 -----G||l||u||d||e||u||l||u||h||i||S||e||u||a||S||p||l||e||S||e||r||L||y||S||a||n||y||S||a||l||l||e||u||e||t|| 302
QY 848 GGTCTGCTGCTGTTAGAACTCATCGTTGGTCTCGGAGAAATTTGAAGAAATGAAGAAAC 907
DB 303 S||e||r||e||u||-----L||y||l||e||P||r||o||t||h||S||e||r||-----L||y||l||e||P||r||o||t||h||S||e||r|| 309
QY 908 TTGGAAGAGTTGACAAATCTGCTCTAGAGGACCTGTGCAATTGGACCATTTGAAGAAATTC 967

```

Db      310  LeuLeuSerIleThrIleGluGluThrSerThrValAlaGluLeuAsnLeuAlaGlyAsn 329
      |||  |||  ::|  |||  ::|
      |||  |||  |||  |||  |||
Oy      968  CGATTAGCAATCTAGACTACTACCTCGATGATATATATGACTTATTAATGTTGACA 1027
      |||  ::|  |||  |||  |||
      |||  |||  |||  |||  |||
Db      330  ArgIleAsnAsnMetSerAspTyrLeu-----IlePheGluHisMetProLeuLeuThr 347
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1028  AATGTTTCT--TCATTTTCCCTGGTAGAGTGACATATTGAAGAAGGTAAAGACTTTTCT 1084
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      348  TyrValAspValSerPheAsnArgIleArgPheIleSerProArgValPheGluLeu 367
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1085  TATAATTTCCGATGGCAATTTAATAATTAGTTAACTGAAATTTGACAGTTTCCACA 1144
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      368  LysAsnLeu-----GluSerLeuPheLeuGlnAsnAsnGlnLeuAlaHisPheProSer 385
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1145  TTG--AAACTCAAAATCTCTCAAAAAGCTTACTTTCACTTCCAAC-----AAAGGT 1192
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      386  LeuPheArgLeuAspLeuArgIleAsnMetLeuAspAsnAsnGlnIleGlnIle 405
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1193  GGAATGCTTTTTCAGAAAGTTGATTCACCAAGCTTGAGTTTCTAGATCTCAGTAGAAAT 1252
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      406  AspAsn---PheSerLeuAlaAspLeuProLysLeuGlnHisLeuSerLeuAlaGlyAsn 424
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1253  GGCCTTGCATTTCAAAAGTTGCTGTTCTGAAGTAGTTTGGACACACAGC----- 1303
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      425  GlnLeuAspIle-----IleThrGlnAsnMetPheGlySerSerSerSerGlu 441
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1304  CTTAAAGTATTTAGATCTGAGCTTCATGAGTGTATTTATTCATGAGTCA---AACTCTTG 1366
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      442  LeuLysSerLeuAsnLeuAlaHisAsnLysIleHisSerIleSerSerArgSerPheSer 461
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1361  GGCCTTAGCAACCTAGAACATCTGGATTTCCAGCACTTCCAAATTGAAACAAATGAGTAG 1420
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      462  AspLeuAspAsnLeuGlnGlnLeuArgLeuSerHisAsnAsnIleArgThrIleHisSer 481
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1421  TTTTCAGTATTCCTATCACTGACGAACCTCAATTATTCCTGATCTTCATATCTCACAC 1480
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      482  MetThr---PheSerAsnLeuArgAsnLeuArgTyrLeuAspLeuSerHisAsnArgIle 500
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1481  AGAGTTCCTTCAATGAGCATCTTCATGAGTCTTCACCTGCACTGCAAGTCTTGAATGAGCT 1540
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      501  IleLysIleLeuProSerAlaLeuTyrGlnLeuProAlaLeuAspValLeuHisLeuAsp 520
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1541  GGCAAATCTTTCCACGAAAACTTCTCCAGATATCTTCACAGAGCTGAGAACTTGACC 1600
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      521  HisAsnAsnLeuAsnGlu---IleAspArgAspAlaPheArgSerPheSerAspLeuGln 539
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1601  TTCCTGACCTCTCTCTCAGTGTCACTGGACGAGTGTCTCCAAACGACATTAACTCACTC 1660
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      540  SerLeuLysLeuSerHisAsnAlaPheArgArgPheSerCysGluPheLeuGlySerIle 559
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1661  TCCAGCTCTTCAGGTACTTAATATATGAGCAACAACATCTTTTCACTGATAGCTTTCT 1720
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      560  SerGlnValHisGlnLeuAspLeuSerSerHisGlnIleAsnGluIleAspIlePhe--- 578
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1721  TATAGTGTCTG--AACTCCCTCCAGGTTTCTTGATTACAGTCTCAATCAATATGACT 1777
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      579  -----CysIleAlaArgGlyIleArgLysLeuSerLeuAlaSerAsnSerValGlnLys 596
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1778  TCCAAAAAACAGAACTACAGACATTTTCCAAAGTACTGAGCTTTCTTAATCTTACTCAG 1837
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      597  IleAsnArgLysLeuLeuGlnAsp---AlaThrGluLeuThrSerIleAspIleSerHis 615
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1838  AAT-----GACTTGCTGTACTGTGGAACACCAAGTTTCTCTG 1876
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      616  AsnGlyIleIleAspValAspSerAspAlaPheCysGluCysArgLysLeuSerHisIle 635
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Oy      1877  CAA 1879
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||
Db      636  Lys 636
      |||  |||  |||  |||  |||
      |||  |||  |||  |||  |||

```

Chacotin precursor - fruit fly (*Drosophila melanogaster*)
N/Alternate names: photoreceptor cell-specific membrane protein
C/Species: *Drosophila melanogaster*
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C/Accession: A29944 #accession
R/Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988
A>Title: Chacotin, a cell surface glycoprotein required for *Drosophila* photoreceptor cell development
A/Reference number: A21123; MUID:84106810; PMID:6420071
A/Accession: A21123
A/Molecule type: protein
A/Residues: 31-43, 'HX', '46-49', 'H' <ZTP>
C/Genetics:
A/Gene: FlyBase:cbp
A/Cross-references: FlyBase:FBgn0000313
A/Intons: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
C/Superfamily: Chacotin; leucine-rich alpha-2-glycoprotein repeat homology
C/Keywords: cell adhesion; glycoprotein; membrane protein
F/1-29/Domin: signal sequence #status predicted <SIG>
F/30-1134/Product: chacotin #status predicted <MAT>
F/80-102/Domin: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR1>
F/103-126/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F/128-151/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
F/152-175/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F/177-200/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F/201-224/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F/226-249/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F/250-273/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F/279-302/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F/303-335/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F/326-349/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F/351-374/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F/375-399/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F/401-424/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F/428-451/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F/453-476/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F/477-500/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F/502-526/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F/527-550/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F/551-574/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
F/577-600/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
F/601-624/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
F/625-648/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
F/649-672/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
F/673-696/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
F/708-731/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
F/733-756/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
F/757-780/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
F/781-804/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
F/805-827/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
F/828-851/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
F/854-877/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
F/879-902/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
F/903-926/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
F/928-948/Domin: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR35>
F/949-972/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
F/973-995/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
F/996-1019/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
F/1021-1044/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
F/1056-1080/Domin: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Best Local Similarity: 22.96% Mismatches: 249
 Query Match: 3.89% Indels: 231
 DB: 1 Gaps: 30

US-09-396-985b-1 (1-4868) x A29944 (1-1134)

```

Qy 251 GACAGCTCCCTTCACCAAGAAAGACCTGACCTTTAATCCCTGAGCATTTA 310
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 346 AspSerLeuValAsnSerLeuGlnIleLeuAspLeuSerGlyAsnAsnLeuThrIleu 365
Qy 311 GGCAGCTAAGCTTCTTCACTTCCAGAACTGACGCTG- 349
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 366 HisHileuSerLeuPheAsnAsnPheAspValIleuArgValIleSerMetArgAspAsnIle 385
Qy 350 -----CTG 352
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 386 IleValIleGlnIleuProThrGlnThrPheAsnAlaValHisTyrThrIleuLeuIleu 405
Qy 353 GATTATTC-----AGGTGGAATCCAGACAATGGAATGGGGCA--- 394
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 406 AspLeuSerGlyAspArgAsnAspProThrAsnLeuGlnThrIleuAspAsnMetThrArg 425
Qy 395 -----TATCAGACCTTAAGC----- 409
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 426 MetArgAsnMetArgSerLeuSerIleSerArgLeuGlySerSerSerValGlyProGln 445
Qy 410 -----CACCTCTCACTTAATATTGACAGAAACCCCATCCAG 448
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 446 AspPheIleAspPheGlyValGlnLeuGlnAspLeuGlnIleThrArgAlaSerLeuSer 465
Qy 449 AGTTAGACCTGGAGCCTTTTGTGACTATCAAGTTTACAGAGAGCTGTGGCTGGAG 508
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 466 GlyIleGlnSerHisAlaPheIleValArgGlyLeuIleuAspGlyAspPheSerGln 485
Qy 509 ACAAACTAGCATCTTACAGAAC-----TTCCCATGTGACATCTCAAACTTGG 559
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 486 AsnGlyIleSerSerIleGlnAsnAspAlaPheHisGlnIleGlnHis-----SerLeu 503
Qy 560 AAAGAACTTAATGCGTCACAACTCTTAATCCAACTTCAAAATTAAGCTGATTTTCT 619
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 504 IleSerLeuIleuMetSerHisGlyTyrSerGlySerIleuProAlaGlnProLeuArg 523
Qy 620 AATGTGACCACTTACAGACCTTTCACAGCAAGAACTTCAAGATTTATATTCG 679
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 524 HisLeuHisSerLeuGlnGlnIleuAspPheSerHisAsnHisIleSerSerMetSerAsp 543
Qy 680 ACAGACTTGGCGGCTTACATCAATGCCCCCTACTCAATCTCTTACAGCTGTCCCTG 739
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 544 ThrSerPheHisPheLeuIleuAsnLeuArgLeu-----LeuGlnIleuHisAsp 559
Qy 740 AATCTTAATGAATTTATCCAAACGAGTCATTTAA-----GAATTAAGCTTCAT 790
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 560 AsnArgIleGlnIleuValIleuIleuValThrPheGlnIleuAspIleHisSerIleuGln 579
Qy 791 AAGCTGACTTAAGAAATTAAT-----TTTGAATAGTTTA 823
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 580 GlnIleSerLeuHisPheAsnHisIleuThrSerIleSerGlnHisThrPheAspLeu 599
Qy 824 AATGTAATGAAGAACTTGTATTCAGAGCTGTGCTGTTTGAAGTCAATCGTTGGTTCTG 883
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 600 GlnAlaLeuArgIleu-----LeuHisLeuAspArgAsnIleAspIleArg 614
Qy 884 GGAAGATTTAGAAATGAAGAAATTTGAAAAGTTTGAACAATGCTCTTAGAGAGC--- 940
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 615 IleGlnIleArgIleAlaPheMetAsnLeuAspGlnIleuGlnIleuSerLeuArgGlyAsn 634
Qy 941 -----CTGTCGAACTTGAAGATTAATC-----CGATTAGCATCTTTCAG 985
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 635 LysIleAsnAsnLeuAlaAspGlnSerPheGlnAsnLeuProIleuGlnIleuIleu 654
Qy 986 TACTACCTCGATGATATT-----ATTGACTTAATTAACTTTGACAAATGTT 1033
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 655 MetAlaPheAsnGlnIleuProAsnPheAsnPheAspTyrPheAspGlnValGlyThrIleu 674

```

```

Qy 1034 TCTTCATTTTCCCTGCTGAGTGAATGATATTGAAAGGTAAGAACTTTTCTTAATATTC 1093
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 675 SerAsnLeuAsn--ValAsnValSerHisAsnGlnIleArgGlnLeuMetTyrAsnSer 693
Qy 1094 GGAATGCAACATTTAAGAAATTAAGTTAACTGAAATTTGACAGCTTCCACATTTGAACTC 1153
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 694 SerTrp----- 695
Qy 1154 AATCTCTCAAAAGCTTACTTTCACTTCCAAACAAAGCTGGAAATCTTTTCAGAACTT 1213
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 696 -----SerGlyArgAsnGlnHisGlyGlyMet 704
Qy 1214 GATTCACAAAGCTTGATTTCTAGATCTCAGTGAAGAAAGGCTTGAAGTTTC-----AAA 1267
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 705 TyrHisSerAsnIleuSerIleuAspSerSerHisAsnAsnIleSerIleIleHisPro 724
Qy 1268 GGTTCGCTGTTCCAAAGATTTTGGACAAAC----- 1300
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 725 GlyTyrPheArgProAlaGlnIleSerLeuThrHisIleuGlnIleuGlyTyrAsnSerLeu 744
Qy 1301 -----AGCTTAAGTATTTAATCTGCAGC 1324
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 745 MetAsnThrThrArgAspValPheGlyAsnMetProHisProIleuGlnIleuAspLeuSer 764
Qy 1325 TTCATGCGTATTATCCATGAGTTCAAC-----TTCTGGGCTTAGAACATAGAAACAT 1381
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 765 TyrAsnThrIleHisGlnIleuAspPheAspAlaPheIleAsnThrIleuGlnIleuGlnIleu 784
Qy 1382 CTGATTTTCACAGCATTCCAATTTGAAACAATGAGTAGTCTTCAATATTTCTTCACTC 1441
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 785 ValPhePheGlyHisAsnGlyIleuSerAspIleProGln---AspIlePheIleuProVal 803
Qy 1442 AGAAACCTCATTTTACCTTTCATTTCTCATCTCAGACAGAA-----CTGCTTTCAATGGC 1498
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 804 GlnGlyLeuArgIleValAspPheSerHisAsnHisIleuArgGlyLeuProAspAsnLeu 823
Qy 1499 ATCTTCATGGC----- 1510
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 824 PheTyrAsnGlyGlyMetGlyIleuAspValSerHisAsnMetLeuIleuIlePro 843
Qy 1511 -----TTGTCAAGCTTCGAAAGCTTGAAGATGCTGGCAATTTCTTCCAGAAAC 1561
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 844 SerSerSerLeuSerSerLeuAlaIleuThrIleuGlnIleuHisIleuSerAsnAsn 863
Qy 1562 TTCTTTCCA-----GATATCTTCAAGAGCTGGAAGAACTTGCCTTCCTG 1606
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 864 PheIleSerThrIleHisSerMetAspLeuSerAsnIleAspPheArgSerLeuArgTyrLeu 883
Qy 1607 GACCTCTCAGTGCAGTCACTGAGAGAGTGTGTCCAAACAGATTTTAATCACTCTCCAGT 1666
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 884 AspIleSerTyrAsnTyrIleuAspArgIleAspArgAlaValAlaPheAlaThrMetCProIle 903
Qy 1667 CTTCAGGTAATTAATTAAGAGCAAC-----AATCTCTTT 1702
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 904 LeuAlaValLeuAspLeuSerHisAsnArgAspLeuIleValMetAspIleuSerPheMet 923
Qy 1703 -----TCATGGAATAGCTTTCT 1720
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 924 GlyLeuGlnAsnSerLeuIleuIleuGlyLeuGlnIleuGlnAsnValSerLeuSerThrValPro 943
Qy 1721 TATAAGTGTGAACCTCCGCAAGCTTCTTGAATTAAGTCAATGATCAATTAAGTACTTC 1780
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 944 GlnIleArgLeuIleuSerTyrIleuAspGlnIleuAspGlyTyrAsnGln---LeuProSer 962
Qy 1781 AAAAAACAGGAACTACAGCATTTTCCAAAGTACTTCTTAAATCTTACTCAGAAAT 1840
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 963 IleProGlnIleuValHisAsnMetSerAsnIleuArgMetLeuAspLeuSerAsnAsn 982
Qy 1841 GACTTGTCTTGACTTGTGAACCAAGAGTTTCTGCAATGATGATCAAGACAGAGGAG 1900
    |||::||| |||::||| |||::||| |||::||| |||::|||
Db 983 Asp----- 983

```

QY 1901 CTCCTGGTGAAGTGAACGAATGTCACACCTTCAGATTAAGAG----- 1951
 Db 984 ---LeuthraenValProleuMetThrGlnAlaLeuProHlsleuAArgGluMetLeu 1002
 QY 1952 ---GGCATGCTGTGCTGAGTATGCAATATCACTGTCAATGATTAAGACCATTCATTGTT 2008
 Db 1003 SerGlyAsnProHlsThrSerLeuAsn-----AsnAsnSerPheAsnGly 1017
 QY 2009 GTGCGGTC---CTCAGTGTGCTGTAGTATTCGTTGTAGACAGTCTGCTAATAGTTC 2065
 Db 1018 ValAsnAluAspLeuGluMetLeuAspHlsSerAsnPheArgLeuHlsTrpPheGluTrp 1037
 QY 2066 TATTTTCACTGATGCTTCTGTGCTGCTGCATA 2098
 Db 1038 -----GlyCysLeu 1040

RESULT 8
 B34087
 hypothetical protein (LJH 3' region) - human
 C/Species: Homo sapiens (man)
 C/Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
 C/Accession: B34087
 R/Scott, A.F.; Schmeckpeper, B.J.; Abdelrazik, M.; Comey, C.T.; O'Hara, B.; Rossiter, J.
 Genomics 1, 113-125, 1987
 A/Title: Origin of the human L1 elements: proposed progenitor genes deduced from a conserved
 A/Reference number: A34087; MUID:88085185; PMID:3692483
 A/Accession: B34087
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-1280 <SC0>
 A/Cross-references: UNIPROT:Q9Y5K0
 C/Superfamily: pol polyprotein

Alignment Scores:
 Pred. No.: 1,33e-16 Length: 1280
 Score: 328.50 Matches: 95
 Percent Similarity: 53.95% Conservative: 28
 Best Local Similarity: 41.67% Mismatches: 70
 Query Match: 3.83% Indels: 36
 Gaps: 4

US-09-396-985b-1 (1-4868) x B34087 (1-1280)

QY 3817 CATTTGGGAAGAGTGATGTTATTCATTGAGAAAACAATGTCGTGGAATTAATGGGGTT 3876
 Db 1084 HisPheSerLysGluAspLeuIleTrpAlaAlaAsnLysHisMet----- 1097
 QY 3877 CTTATTAAGAAGGTTCCAGAAAAGAATGTTCAATTCAGCTTCTTCAGAAACAGAAACA 3936
 Db 1098 -----LysLysCysSerSerSerLeu----- 1104
 QY 3937 TTCAGGAAAAGACATCAATCAGATGTCATCAGGGAATGAATAATTAACCAATGAGA 3996
 Db 1105 -----AlaIleArgGluMetGlnIleLysThrThrMetArg 1116
 QY 3997 TATCACCCTTATACAGGTAGATGGCTACTATAAAA-----AATGAAGTCA 4044
 Db 1117 TyrHisLeuThrProValAlaArgMetAlaIleIleLysLysSerGlyAsnAsn-ArgCysTrp 1136
 QY 4045 TCAAGATATAGAAATTAATGAACCTTCTTCATCTGTCGAGGGAATGAAAATGGTGA 4104
 Db 1136 pArgGlyCysGlyGlnIleGlyThrLeuLeuHisCysTrpTrpAspCysLysLeuValGln 1156
 QY 4105 GCCGTTATGAAGAAACAGTACGAGGTTTCTCAAAA-TTAAATATGAATGCTATATGA 4163
 Db 1156 nProLeuTrpLysThrValAlaTrpArgPheLeuLysAspLeuGlnLeuGlnIleProPheAs 1176
 QY 4164 TCAGCAATCTCACTTGTATATATATACCAAAATATATTGAATTCAGATTCAGAGAAA 4223
 Db 1176 pProHlsIleProLeuLeuGlyIleTrpProLysAspTrpLysSerCysTrpLysAs 1196
 QY 4224 TATTTACACTCCATGTTCAATGTGGCACTTTCACATCACTGTTCCAAAGTTATGA 4283
 Db 1196 -----:::|||

Db 1196 pThrCysThrArgMetPheIleAlaAlaLeuPheThrIle-----AlaLysThr-TrpA 1214
 QY 4284 AACACCCAAATTCATTGGAATAATGAACAAAGGAATGTCATTAACATGACAA 4343
 Db 1214 smGlnProLysCysProSerMetIleAspTrpIleLysLysMetTrpHisIleTrpThr 1234
 QY 4344 TGGGATATATATTCACCTTAATAAAAAGGGGGATCTGTTATTTATGACAAACATGAATA 4403
 Db 1234 etGluTrpTrpAlaAlaIleLysAsnAspGluPheMetSerPheValGlyThrTrpMetL 1254
 QY 4404 ACCCGAGGCCATTATGCTATGTAATAATGACAAATGAACAAAGCAATACTGCCTGA 4463
 Db 1254 yLeuGlnThrIleIleLeuSerLysLeuSerGlnGlnIleLysThrLysHisArgMetP 1274
 QY 4464 TTTCAATTTATGAGGTTCT 4483
 Db 1274 heserLeuIleGlyLysAsn 1280

RESULT 9
 S23650
 retrovirus-related hypothetical protein II - human retrotransposon LINE-1
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
 C/Accession: S23650
 R/Hohjoh, H.; Minakami, R.; Sakaki, Y.
 Nucleic Acids Res. 18, 4099-4104, 1990
 A/Title: Selective cloning and sequence analysis of the human L1 (LINE-1) sequences whi
 A/Reference number: S23649; MUID:90332398; PMID:2165587
 A/Accession: S23650
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-712 <HO>
 A/Cross-references: UNIPROT:O15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:000363; UNI
 PROT:Q14754; UNIPROT:Q9Y5K0; UNIPROT:O00366; UNIPROT:Q8TF30; UNIPROT:000375; EMBL:X5223
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
 C/Genetics:
 A/Mobile element: LINE-1
 A/Start codon: GTG
 C/Superfamily: pol polyprotein

Alignment Scores:
 Pred. No.: 1.65e-16 Length: 712
 Score: 326.50 Matches: 95
 Percent Similarity: 53.51% Conservative: 27
 Best Local Similarity: 41.67% Mismatches: 71
 Query Match: 3.81% Indels: 36
 Gaps: 4

US-09-396-985b-1 (1-4868) x S23650 (1-712)

QY 3817 CATTTGGGAAGAGTGATGTTATTCATTGAGAAAACAATGTCGTGGAATTAATGGGGTT 3876
 Db 516 HisPheSerLysGluAspLeuIleTrp----- 523
 QY 3877 CTTATTAAGAAGGTTCCAGAAAAGAATGTTCAATTCAGCTTCTTCAGAAACAGAAACA 3936
 Db 524 ---AlaAlaLysLysHisMetLysCysSerProSerLeu----- 536
 QY 3937 TTCAGGAAAAGACATCAATCAGATGTCATCAGGGAATGAATAATTAACCAATGAGA 3996
 Db 537 -----AlaIleArgGluMetGlnIleLysThrThrMetArg 548
 QY 3997 TATCACCCTTATACAGGTAGATGGCTACTATAAAA-----AATGAAGTCA 4044
 Db 549 TyrHisLeuThrProValAlaArgMetAlaIleIleLysLysSerGlyAsnAsn-ArgCysTrp 568
 QY 4045 TCAAGATATAGAAATTAATGAACCTTCTTCATCTGTCGAGGGAATGAAAATGGTGA 4104
 Db 568 pArgGlyCysGlyGlnIleGlyThrLeuLeuHisCysTrpTrpAspCysLysLeuValGln 588
 QY 4105 GCCGTTATGAAGAAACAGTACGAGGTTTCTCAAAA-TTAAATATGAATGCTATATGA 4163
 Db 588 nProLeuTrpLysSerValTrpArgPheLeuArgAspLeuGlnProGlnIleProPheAs 608

QY 4164 TCCAGCAATCTCACTTGTATATATACCCAAATAATGAAATTCAGAAATTCAGAAA 4223
||||| ||||| ||||| ||||| ||||| : : : : :
Db 608 pProba1le1pProleu1e1y1le1y1rProlysa1pSer1y1Se1Cy1e1y1r1y1sa1s 628
QY 4224 TATTTACACTCCCATGTTCACTTATGCGACTTTTACAAATCACTGTTTCCAAAGTTATGA 4283
: ||||| ||||| ||||| ||||| : : : : :
Db 628 pThr1Cy1Str1Ar1gMe1Phe1le1Ala1leu1Phe1Thr1le1-----Ala1y1Str1-T1r1p 646
QY 4284 AACAAACCAATTCCTCATGTTGAAATAATGACAAAGCAATGTCATTAACGTACAA 4343
: ||||| ||||| ||||| ||||| : : : : :
Db 646 sm1In1Pro1y1s1Cy1s1Pro1Th1Me1t1le1As1p1Tr1p1le1y1s1Me1t1r1P1h1s1le1y1r1Th1m 666
QY 4344 TGGGATATATATTCAGCTTAAATAAGGGGATCCGTTATTTATGACAACATGAAATA 4403
||||| ||||| ||||| ||||| ||||| : : : : :
Db 666 ec1G1u1y1r1y1r1Ala1Ala1le1y1s1As1n1p1u1p1he1Val1Ser1Phe1Val1G1y1Thr1Tr1p1Me1t 686
QY 4404 ACCCGAGGCAATTAATGCTATGTAATGACAAAGTAACAGAAAGCAAAATACGCTGA 4463
||||| ||||| ||||| ||||| ||||| : : : : :
Db 686 y1s1eu1G1u1l1e1r1le1le1u1Se1r1y1le1u1Se1r1G1n1G1u1n1y1s1Th1r1y1s1H1e1Cy1e1le1r 706
QY 4464 TTTCAATTTATATGAGTTCT 4483
||| ||| ||| ||| : : : : :
Db 706 h1e1Se1r1leu1le1G1y1G1y1As1n 712

RESULT 10

138588
Reverse transcriptase homolog - human retrotransposon L1
N:Alternate names: ORF2 protein
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Acession: I38588
R:Holmes, S.E.; Dombrski, B.A.; Krebs, C.M.; Boehm, C.D.; Kazanian, H.H.
A:Title: A new retrotransposable human L1 element from the LRE2 locus on chromosome 1q
A:Reference number: I38587; MUID:95004577; PMID:7920631
A/Acession: I38588
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1275 <RES>
A:Cross-references: UNIPROT:Q12881; EMBL:U09116; NID:9483914; PIDN:AAB60345.1; PID:94839
C:Superfamily: pol polyprotein

Alignment Scores:

Pred. No.:	5 39e-16	Length:	1275
Score:	320.50	Matches:	93
Percent Similarity:	53.51%	Conservative:	29
Best Local Similarity:	40.79%	Mismatches:	71
Query Match:	3.74%	Indels:	36
DB:	2	Gaps:	4

US-09-396-985b-1 (1-4868) x I38588 (1-1275)

QY 3817 CATTTGGAGAGGTGATGTATCATTTGAGAAAACAATGTCTGGAATTAATGGGTT 3876
||||| ||||| ||||| ||||| ||||| : : : : :
Db 1079 H1s1Phe1Se1r1y1s1e1u1p1r1le1y1r----- 1086
QY 3877 CTTATTAAGAAGGTTCCCAAGAAAGATGTTTCATTCAGCTTTCTTACGAAACAGAAC 3936
||||| ||||| ||||| ||||| ||||| : : : : :
Db 1087 ---Ala1Ala1y1s1y1s1Me1t1y1s1Cy1s1e1Se1Se1r1e1u----- 1099
QY 3937 TTCAGAGAAAAGCAATGATGTCATCAGGAGAAATGAATAATTAACACCAATAGA 3996
||||| ||||| ||||| ||||| ||||| : : : : :
Db 1100 -----Ala1le1Ar1g1u1Me1t1G1n1le1y1s1Th1r1Th1Me1Ar1g 1111
QY 3997 TATCACTTATACCAAGTAGATGGCTACTATAAAA-----AATGAAGTCA 4044
||||| ||||| ||||| ||||| ||||| : : : : :
Db 1112 Ty1H1s1le1u1Th1r1Pro1Val1Ar1gMe1Ala1le1le1y1s1Se1r1y1As1n1Ar1g1Cy1Str 1131
QY 4045 TCAAGGATATAGAAATTCGAAACCTTTCTTACGCTGAGGAGATGAAATGCTGA 4104
: : : : : ||||| ||||| ||||| ||||| : : : : :
Db 1131 pAr1g1y1Cy1e1G1u1l1e1G1y1Th1r1leu1H1e1Cy1e1Tr1p1r1As1r1Cy1e1y1s1e1u1Val1G1 1151

QY 4105 GCCGTTAGAAAACAGTACGAGGTTTCTCAAAA-TTAAAAATAGACTCTATATGA 4163
||||| ||||| ||||| ||||| ||||| : : : : :
Db 1151 nPro1eu1r1p1y1s1e1r1Val1Tr1p1Ar1g1Phe1leu1Ar1g1p1e1u1G1u1le1G1u1le1P1r1o1b1e1 1171
QY 4164 TCCAGCAATCTCACTTGTATATATACCCAAATAATGAAATTCAGAAATTCAGAAA 4223
: ||||| ||||| ||||| ||||| : : : : :
Db 1171 pProba1le1pProleu1e1G1y1le1y1rPro1u1p1r1y1Se1r1y1s1e1Cy1e1y1r1y1sa1s 1191
QY 4224 TATTTACACTCCCATGTTCACTTATGCGACTTTTACAAATCACTGTTTCCAAAGTTATGA 4283
: ||||| ||||| ||||| ||||| : : : : :
Db 1191 pThr1Cy1Str1Ar1gMe1Phe1le1Ala1leu1Phe1Thr1le1-----Ala1y1Str1-T1r1p 1209
QY 4284 AACAAACCAATTCCTCATGTTGAAATAATGACAAAGCAATGTCATTAACGTACAA 4343
: ||||| ||||| ||||| ||||| : : : : :
Db 1209 sm1In1Pro1y1s1Cy1s1Pro1Th1Me1t1le1As1p1Tr1p1le1y1s1Me1t1r1P1h1s1le1y1r1Th1m 1229
QY 4344 TGGGATATATATTCAGCTTAAATAAGGGGATCCGTTATTTATGACAACATGAAATA 4403
||||| ||||| ||||| ||||| ||||| : : : : :
Db 1229 ec1G1u1y1r1y1r1Ala1Ala1le1y1s1As1n1p1u1p1he1le1Se1r1Phe1Val1G1y1Thr1Tr1p1Me1t 1249
QY 4404 ACCCGAGGCAATTAATGCTATGTAATGACAAAGTAACAGAAAGCAAAATACGCTGA 4463
||||| ||||| ||||| ||||| ||||| : : : : :
Db 1249 y1s1eu1G1u1l1e1r1le1le1u1Se1r1y1le1u1Se1r1G1n1G1u1n1y1s1Th1r1y1s1H1e1Cy1e1le1r 1269
QY 4464 TTTCAATTTATATGAGTTCT 4483
||| ||| ||| ||| : : : : :
Db 1269 h1e1Se1r1leu1le1G1y1G1y1As1n 1275

RESULT 11

B28096
line-1 protein ORF2 - human
C:Species: Homo sapiens (man)
C>Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 09-Jul-2004
C/Acession: B28096
R:Skowronski, U.; Fanning, T.G.; Singer, M.F.
Mol. Cell. Biol. 8, 1385-1397, 1988
A:Title: Unit-length line-1 transcripts in human teratocarcinoma cells.
A:Reference number: A28096; MUID:88246405; PMID:2454389
A/Acession: B28096
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1275 <SKO>
A:Cross-references: UNIPROT:Q15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:000363; UNIPROT:000375
PROT:Q9Y5K0; UNIPROT:000366; UNIPROT:Q8TB30; UNIPROT:000375
C:Superfamily: pol polyprotein

Alignment Scores:

Pred. No.:	6 42e-16	Length:	1275
Score:	319.50	Matches:	93
Percent Similarity:	53.07%	Conservative:	28
Best Local Similarity:	40.79%	Mismatches:	72
Query Match:	3.72%	Indels:	36
DB:	2	Gaps:	4

US-09-396-985b-1 (1-4868) x B28096 (1-1275)

QY 3817 CATTTGGAGAGGTGATGTATCATTTGAGAAAACAATGTCTGGAATTAATGGGTT 3876
||||| ||||| ||||| ||||| ||||| : : : : :
Db 1079 H1s1Phe1Se1r1y1s1e1u1p1r1le1y1r----- 1086
QY 3877 CTTATTAAGAAGGTTCCCAAGAAAGATGTTTCATTCAGCTTTCTTACGAAACAGAAC 3936
||||| ||||| ||||| ||||| ||||| : : : : :
Db 1087 ---Ala1Ala1y1s1y1s1Me1t1y1s1Cy1s1e1Se1Se1r1e1u----- 1099
QY 3937 TTCAGAGAAAAGCAATGATGTCATCAGGAGAAATGAATAATTAACACCAATAGA 3996
||||| ||||| ||||| ||||| ||||| : : : : :
Db 1100 -----Ala1le1Ar1g1u1Me1t1G1n1le1y1s1Th1r1Th1Me1Ar1g 1111
QY 3997 TATCACTTATACCAAGTAGATGGCTACTATAAAA-----AATGAAGTCA 4044
||||| ||||| ||||| ||||| ||||| : : : : :
Db 1112 Ty1H1s1le1u1Th1r1Pro1Val1Ar1gMe1Ala1le1le1y1s1Se1r1y1As1n1Ar1g1Cy1Str 1131
QY 4045 TCAAGGATATAGAAATTCGAAACCTTTCTTACGCTGAGGAGATGAAATGCTGA 4104
: : : : : ||||| ||||| ||||| ||||| : : : : :

Db	1131	parGIIyysbglvuiiegIlythIleuLeuHiIsCystrIrrtrrPmPcySylvleuValGI	1151
OY	4105	GCCTGTATGAAAAACAGTACGAGGTTTCTCAAAA-TTAAAAATGAACTGTATATAGA	4163
Db	1151	nProleuTrpIySseValItrpArGpHeIuArGArpIeuGIuIeuGIuIleProPheAs	1171
OY	4164	TTCCAGCAATCTCACATTCTGTATATATATACCCAAAATATGGAATCAGAAATTCAGAANA	4223
Db	1171	pProIaIleProIeuIeuGIuIleIyTrpIAsnAspIyTrIySseCysCyStrIyLysAs	1191
OY	4224	TATTTACACTCCCAATGTCATTTGGAGCACTCTTCACATCACTGTTCCTCAAAAGTTATNGA	4283
Db	1191	pThCyStrhArgMetPheIleAlaIlePheMetIle-----AlaIyStrIrr-TIra	1209
OY	4284	AACAACCCAAATTTCCATTTGGAATAATATAGACAAAGAAATGTCATATATACGTACAA	4343
Db	1209	sngInProIyCySProIhMetIleAspTrIleIySylvIeMetTrpIhIstrIleIyThrm	1229
OY	4344	TGGGAGATTTATTCAGCCTAAAAAAGGGGGAGATCTGTATATTTATGACACATGAATAA	4403
Db	1229	etGIuIyTrYAlaIAlaIleIySAsnAspGIuPheMetSsePheValGIyIrrTrpMet	1249
OY	4404	ACCGGAGGCCATATGCTATGTATATAAGACCAAGTACACAAAGACAAATATCTGCGCTGA	4463
Db	1249	ysIeuGIuThIleIleIeuSerrIySleuSerrGIuGIuIyThIySerrIhAsrIleP	1269
OY	4464	TTTCATTATTTAGAGTTCT	4483
Db	1269	heserIeuIleGIyIyAsn	1275

RESULT 12

reverse transcriptase homolog - human transposon L1.1
C/Species: Homo sapiens (man)
C/Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S65824
R/Dombroski, B.A.
submitted to the EMBL Data Library, January 1992
A/Description: Isolation of an active human transposable element.
A/Reference number: S65823
A/Accession: S65824
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1275 <DOM>
A/Cross-references: UNIPROT:Q15604, EMBL:M80340, NID:G3339767, PID:AAAS1622.1, PID:G3339767, Superfamily: pol polypotein

Alignment Scores:

Pred. No.:	6.42e-16	Length:	1275
Score:	319.50	Matches:	93
Percent Similarity:	53.07%	Conservative:	28
Best Local Similarity:	40.79%	Mismatches:	72
Query Match:	3.72%	Indels:	36
DB:	2	Gaps:	4

US-09-396-985B-1 (1-4868) x S65824 (1-1275)

QY	3817	CATTTTGGGAAGATGTGATGTTATTCATTGAGAAAAACATGCTGTGGAAATTAAAGGGGTT	3876
Db	1079	Hieheserlysgluaplielyr-----	1086
QY	3877	CTTATTAAGAAGCTTCCACAAAAAAGATTGTTTCATTCAGCTTCTTCAGAAAAACAGAAACA	3936
		:::	
Db	1087	---AlaIalylslysh:smellylyltycyserserserleu-----	1099
QY	3937	TTCAAGAAAAAGCAATCAGAGTGCATTCAGGGAATGAATAATTAACCAACCATAGACA	3996
Db	1100	-----AlaileargsluwcglnllystnThrMetArg	1111
QY	3997	TATCACCTTTATACCAAGGTAGATGCTACTATAA-----	4044
		:::	
Db	1112	TyrhisleuthrPrOvalArgMetAlaIlellelyslserserlyanlsen-ArgcysItr	1131

Qy	TCAGAGTATATAGAGAAATTGGAAACCCCTTTCACCTGCGAGGAAATGAAATAGTGTA	4104
Db	1131 pargGlyCyseGlyGluIleGlyThrIleuLeuHisCysTrpTrpAspCysIleuValG1	1151
Qy	4105 GCCGTATTGAAAAACAGTACCGAGGTTTCTCAAAA-TTAAAAATGAACTGCTATATGA	4163
Db	1151 nProleuTrpIyserValTrpArgPheIleuAspIleuGluIleuIleProPheAs	1171
Qy	4164 TCCAGCAATCCACTTGTGTATATATACCCAAAAATAATTGAAATCAGAAATTTCAGAAA	4223
Db	1171 pProIleIleProleuIleuGlyIleTrpProIleuGluTrpIlySerCysGlyTrpIysAs	1191
Qy	4224 TATTACACTCCCATGTTCAATTGTGGACGCTTTCACAATCAGTGTTTCCAAAGTTATGA	4283
Db	1191 pThrCysThrArgMetPheIleIleAlaIleuPheThrIle-----AlaIysThr-TrpA	1209
Qy	4284 AACAAACCAATTTCCATTGGAAAAATAAATGACAAAGAAATGTGCATATTAACGTACA	4343
Db	1209 enGluProIysCysProIleMetIleAspTrpIleIysIysMetTrpHisIleTrpThrM	1229
Qy	4344 TGGGAGATATTAATTCAGCCTAAAAAAGGGGGGATCCCTGTATTATTATGACAACTGAATAA	4403
Db	1229 etGluTrpTrpAlaAlaIleIysAsnAspGluIleSerPheValGlyThrTrpMetI	1249
Qy	4404 ACCCGAGGCCATTATGCTATGTAAAAATGACAAAGTAAACAAAGAAATACCTGCTGA	4463
Db	1249 yIleuGluTrpIleIleIleuSerIysIleuSerGlnGluGlnIysThrIysHisIleArgIleP	1269
Qy	4464 TTTCATTTATATGAGGTTCT 4483	
Db	1269 heSerIleuIleGlyGlyAsn 1275	

RESULT 13

insulin-like growth factor acid-labile chain - baboon
C:Species: Papio sp. (baboon)
C:Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: J05239
R:Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
A:Reference number: J05239; MUID:97040714; PMID:8886027
A:Contents: liver
A:Accession: J05239
A:Molecule type: mRNA
A:Residues: 1-605
C:Comment: This factor is structurally related to proinsulin and have insulin-like met

Alignment Scores:

Pred. No.:	9.97e-16	Length:	605
Score:	316.00	Matches:	157
Percent Similarity:	39.04%	Conservative:	94
Best Local Similarity:	24.42%	Mismatches:	242
Query Match:	3.68%	Indels:	150
DB:	2	Gaps:	23

US-09-396-985B-1 (1-4868) x JC5239 (1-605)

[illegible]

```

Db      113 LeuGIuProGIuAlaLeuLeuGIuLeuGIuAsnLeuCyHisLeuHisLeuGIuArgAsn 132
QY      440 CCATCCAGAGTTAGCCCTGGAGGCGTTTC-----ThrHis 472
Db      133 GlnLeuArgSerLeuAlaValGIuThrPheAlaIYThrProAlaLeuAlaLeuLeuGIu 152
QY      473 -----GACTATCAAGTTTA 487
Db      153 LeuSerAsnAsnArgLeuSerArgLeuGIuAspGIuLeuPheGIuLeuGIuLeuGIuAsnLeu 172
QY      488 CAGAGCTGGTGGCTGTGGAGACAATCTAGCATCTCTAGAGAACTTCCCATTTGGACAT 547
Db      173 TrpAspLeuAsnLeuGIuYTrpAsnSerLeuAlaValLeuProAspAlaIaPheArgGIu 192
QY      548 CTCAAAACTTTGAAGAAGTTAATAGGGCTCAACATCTTATCCAAATCTTCAAAATTACCT 607
Db      193 LeuGIuGIuLeuArgLeuLeuValLeuAlaGIuAsnArgLeu---AlaYrLeuGIuPro 211
QY      608 GAGTATTTTCTAATCTGACCAATCTAGAGCACTTGACCTTTCAGACAAAGATTACA 667
Db      212 AlaLeuPheSerGIuLeuAlaGIuLeuArgGIuLeuAspLeuSerArgAsnAlaLeuArg 231
QY      668 AGTATTTATTGACACAGACTTGGGGTTTACATCAATGCCCCCTACTCAATCTCTCTTA 727
Db      232 AlaIle-----LysAlaAsnValIaPheAlaGIuLeuProArgLeuGIu---LysLeu 247
QY      728 GACCTGCTCCGATCTTATGAACCTTATGACCAAGGTCATTTAAAGAAATTAGG--- 784
Db      248 TyrLeuAspArgAsnLeuIleAlaValaIaProGIuAlaPheLeuGIuLeuLysAla 267
QY      785 CTTCATTAAGCTGACTTAAAGAAATATTTGATAGTTAATGAAATGAAACTTGTATT 844
Db      268 LeuArgTrpLeuAspLeuSerHisAsn---ArgValaIaGIuLeuGIuAspTrpPhe 286
QY      845 CAAGCTCTGGCTGTTTAAAGTCCATCGTTGGTCTGGAGAAATTAGAAATGAAGGA 904
Db      287 ProGIuLeuLeuGIuLeuArgValaLeuArgLeu----- 297
QY      905 AACTTGGAAAAGTTTGACAAATCGCTCTAGAGGGCGCTGCAATTGGACATTGGAAG 964
Db      298 -----SerHisAsnAlaIleAlaSerLeuArgProArgTrpPheGIuAsp 312
QY      965 TTCCGATTAGCATTTAGACTACTACCTGATGATATTTGACTTATTAATTTGTTG 1024
Db      313 Leu-----HisPheLeuGIuLeu----- 319
QY      1025 ACAATGTTTCTTCATTTCCCTGGTGAAGTGAATTAATGAAGGTAAGAACTTTCT 1084
Db      320 -----GlnLeuGIuHisAsnArgTrpLeuArgGIuLeuAlaGIuArgSer 333
QY      1085 TATATTTTGGATGGCAACATTGAATTAATGTAATCTGTAATTTGGACAGTTTCCACA 1144
Db      334 PheGIu---GlyLeuGIuGlnLeuGIuValaLeuThrLeuAspHisAsnGlnLeuGln 352
QY      1145 TTGAACCTCAAACTCTCAAAAGGCTTACTTCACTTCC-----ACAAAGGTGGGAAT 1198
Db      353 ValLysValGIuAlaPheLeuGIuLeuThrAsnValaIaValaMethAsnLeuSerGIuAsn 372
QY      1199 GCTTTTTCAGAGTTGATCTACCAAGCTTGAAGTTTCTAGATCTCACTAGA---AATGGC 1255
Db      373 CysLeuArg-----AsnLeuProGIuGlnValaPheArgGIuLeuGIuLysLeuHisSer 390
QY      1256 TTGAGTTTCAAGGTTGCTGT-----TCTCAAGTGATTTTGGGACAAAC 1300
Db      391 LeuHisLeuGIuGIuSerCysLeuGIuArgTrpProHisThrPheAlaGIuLeuSer 410
QY      1301 AGCCTAAAGTATTTAGATCTGAGCTTCATGCTGTATTTACATGAGTTCAAACTTCTG 1360
Db      411 GYLeuArgArgLeuPheLeuLysAspAsnGIuLeuValaGIuLeuGIuGlnInsertLeu 430
QY      1361 ---GGCTTAGAACCACTTAGAACCTTGATTTCCAGCATTTCCAAATTTGAAACAATGAGT 1417
Db      431 TrpGIuLeuAlaGIuLeuLeuGIuLeuAspLeuThrSerAsnGlnLeu----- 446

```

```

QY      1418 GAGTTTTCAGTATCTCTATCTACAGAAAACCTCATTTACCTTGACATTTCTCATCTCAC 1477
Db      447 -----ThrHis 448
QY      1478 ACCAGAGTTGCTTTCAATGAGCATTTCAATGGCTTTGCCAGTCTTGAAAGT 1537
Db      449 LeuPro-----HisGlnLeuPheGlnGIuLeuGIuLysLeuGIuYrLeuGIuLeuLeu 465
QY      1538 GCTGGCAATCTTTCACAGAAACCTTCTTCA---GATATCTCACAGAGCTGAGAAAC 1594
Db      466 SerHisAsnArgLeuAlaGIu-----LeuProAlaAspAlaLeuGIuProLeuGIuArg 483
QY      1595 TTGACCTTCTGAGACCTCTCTCAGTGTCAACTGAGACAGTTGTCTTCAACAGCATTTAAC 1654
Db      484 AlaPheTrpLeuAspValSerHisAsnArgLeuGIuAlaLeuProGIuSerLeuLeuAla 503
QY      1655 TCACTTCCAGTCTTCAAGCTACTTAATATGAGCCACACAACTTCTTTTCAATTGATACG 1714
Db      504 SerLeuGIuArgLeuArgTrpLeuAsnLeuArgAsnAsn-----SerLeuArgTrp 520
QY      1715 TTTCTTAATAGTGTGTAACCTCCAGGTTCTTGATTACAGTCTCATCATTAATG 1774
Db      521 PheThrProGln----- 524
QY      1775 ACTTCAAAAACAGGAAGTACAGCATTTTCCAAGTATGCTTACTTTTAATCTTACT 1834
Db      525 -----ProProGIuLeuGIuArgLeuTrpLeuGIu 534
QY      1835 CAGATGACTTTCCTTGTACTTGTGAACCAAGCT----- 1870
Db      535 GlyAsnProTrpAspCysProLeuGIuAlaLeuArgAspPheAlaLeuGlnAsn 554
QY      1871 -----TTCGTCAATGATGC-----AAGGACCAAGGGCAGCTC 1903
Db      555 ProSerAlaValaProArgPheValGlnAlaIleCysGIuGIuAspAspCysGlnProPro 574
QY      1904 TTGGTGAAGTTGAAAGCAATGGAATGGCAACACTTTCATAGACAGGAGTCCCTG 1963
Db      575 ValTYrThrTYrAsnAsnHisLeuThrCysAlaSerProProGIuValaIaGIuLeuAspLeu 594
QY      1964 CTGAGTTTG 1972
Db      595 ArgAspLeu 597

RESULT 14
T42218
slit-1 protein homolog - rat
N/Alternate names: MEGF4 protein
C/Species: Rattus norvegicus (Norway rat)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T42218
R/Nakajima, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A/Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A/Reference number: Z14126; PMID:98360089; PMID:9693030
A/Accession: T42218
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1531 <NA>
A/Cross-references: UNIPROT:088279; EMBL:AB011530; NID:93449289; PID:BA32460.1; PID:93
A/Experimental source: strain Sprague-Dawley; brain
C/Genetics:
A/Genes: MEGF4
C/Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

```

```

Alignment Scores:
Pred. No.: 5,46e-15 Length: 1531
Score: 307.50 Matches: 173
Percent Similarity: 34.78% Conservative: 99
Best Local Similarity: 22.12% Mismatches: 271
Query Match: 3.58% Indels: 240
DB: 2 Gaps: 28

```


QY 1895 AGGAGCTCTTGAGGAGTTGAACGAATGAGTGAACACACCTTCAGATTAAGCAGGC 1954
 : : : ||| ||| ||| : : : |||
 Db 885 Tyrlvs-----GluProGlyIleAlaArgCysAlaGlyProProGluMetGluGly 901
 : : : ||| ||| ||| : : : |||
 QY 1955 ATGCTGTGCTAG-----TTTGAATATCACTGTTCAGATGAATAAGAC 1998
 : : : ||| ||| ||| : : : |||
 Db 902 LysLeuLeuLeuThrThrProAlaLysLysPheGlu----- 913
 : : : ||| ||| ||| : : : |||
 QY 1999 CACCATTTGCTGTCGCTCT-----CAGTGTGCTTGAATATCTGTTGT 2043
 : : : ||| ||| ||| : : : |||
 Db 914 -----CysGlnGlyProProSerLeuAlaGlnAlaLysCysAspProCysLeu 930
 : : : ||| ||| ||| : : : |||
 QY 2044 AGCAGT 2049
 : : : ||| ||| ||| : : : |||
 Db 931 SerSer 932
 : : : ||| ||| ||| : : : |||
 RESULT 15
 T17461
 disease resistance protein D - tomato
 C:Species: Lycopersicon esculentum (tomato)
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T17461
 R:Parmlake, M.; Jones, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 96, 5850-5855, 1999
 A>Title: Recombination between diverged clusters of the tomato Cf-9 plant disease resist
 A:Reference number: Z18801; MUID:99254130; PMID:10318973
 A/Accession: T17461
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-853 <PAR>
 A:Cross-references: UNIPROT:Q9ZS82; EMBL:AF119040; NID:g4235640; PID:g4235641; PIDN:AD1
 C:Genetics:
 A:Gene: NUD0
 Alignment Scores:
 Pred. No.: 7.39e-15 Length: 853
 Score: 305.00 Matches: 192
 Percent Similarity: 38.06% Conservative: 106
 Best Local Similarity: 24.52% Mismatches: 291
 Query Match: 3.56% Indels: 194
 Gaps: 35
 US-09-396-985b-1 (1-4868) x T17461 (1-853)
 QY 206 AATATTATCTTATCAATGAGCTGAGCTGAATTTCTAC-----AAATAC 247
 : : : ||| ||| ||| : : : |||
 Db 79 AsnThrThrGlyGlnValIleGlnLeuAspLeuArgCysSerGlnLeuGlnGlyLysLeu 98
 : : : ||| ||| ||| : : : |||
 QY 248 CCCGACAACTCCCTTC-----TCAACCAAGAACTGAGCTGAGCTTAAT 295
 : : : ||| ||| ||| : : : |||
 Db 99 HisSerAsnSerSerLeuPheGlnLeuSerAsnLeuLysArgLeuAspLeuSerTyrAsn 118
 : : : ||| ||| ||| : : : |||
 QY 296 -----CCCTGAGGCAATTAGGCACTTAAGCTTTCCAGTTCCCGAA 340
 : : : ||| ||| ||| : : : |||
 Db 119 AspPheThrGlySerProIle-----SerProLysPheGlnGluPheSerAsn 134
 : : : ||| ||| ||| : : : |||
 QY 341 CTGCAAGTGTGATTTATCCAGGTGTGAATCCAGACATTTGAAGTGGGCAATATCAG 400
 : : : ||| ||| ||| : : : |||
 Db 135 LeuThrHisLeuAspLeuPheAspSerAsnPheThrGlyIleIleProSerGlnLysSer 154
 : : : ||| ||| ||| : : : |||
 QY 401 AGCTTAGCCACCTCTTACCTTAATATGACAGAAACCCATCCAGAGTTTACCCCTG 460
 : : : ||| ||| ||| : : : |||
 Db 155 HisLeuSerLysLeuTyrValLeuArgThrSerThrAspTyrProTyrGlyLeuSerLeu 174
 : : : ||| ||| ||| : : : |||
 QY 461 GGA-----GCCTTTCTGACATCAAGTTACAGATTACAGAGCTGTGGCT 502
 : : : ||| ||| ||| : : : |||
 Db 175 GlyProHisAsnPheGlnLeuLeuLeuLysAsnLeuThrGlnLeuArgGlnLeuAsnLeu 194
 : : : ||| ||| ||| : : : |||
 QY 503 GTGAGACAAATCTAGATCTTGAAGAACTCCCATTTGACATCTCAAAACCTTTGAA 562
 : : : ||| ||| ||| : : : |||
 Db 195 TyrAspValAsnLeuSerSer-----ThrIleProSerAsnPheSerSerHisLeuThr 212
 : : : ||| ||| ||| : : : |||

QY 563 GAATTAATGTGCTCACAACTTATCCAACTTTCAATTAACCTGAGTATTTTCTAAT 622
 : : : ||| ||| ||| : : : |||
 Db 213 AsnLeuArgLeuAlaTyrThrGlnLeuArgGlyIle---LeuProGlnArgPhePheHis 231
 : : : ||| ||| ||| : : : |||
 QY 623 CTGACCAATCTTAGAGCACTTTGACCTTTCCAGACACCAAGATTCGAAGTATTATTGACA 682
 : : : ||| ||| ||| : : : |||
 Db 232 LeuSerAsnLeuGlnSerLeuAspLeuSerPheAsnProGlnLeuThrValArgPhePro 251
 : : : ||| ||| ||| : : : |||
 QY 683 GACTTCGGGTTCTACATCAAAATGCCCTACCAATCTCTTTAGACCTGTCCTGAAT 742
 : : : ||| ||| ||| : : : |||
 Db 252 ThrThrLysTyrAsnSerSerAlaSerLeuValAsnLeuTyrLeu---AlaGlyValAsn 270
 : : : ||| ||| ||| : : : |||
 QY 743 CCTATGAACCTTATCCAAACAGAGTCATTTAAAGAAATTAGGCTTCATTAAGCTGACTT 802
 : : : ||| ||| ||| : : : |||
 Db 271 IleAlaAspArgIle---ProGlnSerPheSerHisLeu----- 282
 : : : ||| ||| ||| : : : |||
 QY 803 AGAAATATATTGATGTTTAAATGTAATGAATACTGTATTCAGAGTCTGGCTGTTA 862
 : : : ||| ||| ||| : : : |||
 Db 283 -----Thr 283
 : : : ||| ||| ||| : : : |||
 QY 863 GAATGCATCGTTTGCTGGGAGAAATTAGAAATGAAGAAATTGAAAAATTGAC 922
 : : : ||| ||| ||| : : : |||
 Db 284 AlaLeuHisLysLeuHisIleMetGlyTyrThrAsnLeuSerGlyProIleProLys----- 301
 : : : ||| ||| ||| : : : |||
 QY 923 AATCTGCTCTAGAGGCTGTGCAATTGACC---ATTGAAGAAATTCGATTAAGCATAC 979
 : : : ||| ||| ||| : : : |||
 Db 302 -----ProLeuThrPheAsnLeuThrHisIleGlnSerLeu-----Phe 313
 : : : ||| ||| ||| : : : |||
 QY 980 TTAGACTAC---TACCTGCATGATATTAATTAATTTAATGTTTGAACAAATGTTCT 1036
 : : : ||| ||| ||| : : : |||
 Db 314 LeuAspTyrLysHisIleLeuGlnGlyProIleSerHisPheThrIlePheGlnLysLeuLys 333
 : : : ||| ||| ||| : : : |||
 QY 1037 TCATTTCCCTGGTGGTGTGACTATTA---AGGTAAGAACTTTCTTAATATTC 1093
 : : : ||| ||| ||| : : : |||
 Db 334 SerLeuSerLeuGlnLysAsnAsnAsnPheAspGlyArgLeuGlnPheLeuSerPheAsnArg 353
 : : : ||| ||| ||| : : : |||
 QY 1094 GGATGCAACATTTAGAAATTAAGTT-----AACTGTAATTTGACAGTTTCCC 1141
 : : : ||| ||| ||| : : : |||
 Db 354 SerThrMetLysLeuGlnLysLeuAspPheSerSerAsnPheLeuThrGlyProIlePro 373
 : : : ||| ||| ||| : : : |||
 QY 1142 ACA-----TTGAATCTCAAAATCTGCAAAAGCTTACTTCACTTCCAAACAA---GGT 1192
 : : : ||| ||| ||| : : : |||
 Db 374 SerAsnValSerGlyLeuGlnAsnLeuGlnGlnLeuIleLeuSerSerAsnHisLeuAsn 393
 : : : ||| ||| ||| : : : |||
 QY 1193 GGGAAATGCTTTTCAAGAGTT---GATCTACCAAGCTTGAAGTTTCTTAAGCTCAGTACA 1249
 : : : ||| ||| ||| : : : |||
 Db 394 GlyThrIleProSerThrIlePheSerLeuProSerLeuThrValLeuAsnLeuSerAsp 413
 : : : ||| ||| ||| : : : |||
 QY 1250 AATGCTTGAATTCAA----- 1267
 : : : ||| ||| ||| : : : |||
 Db 414 AsnThrLeuSerGlyLysIleGlnGluPheLysSerLysThrLeuTyrPheValSerLeu 433
 : : : ||| ||| ||| : : : |||
 QY 1268 -----GGTTCGTCTCTCAAGAGTATTTGGGCAACACAGCTTAAG 1309
 : : : ||| ||| ||| : : : |||
 Db 434 GluGlnAsnLysLeuGlnGlyProIleProArgSerLeuLeuAsnGlnPheLeuGln 453
 : : : ||| ||| ||| : : : |||
 QY 1310 TATTAGATCTGAGCTCAATAGTGTATT---ACATAGAGTTCAAACTTCTTGGGCTTA 1366
 : : : ||| ||| ||| : : : |||
 Db 454 AlaLeuLeuLeuSerHisAsnAsnIleSerGlyHisIleSerSerAlaIleCysAsnLeu 473
 : : : ||| ||| ||| : : : |||
 QY 1367 GAACAACCTGAACATCTGATTTCCAGATTCACATTTCAATTTGAA----- 1408
 : : : ||| ||| ||| : : : |||
 Db 474 LysThrPheIleLeuLeuAsnLeuLysSerAsnAsnLeuGlnGlyThrIleProGlnCys 493
 : : : ||| ||| ||| : : : |||
 QY 1409 -----CAATAGAGTGAATTTCAATTCCTATCACTCAAGAAACCTCATTTACTTTGAC 1462
 : : : ||| ||| ||| : : : |||
 Db 494 LeuGlnGluMetSerGlnLeuGlnVal-----LeuAsp 504
 : : : ||| ||| ||| : : : |||
 QY 1463 ATTCTCATATCTACACACAGAGTGTCTTCAATGGCATCTTCAATGGCTTGTCCAGATTC 1522
 : : : ||| ||| ||| : : : |||
 Db 505 LeuSerAsnAsnSerLeuSerGlyThrMetAsnThrThrPheSerIleGlnLysProLeu 554
 : : : ||| ||| ||| : : : |||
 QY 1523 GAAGCTTGAATAATGTGCTGCAATCTTTCCAGAAACCTTCTTCAGATATCTTCACA 1582
 : : : ||| ||| ||| : : : |||

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:30:23 ; Search time 263.083 Seconds
(without alignments)
18950.714 Million cell updates/sec

Title: US-09-396-985B-1
Perfect score: 8579
Sequence: 1 aaataactccctgcctca.....caaaaaaaaaaaaaaa 4868

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1612378 segs, 512079187 residues
Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US0939685/Runatc_28032005_155743_21146/app_query.fasta.1.85098
-DB=uniprot_03 -QFMT=faatan -SUFFIX=rup -MINMATCH=0.1 -LOOPC=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=bl0sum62 -TRANS=human40.cdd -LIST=45
-DOCALL=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USFR=US0939685.@CCN.1.1.5213.@Runatc_28032005_155743_21146 -NCPU=6 -TFPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Uniprot 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4355	50.8	839	1	TLR4_HUMAN
2	4341	50.6	839	1	TLR4_PANPA
3	4310	50.2	837	2	Q8SPF8
4	4182	48.7	828	1	TLR4_PONPY
5	4043	47.1	826	1	TLR4_PAPAN
6	3342	39.0	843	1	TLR4_HORSE
7	3321.5	38.7	841	1	TLR4_BOVIN
8	3318.5	38.7	841	2	Q8SQS5
9	3316.5	38.6	833	1	TLR4_FELCA
10	3313.5	38.6	841	2	Q6WC4
11	3307.5	38.6	841	2	Q6WC4
12	3197.5	37.3	841	2	TLR4_PIG
13	3102.5	36.2	839	2	Q8MIQ2
14	3017	35.2	838	1	TLR4_CRIGR
15	2860.5	33.3	835	1	TLR4_RAT
16	2852	33.2	835	2	Q8K2T5

17	2847	33.2	835	1	TLR4_MOUSE	Q9quk6 mus musculu
18	2206	25.7	636	2	Q8SQH3	Q8sqh3 canis fam1
19	1847	21.5	843	2	Q7ZRG5	Q7zrg5 gallus gall
20	1285.5	15.0	819	2	Q6TS41	Q6ts41 brachydanio
21	1274.5	14.9	817	2	Q6NV08	Q6nv08 brachydanio
22	834.5	9.7	258	2	Q70EK4	Q70ek4 sus scrofa
23	690	8.0	945	2	Q801F9	Q801f9 carassius a
24	685	8.0	961	2	Q76CT9	Q76ct9 paralicthys
25	678.5	7.9	940	2	Q8RT53	Q8rt53 brachiocto
26	677	7.9	961	2	Q76CT7	Q76ct7 paralicthys
27	668.5	7.8	991	2	Q6R5N8	Q6r5n8 mus musculu
28	663	7.7	661	1	C180_MOUSE	Q62122 mus musculu
29	645	7.5	661	2	Q8C251	Q8c251 mus musculu
30	641.5	7.5	784	2	Q6YGU2	Q6ygu2 rattus norv
31	633.5	7.4	973	2	Q6KCC7	Q6kcc7 oncochynch
32	629.5	7.3	661	1	C180_HUMAN	Q99467 homo sapien
33	617.5	7.2	784	1	TLR2_MOUSE	Q9qu7 mus musculu
34	616.5	7.2	784	2	Q8K3D9	Q8k3d9 mus musculu
35	613.5	7.2	784	2	Q811T5	Q811t5 mus musculu
36	610.5	7.1	661	2	Q7YRL4	Q7yrl4 sus scrofa
37	602.5	7.0	784	1	TLR2_HUMAN	Q60603 homo sapien
38	601.5	7.0	785	2	Q76LZ4	Q76l24 sus scrofa
39	600.5	7.0	785	2	Q6TN21	Q6tn21 sus scrofa
40	597	7.0	784	2	Q6T752	Q6t752 equus cabal
41	595.5	6.9	784	1	TLR2_MACFA	Q95m53 macaca fasc
42	591.5	6.9	784	1	TLR2_CRIGR	Q9rlf8 cricetus
43	580.5	6.8	793	1	TL21_CHICK	Q9dd78 gallus gall
44	580.5	6.8	1032	1	TLR8_MOUSE	P58682 mus musculu
45	580	6.8	781	1	TL22_CHICK	Q9dgb6 gallus gall

ALIGNMENTS

RESULT 1
TLR4_HUMAN STANDARD; PRT; 839 AA.
AC 000206; Q9UK78; Q9UM57;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Toll-like receptor 4 precursor (Toll1).
GN Name=TLR4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=97379437; PubMed=9237759; DOI=10.1038/41131;
RA Medzhitov R., Preston-Hurlbut P., Janeway C.A. Jr.;
RT "A human homologue of the Drosophila Toll protein signals activation
RT of adaptive immunity.";
RL Nature 388:394-397(1997).
RN [2]
RP SEQUENCE OF 41-839 FROM N.A.
RC TISSUE=Retal liver, lung, and Placenta;
RX MEDLINE=98118556; PubMed=9435236; DOI=10.1073/pnas.95.2.586;
RA Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RT "A family of human receptors structurally related to Drosophila
RT Toll.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.
RX MEDLINE=20558910; PubMed=11104518;
RA Shulimova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
RT locus (TLR4).";
RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.
RX MEDLINE=20296622; PubMed=10835634; DOI=10.1038/76048;
RA Adbour N.C., Lorenz E., Schutte B.C., Zahner J., Kline J.N., Jones M.,

FT VARIANT 299 299 /FtId=VAR_018730.
D -> G (in allele TUR4*B; reduced LPS-
response; dbSNP:4986790).
/FtId=VAR_012739.
FT VARIANT 329 329 N -> S.
/FtId=VAR_018731.
FT VARIANT 399 399 T -> I (in allele TUR4*B; reduced LPS-
response; dbSNP:4986791).
/FtId=VAR_012740.
FT VARIANT 443 443 F -> L.
/FtId=VAR_018732.
FT VARIANT 474 474 E -> K.
/FtId=VAR_018733.
FT VARIANT 510 510 Q -> H.
/FtId=VAR_018734.
FT VARIANT 694 694 K -> R.

Alignment Scores:
Pred. No.: 0 Length: 839
Score: 4355.00 Matches: 839
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.76% Indels: 0
Gaps: 0

US-09-396-985b-1 (1-4868) x TUR4_HUMAN (1-839)

QY 104 ATATATGTCTGCTCGGCGCTGGAGCTCTGATCCAGCATGGCCCTCTCTCTCTGC 163
Db 1 MetMetSerLaseRrXgluValaglyThrLeuileProLametrAlpheLeuSerCys 20

QY 164 GTGAGCCGAAGAGCTGGAGGCGCTGGAGAGTGCTCTATATTAATTACTTCAATGC 223
Db 21 ValAlrProGluSerThrGluProCysValGluValAlProAsnIleMrTrYrGlnCys 40

QY 224 ATGAGAGCTGAATTTCTACAAATATCCCGACAACTCCCTCTTCAACCAAGAACTGGAC 283
Db 41 MetGluLeuAsntheYrlyrslleProAspAsnLeuProPheSerThrlySaenLeuAsp 60

QY 284 CTGAGCTTTAATCCCTGAGGAGCTTTAGGAGCTATAGCTTCTTCAGTTCCAGAACTG 343
Db 61 LeuSerPheAsnProLeuArghIleuGlySerYrSerPhePheSerPheProGluLeu 80

QY 344 CAGGTCTGATTTATCCAGGTGGAATCCAGACATTCAGAACTTGAAGTGGGAGCTATCAGAG 403
Db 81 GlnValLeuAspLeuSerArghCysGluIleGlnThrIleGluAspGlyAlaIlyrGlnSer 100

QY 404 CTAGCCACCTCTCTAATTAATTTAGACAGAAACCCCATCCAGAGTTTACGCTGGAG 463
Db 101 LeuSerHisLeuSerThrLeuileLeuThrGlyAsnProIleGlnSerLeuAlaleuGly 120

QY 464 GCGTTTCTGGAGCTATCAAGTTTACAGAGCTGGGCTGGAGCAAACTTACGATCT 523
Db 121 AlaPheSerClyLeuSerSerLeuGlnlyLeuValAlaValGluThrAsnLeuAlaSer 140

QY 524 CTAGAAACTTCCCGCATTTGACATCTCAAACTTTGAAAGAACTTAAATGGGCTCAAA 583
Db 141 LeuGlnAsntheProIleGlyHisLeuLySThrLeuLySThrLeuAsnValAlaHisAsn 160

QY 584 CTTATCAATCTTTCAAAATTAACCTGAGTATTTTCTTATCTGACCAATCTAGAGCACTTG 643
Db 161 LeuileGlnSertheYrleuProGluYrPheSerAsnLeuThrAsnLeuGluHisLeu 180

QY 644 GACCTTTCCAGACAAAGATTCAAGATTATTTAGCAGAGCTTGGGGTTTCAATCA 703
Db 181 AspLeuSerSerAsnlyrIleGlnSerIleYrCysThrAspLeuArghValIleuHisGln 200

QY 704 ATGCCCTACTCATCTCTTTAGACCTTCCTCAATTCCTAATCTTGAACCTTATCCAA 763
Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220

QY 764 GGTGATTTAAAGAAATTAAGCTTCAATAGCTTAAAGATTAAGAATATTTGATAGTTTA 823
Db 764 GGTGATTTAAAGAAATTAAGCTTCAATAGCTTAAAGATTAAGAATATTTGATAGTTTA 823

Db 221 GlyAlaPheLeuGluIleArghLeuHislyLeuThrLeuArghAsnAsntheAspSerLeu 240
QY 824 AATGTAAATGAAAACCTGTATTCAGAGTCTGGCGTGTATGAGTCCATGCTGTGCTTCG 883
Db 241 AsnValMetCysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArghLeuValLeu 260
QY 884 GGAGAAATTTAGAAATGAGAAACCTTGAAAAAGTTTGACAAATCTGCTAGAGGCGCTG 943
Db 261 GlyGluPheArghAsnIleGluAsnLeuGluYrPheAspLySerAlaLeuGluGlyLeu 280
QY 944 TGCATTTGACCATTTGAGAAATTCGATTTAGCATTAATGACTACTCTCGATGATATT 1003
Db 281 CysAsnLeuThrIleGlnGluPheArghLeuAlaYrLeuAspYrTrYrLeuAspArpIle 300
QY 1004 ATTTGATTTATTAATTTGTCACAAATGTTTCTCAATTTCCCTGGTGGAGTGACTATT 1063
Db 301 IleAspLeuPheAsnlyLeuThrAsnValSerSerPheSerLeuValSerValInrIle 320
QY 1064 GAAAGGGTAAAAAGACTTTTCTTAATATTTCCGATGCGCAACATTTAGAAATTAAGTTCG 1123
Db 321 GluArghValIlyAspPheSerYrAsnPheGlyTrpGlnHisleuGluLeuValAsnlyCys 340
QY 1124 AATTTGACAGTTTCCACATTTGAATCTCAAAATCTTCAAAAGCTTACTTCACTTCC 1183
Db 341 LysPheGlyGlnPheProThrLeuYrleuYrSerLeuYrArghLeuThrPheThrSer 360
QY 1184 AACAAAGTGGGAATGCTTTTTCAGAACTTGATCTACCAAGCTTGATTCAGATCTTC 1243
Db 361 AsnLySGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuIlePheLeuAspLeu 380
QY 1244 AGTAGAAATGCTGATTTCAAAAGTGTCTGTCTCAAGAGTATTTGGGACCAACACAG 1303
Db 381 SerArghAsnGlyLeuSerPheYrleuYrGlyCysSerSerGlnSerArghPheGlyThrTrSer 400
QY 1304 CTAAAGTATTTAGATCTGAGCTTCAATGGGTGTTATTCAGATGATTCAAACTTCTTG 1363
Db 401 LeuYrYrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1364 TTAGAACACTGACATCTGATTTCCAGCACTTCCAAATTTGAAACAAATGAGTGAGTT 1423
Db 421 LeuGlnGlnLeuGlnHisleuAspPheGlnHisSerAsnLeuYrGlnMetSerGluPhe 440
QY 1424 TCAGTATTCCTATCACTCAGAAACCTCATTTACCTTTCAGATTTTCGATCTCACACAG 1483
Db 441 SerValPheLeuSerLeuArghAsnLeuIleYrLeuAspIleSerHisThrHisArgh 460
QY 1484 GTTGCTTTCAATGACATCTTCAATGGCTTGTCCAGCTTCCAGAACTTGAATGGCTGC 1543
Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuYrSmetAlaGly 480
QY 1544 AATTTCTTCCAGAAACCTTCTCCAGATATCTTACAGAGCTGAGAACTTGAACCTTC 1603
Db 481 AsnSerPheGlnGluAsntheProAspIlePheThrGluLeuArghAsnLeuThrPhe 500
QY 1604 CTGAGACCTCTCAGAGTCAACCTGAGAGCTGTCTCCAAACAGCATTTAACTCACTCC 1663
Db 501 LeuAspLeuSerGlnCysGlnLeuGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 520
QY 1664 AGTCTTCAGGTAATAATATGAGCCACAAACCTTCTTTCATTTGAGTACGTTTCTCTAT 1723
Db 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProYr 540
QY 1724 AAGTGTCTGAATCTCCTCCAGGTTCTTGATTTACAGTCTCAATCACATAATGACTTCA 1783
Db 541 LysCysLeuAsnSerLeuGlnValLeuAspYrSerLeuAsnHisIleIleMetThrSerLyS 560
QY 1784 AAAACAGAGACTCAGCATTTTCCAGTAGCTTAGCTTCTTAAATTTACTCAGATGAC 1843
Db 561 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1844 TTTGCTTGACTTGAGAACACAGAGTTTCTGCAATGGATCAGAGGACGAGCTC 1903
Db 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArghGlnLeu 600

FT REPEAT 543 566 LRR 20.
 FT REPEAT 568 592 LRR 21.
 FT DOMAIN 672 818 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 282 282 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 624 624 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 630 630 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 839 AA; 95637 MW; 3B328C5682127D37 CRC64;

Alignment Scores:

Pred. No.: 0 Length: 839
 Score: 4341.00 Matches: 836
 Percent Similarity: 99.88% Conservative: 2
 Best Local Similarity: 99.64% Mismatches: 1
 Query Match: 50.60% Indels: 0
 DB: 1 Gaps: 0

US-09-396-985b-1 (1-4868) x TLR4_PANPA (1-839)

QY 104 ATGATGTCGCTCGCGCTGCGGAGCTGTGATCCGACGAGCCCTCTCTCTGC 163
 DB 1 MetMetSerHisLeuSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 164 GTGAGACGAGAAAGCTGGAGGCCCTGCGTGGAGGTGCTCTAATATTACTTATCATGC 223
 DB 21 ValArgProGluSerThrGluProCysValGluValAlaProAlaIleThrTyrglnCys 40
 QY 224 ATGAGAGTGAAATTTTACAAATCCCGAGAACCTCCCTTCCACCAAGAACCTGGAC 283
 DB 41 MetGluLeuAsnMetPheTyrlsIleProAspAsnLeuProPheSerThrIlyAsnLeuAsp 60
 QY 284 CTGAGCTTTAATCCCTGAGGAGCAATTTAGGAGCTATGCTTCTTCAGTTTCCGAAAGCTG 343
 DB 61 LeuSerPheAsnProLeuAlaGlyIleuGlySerTyrlsSerPhePheSerPheProGluLeu 80
 QY 344 CAGGTGCTGATTTATTCAGGTGTGAATCCAGCAATGGAAGTGGGGCATATCAGAGC 403
 DB 81 GluValIleuAsnProLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrglnSer 100
 QY 404 CTAGACCACTCTCTACCTTAATATTGACGAGAAACCCCATCCAGAGTTTAGCCCTGGGA 463
 DB 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
 QY 464 GCGTTTCTGAGCTATCAAGTTTACAGAGCTGTGCTGGAGCAAACTTAGCATCT 523
 DB 121 AlaPheSerGlyLeuSerSerLeuGlnIlyLeuValAlaValGluThrAsnLeuAlaSer 140
 QY 524 CTAGAGAACTTCCCATTTGAGACATCTCAAACTTTGAAAGACTTATGTGGCTCAAT 583
 DB 141 LeuGluAsnMetPheProIleGlyHisLeuTyrlsThrLeuIlyGluLeuAsnValAlaHisAsn 160
 QY 584 CTTATCCATCTTTCAATTAATCTGAGATTTTCTAATCTGACCAATCTAGGACACTTG 643
 DB 161 LeuIleGlnSerPheTyrlsLeuProGluTyrlsPheSerAsnLeuThrAsnLeuGluHisLeu 180
 QY 644 GACCTTCCAGCAACAAGATTCAAGATTATTTGACAGACTTGGGGGCTTCTACATCAA 703
 DB 181 AsnLeuSerSerAsnIlyIleGlnSerIleTyrlsCysThrAsnLeuAlaGlyValIleuHisGln 200
 QY 704 ATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGATCTTATGAACTTTATCCAAACA 763
 DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 764 GGTGCAATTTAAAGAAATTAGGCTTCATAGCTGACTTAAAGAAATTAATTTGATAGTTTA 823
 DB 221 GlyAlaPheTyrlsGluIleArgLeuHisIlyLeuThrLeuArgAsnAsnPheAspSerLeu 240

QY 824 AATGTAATGAAAACTTGATATTCAGAGCTGTGGCTGTTTAGAGCTCATGCTTGTCTG 883
 DB 241 AsnValIleuTyrlsThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 260
 QY 884 GGAAGATTTTGAAGAAATGAGAAACTTGGAAAACTTTGACAAATCTCTCTAGAGGGCTG 943
 DB 261 GlyGluPheArgAsnGluGlyAsnLeuGluTyrlsPheAspIlySerHisLeuGluGlyLeu 280
 QY 944 TGCATTTTGACCACTTGAAGAAATCCGATTAGCATCTACTGACTACCTGATGATATT 1003
 DB 281 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrlsLeuAspTyrlsTyrlsLeuAspPheIle 300
 QY 1004 ATGACTTATTTAATGTTTGAACAAATGTTTCTTCATTTTCCCTGAGTGTGACTATT 1063
 DB 301 IleAspLeuPheAsnProLeuThrAsnValIleSerSerPheSerLeuValIleThrIle 320
 QY 1064 GAAAGGTTAAAGACTTTTCTTATTAATTTCCGATGGCAACATTAGAAATTGATTACTGT 1123
 DB 321 LysSerValIlyAspPheSerTyrlsAsnPheGlyTyrlsGlnHisLeuGluLeuValAsnCys 340
 QY 1124 AAATTTGACAGTTTCCCATTTGAAACTGAAATCTCAATCTCTCAAAAGGCTTACTTCACTTC 1183
 DB 341 LysPheGlyGlnPheProThrLeuTyrlsLeuTyrlsSerLeuTyrlsArgLeuThrPheThrSer 360
 QY 1184 AACAAAGTGGGAATCTTTTTCAGAACTTGATCTTCAAGCCTTGAGTTCTAGATCTC 1243
 DB 361 AsnIlyGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
 QY 1244 AGTAGAAATGGCTTGAGTTTCAAGGTTGCTGTCTCAAAAGTATTTGGGACACACAGC 1303
 DB 381 SerArgAsnGlyLeuSerPheTyrlsGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1304 CTAAAGTATTTGATGTGAGCTTCAATGGGTTATTAACATGATGTTCAAACTTCTGGGC 1363
 DB 401 LeuTyrlsTyrlsLeuAspPheSerPheAsnGlyValIleThrMetSerAsnPheLeuGly 420
 QY 1364 TTAGAACACTAGAACATCTGTGATTTCCAGACTTCCAAATTTGAAAGAGTGTGATT 1423
 DB 421 LeuGluGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuTyrlsGlnMetSerGluPhe 440
 QY 1424 TCAGTATTCCTATCACTCAAGAAACCTCAATTTACCTTGACATTTCTCATCTCACACAGA 1483
 DB 441 SerValPheLeuSerLeuArgAsnLeuIleTyrlsLeuAspIleSerHisThrHisArg 460
 QY 1484 GTTGCTTTGAATGGCATCTTCAATGAGCTGTGTCAGCTGGAAGTCTTGAAGAAATGGCTGGC 1543
 DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValIleuTyrlsMetAlaGly 480
 QY 1544 AATTTCTTCAGGAAAACTTCTTCAGATATCTTCAAGAGCTGAGAAACTTGACCTTC 1603
 DB 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
 QY 1604 CTGAGCTTCTTCAGTGTCACTGAGCAAGTGTCTTCAACAGCAATTTAACTCATCTTCC 1663
 DB 501 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 520
 QY 1664 AGCTTTCAGGACTTAATATGAGCCCAACAACCTTTTCAATGGATACGTTTCCCTTAT 1723
 DB 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyrls 540
 QY 1724 AAGTGTCAAGACTCCCTCCAGGTTCTTGATTACAGTCTCAATCACTCAATGACTTCCAA 1783
 DB 541 LysCysLeuAsnSerLeuGlnValLeuAspTyrlsSerLeuAsnHisIleLeuThrSerTyrls 560
 QY 1784 AAAAGAACTACAGCAATTTTCCAGTAGTCTTACTTCTTTAAATCTTACAGAAATGAC 1843
 DB 561 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
 QY 1844 TTTGCTTTATCTTGTGAACACAGAGTTTCCGCAATGATACAGGACGAGGCGAGCTC 1903
 DB 581 PheAlaCysThrCysGluHisGlnSerPheLeuGlnTyrlsIleLysAspGlnArgGlnLeu 600
 QY 1904 TTGCTGAAGTTGAACGAATGGAATGTGCAACCTTCAGATTAAGCAGGAGCTGTG 1963

```

Db      601 LeuValGIuValGIuArgMetGIuCySAIaThrProSerAspIysGlnIyMetProVal 620
QY      1964 CTGACGTTGAATTCACCTGTCAGATGAATAAACAACATCTTGGTGTGGCTCCAG 2023
Db      621 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGIuValSerValLeuSer 640
QY      2024 GTCCTTGATGATCTGTGTGAGAGATTCGTGTATATAGTTCTATTATTCCTGATGCTT 2083
Db      641 ValLeuValValSerValValAlaValLeuValTylLysPheTyrPheHisLeuMetLeu 660
QY      2084 CTTGCTGGCTGCATTAAGTATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2143
Db      661 LeuAlaGIuCySileIySlyArgGIuValAsnIleTyrAspAlaPheValIleTyr 680
QY      2144 TCAAGCCAGATGAGAGCTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2203
Db      681 SerSerGIuAsnSpIuAspIyrValArgAsnGIuLeuValLysAsnLeuGIuGIuVal 700
QY      2204 CTTCCATTTGAGCTGCTGCTTCACTACAGAGACTTATTCCTGCTGCTGCTGCTGCTGCTGCTG 2263
Db      701 PropIophenIleuCySleuHisTyrAspAspPheIleProGIuValAlaIleAla 720
QY      2264 AACATCATCCATGAAGTTTCCATTAAGCCGGAAGGTGATTTGTGTGCTGCACGAC 2323
Db      721 AsnIleIleIleGIuGIuPheHisTyrSerArgLysValIleValValValSerGIuHis 740
QY      2324 TTTCATCCAGAGCCGCTGGTGTATCTTGAATTAAGATTTGCTGACGCTGCTGCTGCTGCTG 2383
Db      741 PheIleGIuSerArgIyrCysIlePheGIuTyrGIuIleGIuIleGIuIleGIuIleGIuIle 760
QY      2384 AGCAGTGTGCTGTATCATCTTCATTTGCTGCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 2443
Db      761 SerSerArgAlaIleIleIlePheIleValLeuGIuIleValGIuIleValGIuIleValGIu 780
QY      2444 CAGCAGGTGAGTGTATCCGCTTCTCAGCAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2503
Db      781 ArgGIuValGIuLeuTyrArgLysLeuSerArgAsnThrTyrLeuGIuIleGIuIleGIuIle 800
QY      2504 GTCTGTGGGGGCGACATCTTCTGAGAGCAGTCAAGAAAGCCCTGCTGATGTGAATCA 2563
Db      801 ValLeuGIuYArgHisIlePheTyrArgLysValArgLysAlaLeuMetAspGIuLysSer 820
QY      2564 TGGATTCAGAGAGACAGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2620
Db      821 TrrAsnProGIuGIuThrValGIuIleGIuIleGIuIleGIuIleGIuIleGIuIleGIuIle 839

```

RESULT 3

```

Q8SP88 PRELIMINARY; PRT; 837 AA.
ID      08SP88
AC      08SP88;
DT      01-JUN-2002 (TrEMBLrel. 21, Created)
DT      01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Toll-like receptor 4.
GN      Name=TLR4;
OS      Gorilla gorilla.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX      NCBI TaxID=9593;
RN      [1]
RP      SEQUENCE FROM N.A.
RP      MEDLINE=21405531; Pubmed=11514453;
RA      Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RT      "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
RL      in humans."
RN      Genetics 158:1657-1664(2001).
RP      SEQUENCE FROM N.A.
RP      Beutler B., Smirnova I., Hamblin M.T., McBride C., Di Rienzo A.;
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF497563; AAM18617.1; JOINED.

```

```

DR      EMBL; AF497564; AAM18617.1; JOINED.
DR      HSSP; 060603; 1077.
DR      GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR      GO; GO:0001530; P:lipopolysaccharide binding; ISS.
DR      GO; GO:0004888; P:transmembrane receptor activity; ISS.
DR      GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR      GO; GO:0016046; P:detection of fungi; ISS.
DR      GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR      GO; GO:0042116; P:macrophage activation; ISS.
DR      GO; GO:0045576; P:macr cell activation; ISS.
DR      GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR      GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR      GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR      GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR      GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR      GO; GO:0042089; P:T-helper 1 type immune response; ISS.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR000483; LRR_Cterm.
DR      InterPro; IPR003591; LRR_Typ.
DR      InterPro; IPR000157; TIR.
DR      Pfam; PF01463; LRRCT; 1.
DR      Pfam; PF00560; LRR_1; 10.
DR      Pfam; PF01582; TIR; 1.
DR      PRINTS; PR00019; LEURICRPT.
DR      SMART; SM00082; LRRCT; 1.
DR      SMART; SM00369; LRR_Typ; 2.
DR      SMART; SM00255; TIR; 1.
DR      PROSITE; PS50104; TIR; 1.
DR      Receptor.
SQ      SEQUENCE 837 AA; 95497 MW; 5A177BABA341396DD CRC64;

```

Alignment Scores:

```

Pred. No.: 8 55e-314 Length: 837
Score: 4310.00 Matches: 832
Percent Similarity: 99.52% Conservative: 3
Best Local Similarity: 99.17% Mismatches: 2
Query Match: 50.24% Indels: 2
DB: 2 Gaps: 1

```

US-09-396-985b-1 (1-4868) x Q8SP88 (1-837)

```

QY      104 ATGATGTCTGCTGGCGCTGCTGAGACTGTATCCAGCAGTGCCTTCTCTCTGCTG 163
Db      1 MetMetSerAlaSerArgLeuAlaGIuThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY      164 GTGAGACCGAAGAGCTGGAGCCCTGCGTGAAGTGTCTTAAATTTCTTATCAATGC 223
Db      21 ValArgProGIuIleTyrGIuProCys-----ValValProAsnIleThrTyrGIuCys 38
QY      224 ATGAGAGCTGAATTTCTCAAAATCCCGACAACTCCCTTCTCAACGAAGCTGAGC 283
Db      39 MetGIuLeuAsnPheTyrIleProAspAsnLeuProPheSerThrIysAsnLeuAsp 58
QY      284 CTGAGCTTAAATCCCTGAGGATTTAGGACGTATAGCTTCTTCAAGTTCCAGAACTG 343
Db      59 LeuSerPheAsnProLeuArgHisLeuGIuIleGIuIleGIuIleGIuIleGIuIleGIuIle 78
QY      344 CAGGTCTGATTTATCCAGGTGTGAATCCAGACATTTGAAGATGGGCTATTCAGAGC 403
Db      79 GlnValLeuAspLeuSerArgCysGIuIleGIuIleGIuIleGIuIleGIuIleGIuIleGIuIle 98
QY      404 CTAAGCCACTCTCTCACTTAATATGACAGAAACCCCATCCAGAGTTTAAAGCCCTGGGA 463
Db      99 LeuSerHisLeuSerThrLeuIleuTrGIuAsnProIleGlnSerLeuAlaLeuGIu 118
QY      464 GCCTTTCTGACTATCAAGTTTACAGAGCTGTGTGCTGTGGAGCAAAATCTTACGATCT 523
Db      119 AlaPheSerGIuLeuSerSerLeuGIuIleValAlaValGIuThrAsnLeuAlaSer 138
QY      524 CTAGAGACTTCCCATTTGAGACATCTCAAACTTTGAAGAACTTATGTGCTCAAT 583
Db      139 LeuGIuAsnPheProIleGIuHisLeuIleGIuIleGIuIleGIuIleGIuIleGIuIleGIuIle 158

```

QY 584 CTTATCCAACTCTTCAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTG 643
DB LeuIIeGIserPheIysleuProGIuTyPheSerAsnleuThrAsnleuGIuTyLeu 178
QY 644 GACCTTCCAGCAACAAGATTCAAGATTATTTATTCACAGACTTGGGGTTCTACATCAA 703
DB AspleuSerSerAsnIysIleGIuSerIleTyrcysThrAspleuArgValIeuHISGln 178
QY 704 ATGCCCTACTGATCTCTTTAGACCTGTCCCTGAACTCTTAATGAACTTTATCCAAACA 763
DB MetProIeuAsnleuSerIleuAspleuSerIleuAsnProMetThrPheIIeGIuPro 218
QY 764 GGTGATTTAAAGAAATTAGGCTTCAATAGCTGACTTAAAGAAATAATTTGATAGTTA 823
DB GIIyAlAphelysGIuIleArgIeuHIleTyIeuThrIeuArgAsnPheAspSerIeu 238
QY 824 AATGTAATGAAACTTGATATTCAAGGTCTGGCTGTTTAAAGATCCATGCTTTGGTTCTG 883
DB AsnValMetIysThrCysIIeGIuIysIleuAlaGIuIleuGIuValAlaArgArgIeuValIeu 258
QY 884 GGAGAAATTTAGAAATGAGGAACTTGAGAAAGTTTGACAAATCTGCTTAGAGGGGCTG 943
DB GIIyGIuIlePheArgAsnGIuIleAsnleuGIuIlePheAspIysSerAlaIeuGIuIleu 278
QY 944 TGCAAATTTGACATTTGAGAAATTCGATTTAGACTACTTACTGATCTGATGATATT 1003
DB CysAsnleuThrIIeGIuIleuPheArgIeuAlaTyIleuAspIlyTyIleuAspAspIle 298
QY 1004 ATTGACTTATTTAATTTGTTGACAAATGTTTCTTCAATTTCCCTGGTGAAGTGTGACTATT 1063
DB ILeAspleuPheAsnCysIleuThrAsnValSerSerPheSerIeuValSerValIleThrIle 318
QY 1064 GAAAGGTTAAACACTTTCTTATTAATTTGAGTGGCAACTTAAAGTAAATTAAGTAACTG 1123
DB GIIuArgValAllysAspPheSerTyraAsnIleGIuIleArgIleuGIuIleuValAsnCys 338
QY 1124 AATTTGACAGATTTCCTCCATTTGAAATCTCAATCTCTCAAAAGGCTTACTTCACTTCC 1183
DB IysPheGIuIleuPheThrIleuTyIleuIysSerIleuIysArgIleuThrIleThrIleSer 358
QY 1184 AACAAAGGTGGGAATGCTTTTTCAGAAAGTTGATCTCAACAAAGCTTGATTTGAGATCTTC 1243
DB AsnIlyGIuIleAsnAlaPheSerGIuValAlaAspleuProSerIeuGIuIleuAspleu 378
QY 1244 AGTAGAAATGGCTTGATTTCAAGGTTGCTGTCTCAAGTATTTTGGAGCAACACAG 1303
DB SerArgAsnIlyIeuSerIleuIysGIuIysCysSerGIuSerAspPheGIuIleThrIleSer 398
QY 1304 CTTAAATATTAGATCTGAGCTTCAATGTGTATTATTCATGAGTTCAAACTTCTGGGC 1363
DB IeuIlyTyIleuAspleuSerIleuAsnGIuValIleThrMetSerSerAsnPheIeuGIu 418
QY 1364 TTAGAACAACTAGAACATCTGATTTCCAGCATTTCCAAATTTGAAACAAATGAGTGAATT 1423
DB IeuGIuIleuGIuIleuIleuAspPheGlnHISerAsnleuIysGIuIleMetSerGIuPhe 438
QY 1424 TCAGTATTCCTATCACTCAGAAACCTCATTTACTGATCTGATCTGATCTGACACACAA 1483
DB SerValPheIeuSerIleuArgAsnleuIleTyIleuAspIleSerHISerHISerHISer 458
QY 1484 GTTGCTTTCAATGAGCATCTTCAATGAGCTTGTCTGAGTCTGAAATCTTGAATGAGCTGGC 1543
DB ValAlaPheAsnIlyIlePheAsnGIuIleuSerSerIleuGIuValIleuIysMetAlaGIu 478
QY 1544 AATTTCTTCCAGGAAACTTCTTCCAGATATCTTCCAGAGCTGAGAACTTGACCTTC 1603
DB AsnSerPheGIuIleuAsnPheIeuProAspIlePheThrGIuIleuArgAsnleuThrPhe 498
QY 1604 CTGGAGCTCTCTCAGGTCAACTGAGCACTGTTCTCCCAACAGATTTAACTGACTTCC 1663
DB IeuAspleuSerIleuIysGIuIleuGIuIleuIleuSerProThrAlaPheAsnSerIleuSer 518
QY 1664 AGTCTTCAGGTACTAATATAGACCACAAACAATCTTTTCAATGATAGTTTCTTAT 1723

DB 519 SerIeuGIuValIeuAsnMetSerHISAsnAsnPheSerIleuAspThrPheProTyrc 538
QY 1724 AAGTCTGAACTCCCTCCAGGTTCTTGATTTACAGTCTCAATCACTAATGACTTCCAA 1783
DB IysCysIeuAsnSerIleuArgValIeuAspTyrcSerIeuAsnHISerIleMetThrSerIys 558
QY 1784 AACAGGAAGTACAGCAATTTTCCAGTAGCTGCTTTCTTAATCTTACTCAGAAATGAC 1843
DB IysGIuIleuGIuIleuHISerPheProSerSerIleuAlaPheIeuAsnleuThrGlnAsnAsp 578
QY 1844 TTTGCTTGTATCTTTGAGAACACAGATTTCTTGCAATGATCAGAGGACAGCTC 1903
DB PheAlaCysThrCysGIuIleuIleGIuSerPheIeuGIuIleuIleuIleuAspGlnArgIleu 598
QY 1904 TTGGTGGAAAGTTGAAAGATTTGAAATTTGCAACCTTCCAGATTAAGAGGCAAGCTCTG 1963
DB IeuValGIuValGIuIleuArgMetGIuIleuValAlaThrProSerAspIysGIuIleuMetProVal 618
QY 1964 CTGAGTTGAATATCACTGCTGAGATGAATGAATGACATGATGTTGGTGGTCTCAGT 2023
DB IeuSerIleuAsnIleThrCysGlnMetAsnIysThrIleIleGIuValSerValIleuSer 638
QY 2024 GTGCTTGTAGTATCTGTTGAGCACTTGTGCTATAGCTTCTAATTTTCACTGATGCTT 2083
DB ValIeuValIleuSerValIleuAlaValIleuValIleuValIleuPheTyrcPheHISleuMetIeu 658
QY 2084 CTGCTGCTGCTCAATAAGTATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2143
DB IeuAlaGIuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 678
QY 2144 TCAGCCAGAGATGAGGAGCTGGGTAAGAAATGAGCTGTAAGAAATTTAGAAAGAGGGGTG 2203
DB SerSerGlnAspIleuAspIleuValAlaArgAsnGIuIleuValIleuAsnleuGIuIleuVal 698
QY 2204 CCTCATTTCAAGCTCTGCTTCACTGACAGAGCTTATTTCCCGTGTGGCATTTGCTGCC 2263
DB PropIleuGIuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 718
QY 2264 AACATATCAATGAAAGCTTTCCATTAAGCCGAAAGGTGATTTGTGTGTCCAGCAC 2323
DB AsnIleIleHISGIuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 738
QY 2324 TTTCATCAGAGGCGCTGATCTTCAATTTGATGATGATGATGATGATGATGATGATGATGAT 2383
DB PheIleGIuIleuSerArgIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 758
QY 2384 AGCAGTCTGCTGATCATCTTCAATTTGCTGTCAGAAAGTGGAGAAAGCCCTGCTCAG 2443
DB SerSerArgAlaGIuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 778
QY 2444 CAGCAGGTGAGCTGTACCGCTTCTCAGCAGAGAACATTTACTGAGTGGAGAGCAGT 2503
DB GlnGIuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 798
QY 2504 GTTCTGGGGGCGACACTTCTTGAGAGAGAGCTCAGAAAGCCCTGATGGTGAATGAATGA 2563
DB 799 ValIeuGIuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 818
QY 2564 TGGAAATCCAGAAAGAACTGGGTACAGAGTCAATTTGACAGAAAGCAACATCTATC 2620
DB 819 TrpAsnProGIuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 837

RESULT 4
TLR4_PONPY
ID TLR4_PONPY STANDARD; PRT; 828 AA.
AC 08Sep9;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Toll-1-like receptor 4, precursor.
GN Name=TLR4;
OS Pongo pygmaeus (Orangutan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21405531; PubMed=11514453;
RA Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
in humans."; 157-1664(2001).
RL Genetics 158:1657-1664(2001).
CC -I- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
immune response to bacterial lipopolysaccharide (LPS). Acts via
Myd88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
secretion and the inflammatory response (By similarity).
CC -I- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds Myd88 and TIRAP via
their respective TIR domains (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the Toll-like receptor family.
CC -I- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; AF497562; AAM18616.1; -;
DR EMBL; AF497560; AAM18616.1; JOINED.
DR EMBL; AF497561; AAM18616.1; JOINED.
DR HSSP; O60603; LFYM.
DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR GO; GO:0001530; P:lipopolysaccharide binding; ISS.
DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR GO; GO:0007250; P:activation of NF-kappa-B inducing kinase; ISS.
DR GO; GO:0016046; P:detection of fungus; ISS.
DR GO; GO:0009398; P:detection of pathogenic bacteria; ISS.
DR GO; GO:0042116; P:macrophage activation; ISS.
DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR GO; GO:0045168; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Cyp.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR_12.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO0019; LEURCHRP.
DR SMART; SM00369; LRR_TYR; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KW Glycoprotein; Immune response; Inflammatory response;
KW leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 828 Toll-like receptor 4.
FT DOMAIN 24 629 Extracellular (Potential).
FT TRANSMEM 630 650 Potential.
FT DOMAIN 651 828 Cytoplasmic (Potential).
FT REPEAT 50 74 LRR 1.
FT REPEAT 75 98 LRR 2.
FT REPEAT 99 122 LRR 3.
FT REPEAT 126 147 LRR 4.
FT REPEAT 148 171 LRR 5.

FT REPEAT 172 195 LRR 6.
FT REPEAT 201 223 LRR 7.
FT REPEAT 226 250 LRR 8.
FT REPEAT 275 301 LRR 9.
FT REPEAT 325 348 LRR 10.
FT REPEAT 349 370 LRR 11.
FT REPEAT 371 396 LRR 12.
FT REPEAT 398 419 LRR 13.
FT REPEAT 420 443 LRR 14.
FT REPEAT 445 467 LRR 15.
FT REPEAT 468 492 LRR 16.
FT REPEAT 493 516 LRR 17.
FT REPEAT 518 539 LRR 18.
FT REPEAT 541 564 LRR 19.
FT REPEAT 566 590 LRR 20.
FT DOMAIN 670 816 TIR.
FT CARBOHYD 33 33 N-linked (GlcNAc . . .) (potential).
FT CARBOHYD 171 171 N-linked (GlcNAc . . .) (potential).
FT CARBOHYD 203 203 N-linked (GlcNAc . . .) (potential).
FT CARBOHYD 260 280 N-linked (GlcNAc . . .) (potential).
FT CARBOHYD 307 307 N-linked (GlcNAc . . .) (potential).
FT CARBOHYD 495 495 N-linked (GlcNAc . . .) (potential).
FT CARBOHYD 524 524 N-linked (GlcNAc . . .) (potential).
FT CARBOHYD 573 573 N-linked (GlcNAc . . .) (potential).
FT CARBOHYD 622 622 N-linked (GlcNAc . . .) (potential).
FT CARBOHYD 628 628 N-linked (GlcNAc . . .) (potential).
SQ SEQUENCE 826 AA; 94340 MW; 51AC0984E5970FDF CRC64;

Alignment Scores:

Pred. No.: 3, 24e-304 Length: 828
Score: 4182.00 Matches: 808
Percent Similarity: 98.31% Conservative: 8
Best Local Similarity: 97.35% Mismatches: 12
Query Match: 48.75% Indels: 2
DB: 1 Gaps: 1

US-09-396-985B-1 (1-4868) x TLR4_PONPY (1-828)

QY 104 ATGATGTCGCTCGGCTGGCTGGACTCGATCCGACGATGCGCTTCCTGCTGCG 163
|||
DB 1 MetMetSerLaserArgLeuAlaGlyThrLeuIleProAlaMetAlaLeuSerCys 20
164 GTGAGACGAGAAAGCTGGAGCGCTGGAGGTGCTCTAATATTACTTATCAATGC 223
|||
DB 21 ValArgProGluSerThrProIuProCys-----ValValProAsnIleThrTyGlnCys 38
QY 224 ATGAGACTGAATTTCTACAAAATCCCGACAACTCCCTTCTCAACCAAGAACTGAGC 283
|||
DB 39 MetGluLeuAsnPhenTyrlsIleProAsnLeuProPheSerThrIysAsnLeuAsp 58
QY 284 CTGAGCTTTAATCCCTGAGGACTTTAGGCACCTAAGCTTCTTCAGTTTCCAGAACG 343
|||
DB 59 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerThrProGluLeu 78
QY 344 CAGGTGCTGATTTATCCAGTGTGAAATCCAGACAATTAAGATGGGCATATCAGAGC 403
|||
DB 79 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGluAspGlyAlaTyrglnSer 98
QY 404 CTAAAGCCACTTCTTACCTTAATATTGACAGAGAAACCCATCCAGATTAGCCCTGGGA 463
|||
DB 99 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnAsnLeuAlaLeuGly 118
QY 464 GCTTTTCTGAGACTATCAGTTTATCAGAGCTGCGGCTGTGGAGCAATCTAGAGACT 523
|||
DB 119 AlaPheSerGlyLeuSerSerLeuGlnIlySleuValAlaValGluThrAsnLeuAlaSer 138
QY 524 CTAGAGAACTTCCCATTTGAGCATCTCAAAACTTTGAAGAAGACTTAATGTGCTCAAT 583
|||
DB 139 LeuGluAsnPhenProIleGlyHisLeuTySThrLeuGlyGluLeuAsnValAlaHisAsn 158
QY 584 CTATTCGAATCTTTCAATTAATCTGAGATATTTTCTTAATCTGACCAATCTGAGACTTG 643
|||
DB 159 LeuIleGlnSerPheIysLeuProGluTyrrPheSerAsnLeuThrAsnLeuGluHisLeu 178

QY 644 GACCTTTCCAGCAACAGATTCAAGATTATTTGACAGACTTGCGGTTTCAATCAA 703
 DB 179 AspLeuSerSerLeuIleGlnSerIleTyCysIleAspLeuGlnValIleHisGln 198
 QY 704 ATGCCCCCTCAATCTCTCTTTAGACCTGTCCCTGAATCTTATGAACCTTTATCCACA 763
 DB 199 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnIleMetAsnPheIleGlnPro 218
 QY 764 GGTGCAATTTAAAGAAATTAGCTTCATTAAGCTTAAAGAAATAATTTGATAGTTA 823
 DB 219 GlyAlaPheLeuGlnIleArgLeuHisIleLeuThrLeuArgAsnSerPheAspSerLeu 238
 QY 824 AATGATATGAAGAACTTGATTTCAAGCTGTGGCTGTTTGAAGTCCATCTTGTTGTTCTG 883
 DB 239 AsnValMetLeuSerThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisIleValLeu 258
 QY 884 GAGAAATTTAGAAATGAGGAACTTGAGAAAGTTTGACAAATCTGCTTGAAGGGCTG 943
 DB 259 GlyGluPheArgAsnGlnIleGlnIlePheAsnLeuGluIlePheAspThrSerAlaLeuGlnGlyLeu 278
 QY 944 TGCATTTGACCATTTGAAGAAATTCGATTTAGCATCTACTACTACTACTGATATTT 1003
 DB 279 CysAsnLeuThrIleGlnGlnPheArgLeuAlaTyLeuAspTyrTyLeuAspAspIle 298
 QY 1004 ATTGCTTAATTTAATTTGACAAATGTTTCAATTTTCCCTGGAGTGGAGTCAATT 1063
 DB 299 IleAspLeuPheAsnGlyLeuAlaAsnValSerSerPheSerLeuValSerValIle 318
 QY 1064 GAAAGGGTAAAGACTTTTCTTAATTTGAGATGGCAATTTAGATTTAACTGT 1123
 DB 319 LysSerValIleAspPheSerIleTyAsnPheGlyTyrGlnHisIleGlnIleValAsnGly 338
 QY 1124 AATTTTGACACTTTCCCAATTTGAACCTCAATCTCTCAAAAGGCTTACTTCACTTCC 1183
 DB 339 LysPheGlyGlnPheThrIleGlnIleLeuIleLysSerLeuLysArgLeuThrPheIleAla 358
 QY 1184 AACAAAGGTGGAGATGCTTTTTCAGAAATGATCTCAAGCTTGAATTTAGATCTG 1243
 DB 359 AsnIleGlyGlyIleAsnAlaPheSerGluValAspLeuProSerLeuGlnPheLeuAspLeu 378
 QY 1244 AGTAGAAATGGCTTGAGATTCAAGGTTGCTGTTCTCAAGATTTTGGAGAACACAGC 1303
 DB 379 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 398
 QY 1304 CTAAATGATTTAGATCTGAGCTTCAATGCTGTTATTAACATGAGTTCAAACTTTGGGC 1363
 DB 399 LeuIleTyLeuAspLeuSerPheAsnAspValIleThrMetGlySerAsnPheLeuGly 418
 QY 1364 TTGAGCAACTAGAACATCTGATTTCCAGACTTCCAAATTTGAAACAAATGAGTGAATT 1423
 DB 419 LeuGlnIleLeuGlnIleHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 438
 QY 1424 TCAGATTTCTATCACTAGAAACCTCATTTACTTGAATTTCTCATATCTCACACAGC 1483
 DB 439 SerValPheLeuSerLeuArgAsnLeuIleTyLeuAspIleSerHisThrHisIleThrArg 458
 QY 1484 GTTGCTTTCAATGCAATCTTCAATGCTGTGCTCAAGTCTGCAAGTCTTGAATGCTGGC 1543
 DB 459 ValAlaPheAsnIleTyLeuAsnGlyLeuSerSerLeuLysValIleLysMetAlaGly 478
 QY 1544 AATTTCTTCCAGGAAACTCTTCCAGATATCTTCCAGAGCTGAGGAACTTGACCTTC 1603
 DB 479 AsnSerPheGlnIleAsnPheLeuProAspIlePheThrGlnIleuArgAsnLeuThrPhe 498
 QY 1604 CTGACACTCTCTCAAGTGTCAACTGAGAGCTGTCTTCAACAGCATTTTAATCACTCTCC 1663
 DB 499 LeuAspLeuSerGlnCysGlnLeuGlnIleLeuSerProThrAlaPheAsnSerLeuSer 518
 QY 1664 AGCTTTCAAGTACTTAATATGAGCCACACAACTTCTTTCAATGATGATGCTTCTTAT 1723
 DB 519 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 538

QY 1724 AAGTGTCTGAACCTCCCTCCAGGTTCTTGATTTACAGTCTCAATCATAATGACTTCCAA 1783
 DB 539 LysCysLeuAsnSerLeuGlnValIleAspTyrSerLeuAsnHisIleMetThrSerLys 558
 QY 1784 AAACAGAACTACAGCATTTTCCAGTACTTACGTTTCTTAAATCTTACTGCAATGAC 1843
 DB 559 LysGlnGlnLeuGlnHisIlePheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 578
 QY 1844 TTGCTTTGACTGTGTAACACCGAGATTTCTCGCAATGGATCAAGAGCCAGGACGCTC 1903
 DB 579 PheAlaCysThrCysGlnIleGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu 598
 QY 1904 TTGGTGAAGTTGACGAATGGAATGGAATGGAACACTTTCAGATTAAGAGGCGATGCTGTG 1963
 DB 599 LeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnIleMetProVal 618
 QY 1964 CTGAGTTGAATATCACTGTCAGATGAATTAAGACCATCATGTTGGTGTGCTTCAGT 2023
 DB 619 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrValIleGlyValSerValPheSer 638
 QY 2024 GTGCTTGATGATCTGTTGATGAGACTTGTGCTATTAAGTTCATTTTCACTGATGCTT 2083
 DB 639 ValLeuValValSerValValAlaValAlaValIleValTyLeuPheTyrPheHisLeuMetLeu 658
 QY 2084 CTGCTGCGCTGCAATAAGTATGAGTGAAGGTAAGAAACATCATGATGCTTGTATCTAC 2143
 DB 659 LeuAlaGlyCysAlaIleLysTyGlyArgGlyGlnAsnThrTyAspAlaPheValIleTyr 678
 QY 2144 TCAGGCGAGATGAGAGACTGGGTAAAGATGAGCTGTAAGAAATTTAGAAAGAGGCTG 2203
 DB 679 SerSerGlnAspGluAspIleThrValArgAsnGlnLeuValLysAsnLeuGlnGlyVal 698
 QY 2204 CTTCACTTTCAAGTCTGCTTCACTACAGACTTAAATCCCGGTTGGCATTTGCTGCC 2263
 DB 699 ProThrPheGlnLeuCysLeuHisTyTyArgAspPheIleProGlyValAlaIleAlaAla 718
 QY 2264 AACATCATCAAGAAAGTTCATTAAGAAACCGGAAGGATGTTGTGTGTCCTCCAGAC 2323
 DB 719 AsnIleIleHisGlnIlePheHisIleTySerAspArgValIleValValValSerGlnHis 738
 QY 2324 TTCAATCAGAGCGGCTGTGTATCTTTGAATATGATGATGCTCAGACTGGAGTTTCTG 2383
 DB 739 PheIleGlnSerArgTyrCysIlePheGlnTyGlnIleAlaGlnThrTyGlnPheLeu 758
 QY 2384 AGCAGTCGCTGCTATCATCTTCAATTCCTCGCAAGAGTGAAGAGCCGCTCAGG 2443
 DB 759 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnTyThrLeuLeuArg 778
 QY 2444 CAGCAGGTGAGCTGTAACCGCTTCTCAGCAGGAACACTTACCTGAGTGGAGAGCAGT 2503
 DB 779 GlnGlnValGlnLeuTyArgLeuLeuSerArgAsnThrTyLeuGlnTrpGluAspSer 798
 QY 2504 GTCTGCGGCGGACATCTTCTGAGACGACTCAGAAAGCCCTGCTGATGGTAAATCA 2563
 DB 799 ValLeuGlyArgHisIlePheThrPargArgLeuArgValAlaLeuLeuAspGlyLysSer 818
 QY 2564 TGGATCCGAAGAGAACTGGGTACAGCA 2593
 DB 819 TrpAsnProGlnGlyThrValGlnTyThrGly 828

RESULT 5
 ID TLR4_PAPAN STANDARD; PRT; 826 AA.
 AC Q9TSE2;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE TOLL-like receptor 4 precursor.
 GN Name-TLR4;
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.

OX NCBI_TaxId=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:20558910; PubMed:11104518;
 RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
 RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
 locus (TLR4).";
 RL Genome Biol. 1:RESEARCH002.10(2000).
 CC -! FUNCTION: Cooperates with MyD88 and CD14 to mediate the innate
 immune response to bacterial lipopolysaccharide (LPS). Acts via
 MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 secretion and the inflammatory response (By similarity).
 CC -! SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 multi-protein complex containing at least CD14, MyD88 and TIRAP, via
 binds MyD88 via the extracellular domain. Binds MyD88 and TIRAP via
 their respective TIR domains (By similarity).
 CC -! SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -! SIMILARITY: Belongs to the Toll-like receptor family.
 CC -! SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
 CC -! SIMILARITY: Contains 1 TIR domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF180964; AAF07059.1; -;
 DR EMBL; AF180962; AAF07059.1; JOINED.
 DR EMBL; AF180963; AAF07059.1; JOINED.
 DR HSSP; 015399; 1FVY.
 DR GO; GO:0046596; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045576; P:osteoclast activation; ISS.
 DR GO; GO:0045571; P:negative regulation of osteoclast different. . .; ISS.
 DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR_13.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO0019; LEURICHRPT.
 DR SMART; SM00369; LRR_Typ; 2.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 DR GlycoSite; PS50104; TIR; 1.
 KW Glycoprotein; Immune response; Inflammatory response;
 KM Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 826
 FT DOMAIN 24 631 Extracellular (Potential).
 FT TRANSMEM 632 652 Transmembrane.
 FT DOMAIN 653 826 Cytoplasmic (Potential).
 FT REPEAT 53 76 LRR 1.
 FT REPEAT 77 100 LRR 2.
 FT REPEAT 101 124 LRR 3.
 FT REPEAT 128 149 LRR 4.
 FT REPEAT 150 173 LRR 5.
 FT REPEAT 174 197 LRR 6.
 FT REPEAT 203 225 LRR 7.

FT REPEAT 228 252 LRR 8.
 FT REPEAT 277 303 LRR 9.
 FT REPEAT 327 350 LRR 10.
 FT REPEAT 351 372 LRR 11.
 FT REPEAT 373 398 LRR 12.
 FT REPEAT 400 421 LRR 13.
 FT REPEAT 422 445 LRR 14.
 FT REPEAT 447 469 LRR 15.
 FT REPEAT 470 494 LRR 16.
 FT REPEAT 495 518 LRR 17.
 FT REPEAT 520 541 LRR 18.
 FT REPEAT 543 569 LRR 19.
 FT REPEAT 571 592 LRR 20.
 FT DOMAIN 612 818 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc . . .) (potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc . . .) (potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc . . .) (potential).
 FT CARBOHYD 282 282 N-linked (GlcNAc . . .) (potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (potential).
 FT CARBOHYD 624 624 N-linked (GlcNAc . . .) (potential).
 FT CARBOHYD 630 630 N-linked (GlcNAc . . .) (potential).
 SQ SEQUENCE 826 AA; 94678 MW; 4227773185F1769 CRC64;
 Alignment Scores:
 Pred. No.: 8, 35e-294 Length: 826
 Score: 4043.00 Matches: 776
 Percent Similarity: 96.97% Conservative: 23
 Best Local Similarity: 94.17% Mismatches: 25
 Query Match: 47.13% Indels: 0
 DB: 1 Gaps: 0
 US-09-396-985b-1 (1-4868) x TLR4_PAPAN (1-826)
 QY 104 ATGATGCTGCTGCTGGCGCTGGAGCTGATCCAGACGCTTCTCTCTGC 163
 DB 1 MetInSerAlaLeuArgLeuLaglyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 164 GTGAGACCAAGAAAGCTGGAGCGCTGGAGGTGCTTCTTATTTATTCATATGC 223
 DB 21 ValArgProGluSerTyrPheIleProCysValAlaGluValAlaProAsnIleThrTyrGlnCys 40
 QY 224 ATGGAGCTGAATTTTACAAATATCCCGCAACCTCCCTTCAACCAAGACCTGAGC 283
 DB 41 MetGluLeuAspPheThrTyrIleProAspAsnIleProPheSerThrTyrAsnLeuAsp 60
 QY 284 CTGAGCTTATATCCCTGAGGACATTTAGCAGCTATAGCTTTCAGTTTCCAGAACTG 343
 DB 61 LeuSerPheAsnProLeuArgIleLeuGlySerTyrSerPheLeuArgPheProGluLeu 80
 QY 344 CAGGTGCTGATTTATTCAGGTGTGAATTCAGACATTTGAAGATGGGCAATTCAGAC 403
 DB 81 GlnValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 100
 QY 404 CTAGAGCACTCTGATCTTATATTTAGCAGAAACCCATCCAGAGTTTGGCCCTGGAG 463
 DB 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
 QY 464 GCGTTTTCGACTATCAAGTTTACAGAGCTGTGTGCTGTGGAGCAAAATCTAGCATCT 523
 DB 121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGluThrAsnLeuAlaSer 140
 QY 524 CTAGAGCACTTCCCATTTGAGACATTCGAAACTTTGAAGAACTTATGTGCTCAAT 583
 DB 141 LeuGluAsnPheProIleGlyHisLeuIleGluValGluLeuAsnValAlaHisAsn 160
 QY 584 CTATGCAATCTTTGAAATTTACCTGATTTTCTTCAATCTAGCAATCTAGGACCTTG 643
 DB 161 LeuIleGlnSerPheIleLeuProGlyTyrPheSerAsnLeuThrAsnLeuGluHisLeu 180
 QY 644 GACCTTTCAGCAACAAGATTCAAAGTATTTATTCAGACAGACTTGGGGTTCATCA 703

```

|||||.....
Db 181 AspreuserSerAenLysileGlnAsnileTyrCysLysAspLeuGlnValLeuHisGln 200
Qy 704 ATGCCCTACTCAATCTCTCTTAGACCTGTCCCTGAATCCTATGAACCTTATTCACCA 763
Db 201 MetProLeuProAsnLeuSerLeuAspLeuSerLeuAsnProIleAsnPhelileGlnPro 220
Qy 764 GGTCATTTAAGAAATTAAGCTTCATAGCTGACTTAAAGAAATTAATTTGATAGTTA 823
Db 221 G1ValAheLysGlnLileArgLeuHisLysLeuThrLeuArgSerAsnPhenAspLeu 240
Qy 824 AATGTAAAGAAACCTTGTATCAAGCTCTGGCTGGTTAAGAGTCAATCGTTGGTCTG 883
Db 241 AsnValMetLysThrCysileGlnGlyLeuAilaGlyLeuGlnValHisArgLeuValLeu 260
Qy 884 GGAGATTTTGAATTAAGAAACTTGAAGAAAGTTTGAACAAATTCCTCTAGAGGCTG 943
Db 261 G1YglLuhPheArgAsnGluArgAsnLeuGlnLuhPheAspLysSerAlaLeuGlnGlyLeu 280
Qy 944 TGCAATTTGACCATTTGAAGAAATTCGATTAAGCATTAAGCTACTGATCATATTT 1003
Db 281 CysAsnLeuThrIleGlnGlnLuhPheArgLeuThrTyrLeuAspLys 300
Qy 1004 ATTGACTTATTTAATTTGTCACAAATGTTTCTCATTTTCCCTGTAGAGTGTACTATT 1063
Db 301 ILeAspLeuPheAsnGlySerLeuAlaAsnAlaSerSerPheSerLeuValSerValAsnIle 320
Qy 1064 GAAAGGTAAAGACCTTTCTTATATTTGAGATGGACACATTTAAGATTAAGTACTGT 1123
Db 321 LysArgValGlnAspPheSerTyrAsnPhenArgPheGlnHisLeuGlnLeuValAsnGly 340
Qy 1124 AAATTTGACAGTTTCCCATTTGAACCTGAATCTCAAAAGGCTTACTTTCACCTCC 1183
Db 341 LysPheGlnLuhPheProThrLeuGlnLuhPheLysLeuLysArgLeuThrPheThrAla 360
Qy 1184 AACAAAGGTGGAGATCTTTTTCAGAGTGTATCTACCAAGCCTTGAATTTCTAGATCTC 1243
Db 361 AsnLysGlnLuhPheAsnAlaPheSerGlnValAspLeuProSerLeuGlnLuhPheLeuAspLeu 380
Qy 1244 AGTGAATAGCTTGAATTCAGAAAGTTGCTGTCTCAAAAGTGAATTTGGAGACACAGC 1303
Db 381 SerArgAsnGlnLysLeuSerPheLysGlnCysSerSerLeuSerAspPheGlnThrThrSer 400
Qy 1304 CTAAGATTTTGAATCTGAGGTTCAATGCTGATTAATCAATGATTTCAAACTTCTGGGC 1363
Db 401 LeuLysTyrLeuAspLeuSerPheAsnAspValIleThrMetGlnLysArgAsnPhenLeuGly 420
Qy 1364 TTAGAACACTAGAACATCTGATTTCCAGATTTCCAAATTTGAAACAAATGAGTGAATTT 1423
Db 421 LeuGlnLuhPheGlnLuhPheLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPhe 440
Qy 1424 TCAGTATTTCTATCACTGACGAACTTCATTAATCTTGAATTTCTCAATCTCACACGAG 1483
Db 441 SerValPheLeuSerLeuArgAsnLeuLileTyrLeuAspLieserHisThrHisThrThr 460
Qy 1484 GTTGCTTTCAATGAGCATCTTCAATGCTTGGCCAGTGTGCAAGCTTGAAGAAAGGCTGCG 1543
Db 461 ValAlaPheAsnGlnLilePheAspGlnLysLeuSerLeuLysValLeuLysMetAlaGly 480
Qy 1544 AATTTCTTCCAGGAAACCTTCCATTCAGATATCTTCCAGAGCTGAGAAACCTTGACCTTC 1603
Db 481 AsnSerPheGlnGlnLuhPheLeuProAspLilePheThrAspLeuLysAsnLeuThrPhe 500
Qy 1604 CTGAGACTTCTCTCAGTCTCACTGAGACAGTGTCTCCAAACAGATTTAACTCACTCTCC 1663
Db 501 LeuAspLeuSerGlnCysGlnLeuGlnLuhPheLysLeuSerProThrAlaPheAspThrLeuAsn 520
Qy 1664 AGCTTGAAGTAAATATGAGCACAACAACCTTTTCAATGATGATGATGATGATGATGAT 1723
Db 521 LysLeuGlnValLeuAsnMetSerHisAsnAsnPhenPheSerLeuAspValPheProTyr 540
Qy 1724 AAGTGTGAACTCCCTCAGGTTCTGATTAAGTCAAGTCAATCAATCAATCAATCAATCA 1783

```

```

Db 541 LysCysLeuProSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 560
Qy 1784 AAACAGAACTAAGACTTTTCCAAAGTACTGATCTTTCTTAATCTTACTCAAGAAATGAC 1843
Db 561 AsnGlnLuhProGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
Qy 1844 TTTGCTTGTACTTGTGAACACACAGATTTCTTCAATGATGATCAAGACACAGAGCAGCTC 1903
Db 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrLileLysAspGlnAlaGlnLeu 600
Qy 1904 TTGGTGAAGTGAACGAAATGGAATGTGCAACCTTCAGATTAAGACAGGACGCTGTG 1963
Db 601 LeuValGlnLuhLuhArgMetGlnCysAlaThrProSerAspLysGlnLysMetProVal 620
Qy 1964 CTGAGTTGAATTCACCTGTGATGATTAAGATTAACATCACTTGGTGTGGCTGCTGACT 2023
Db 621 LeuSerValAsnLileThrCysGlnMetAsnLysThrLileLysValSerValPheSer 640
Qy 2024 GTGCTGTAGTATCTGTGTGACAGATTTGCTGATTAAGTTCATTTTCACTGATGCTT 2083
Db 641 ValLeuValValSerValValAlaValLeuValTyrLysPheThrPheHisLeuMetLeu 660
Qy 2084 CTGCTGTGCTGCTCAATTAAGTGTGAGTGAAGTGAACATCTATGATGCTTTGATCTAC 2143
Db 661 LeuAlaGlnCysIleLysTyrGlnArgGlnGlnAsnIleTyrAspAlaPheValIleTyr 680
Qy 2144 TCAGGACAGATTAAGACCTGGCTGAAGAAATGACTGTGAAGAAATTAAGAAAGGCTG 2203
Db 681 SerSerGlnAspLuhAspThrValArgAsnGlnLeuValLysAsnLeuGlnGlnGlyVal 700
Qy 2204 CTTCAATTTCAAGCTTCCCTTCACTACAGAGCTTATTTCCGCTGTGGCCTTGTGCTCC 2263
Db 701 ProProPheGlnLeuCysLysLeuHisTyrArgAspPheIleProGlnValAlaIleAla 720
Qy 2264 AACATCATCCATGAAGTTCATTAAGAGCCGAAAGCTGATTTGTGTGTGCTCCAGAC 2323
Db 721 AsnIleIleHisGlnLuhPheHisLysSerArgLysValIleValValValSerGlnHis 740
Qy 2324 TTGATCCAGAGCCGCTGTGATCTTTGAAATGAGATTTGCTCAAGCTTGGCAGTTTCTG 2383
Db 741 PheIleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGlnThrTyrGlnPheLeu 760
Qy 2384 AGCAGTGTGCTGTATCATCTTCAATTTCTCAGAGGTGAGAGAACCTGTCTCAG 2443
Db 761 SerSerArgAlaLileLilePheIleValLeuGlnLysValGlnLysThrLeuAspSer 780
Qy 2444 CAGCAGGTGAGCTGTACCGCTTCTCAGCAGGAAACCTTACCTGAGTGGAGACAGT 2503
Db 781 GlnGlnValGlnLuhLuhTyrArgLeuLeuSerArgAsnThrTyrLeuGlnLuhAspSer 800
Qy 2504 GTCTGTGGGGGAGCAATCTTTCTGAGACGACTCAAGAAAGCCCTGTGATGTTAAATCA 2563
Db 801 ValLeuGlnGlnHisIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlnArgSer 820
Qy 2564 TGGATTCAGAA 2575
Db 821 TrpAsnProGln 824

```

RESULT 6
 ID TLR4 HORSE STANDARD; PRT; 843 AA.
 AC GMYV3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE T011-like receptor 4 precursor.
 GN Name=TLR4;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OC NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.

QY	824	AATGAAATGAAAACCTTGATTCACAAAGTCGGCGGTGTTTAAAGATCCATCGTTGGTTCG	883
Db	241	AspValMetLysSerCysIleGlnIleuAlaGlyLeuLysValAsnArgLeuValLeu	260
QY	884	GGAGAAATTTAGAAATGAAGAAACCTTGAAAAAGTTTGCAAAATCGCTCTAGAGGGCGCTG	943
Db	261	GlyIuPheLysAsnGluArgLysLeuGluArgPheAspThrIleAsnArgGlyLeu	280
QY	944	TGCATTTTGACCATTTGAAGAAATCCGATTAGCATCTTAAAGCTACTACCTCGAT--GAT	1000
Db	281	HisAsnLeuThrIleGluGluPheArgLeuAlaTyrIleAspAsnTyrSerSerLysAsp	300
QY	1001	ATTATTTGACTATTTAATTTATGTTTGACAATGTTTCTCATTTTCCCTGGTGAAGTGTACT	1066
Db	301	SerIleAspLeuLeuAsnCysLeuAlaAspIleSerLysIleSerLeuValSerLeuAsn	320
QY	1061	ATTGAAAGGATTAAGAACTTTTCTTATATTTCCGATGGCAACATTTTGAATTTGTTTAACT	1120
Db	321	LeuGlyAsnLeuLysAspPheProLysGlyPheGlyTyrGlnAspPheGluLeuValAsn	340
QY	1121	TGTAAATTTTGACAGCTTTCCACATTTGAAACTCAAAATCTCAAAAGGCTTACTTTCAC	1180
Db	341	CysArgIleGluGlyPheProThrLeuGluLeuThrSerLeuLysArgLeuValPheThr	360
QY	1181	TCCAACAAAGGTGGGAATGCTTTTTCAGAACTGATCTACCAAGCTTGAGTTCTAGAT	1240
Db	361	SerAsnLysAspMetLysSerPheAsnIleValLysLeuProSerLeuGluPheLeuAsp	380
QY	1241	CTCAGTGAATATGGCTGAGTTTCAAAAGTTCGTTTCAAAAGATTTTGGGCAACC	1300
Db	381	LeuSerArgAsnArgLeuSerPheLysSerCysSerGlyAlaAspLeuLysThrThr	400
QY	1301	AGCCTAAAGTATTTAGATCTGAGCTTCATGATGTTATTTACCATGAGTTCAACTTCTTG	1360
Db	401	ArgLeuLysHisIleLeuAspLeuSerPheAsnAspValIleSerMetSerSerAsnPheMet	420
QY	1361	GGCTTAGAACCACTGAAACATCTGGATTTCCAGCACTTCCAAATTTGAAACAAATAGTAG	1420
Db	421	GlyLeuGluGluGlnLeuGlnHisIleAsnAspPheGlnHisSerThrLeuLysGlnAlaSerAsp	440
QY	1421	TTTTCAGATTTCCATCACTCAGAAACCTCAATTATTCCTGACATTTCCATATCAACACC	1480
Db	441	PheProValPheLeuSerLeuLysAsnLeuArgTyrLeuAspIleSerTyrThrAsnThr	460
QY	1481	AGAGTTGCTTTCAATGGCATCTTCAATGGCTGTCTCAGCTTCGAAGTCTTAAAAATGGCT	1540
Db	461	ArgValValPheHisIleGlyIlePheAspGlyLeuValSerLeuGlnValLeuLysMetAla	480
QY	1541	GGCAATTTCTTCCAGAAACCTTCTCTCCAGATATCTTCAAGAGCTGAGAACTTGACC	1600
Db	481	GlyAsnSerPheLysAspAsnPheLeuProAsnIlePheArgGluMetThrAsnLeuThr	500
QY	1601	TTCTCGACCTCTCTCAGTGTCACTGGAGAGATTTGTCCAAACAGCATTTAACTCACTC	1660
Db	501	ThrLeuAspLeuSerLysCysAsnLeuGluGlnValSerGlnGluAlaPheCysLeuLeu	520
QY	1661	TCCAGTCTTTCAGTACTAAATATATAGCCACAACAACCTTTCTTCAATGGATACGTTTCT	1720
Db	521	ProArgLeuAlaGlyValLeuAsnMetSerHisAsnAsnLeuLeuPheLeuAspMetLeuPro	540
QY	1721	TATAAGTGTCTGAACCTCCCTCCAGGTTCTTGATTACAGTCTCAATTCACATATACATTC	1780
Db	541	TyrItyrProLeuHisIleSerLeuGlnIleLeuAspCysSerPheAsnArgIleValAlaPhe	560
QY	1781	AAAAAACGGAACCTACAGCATTTTTCAAAGTAGCTAGCTTCTTAAATCTTACTCGAGAT	1840
Db	561	LysTrpGlnGluLeuGlnHisPheProSerSerLeuAlaSerLeuAsnLeuThrGlnAsn	580
QY	1841	GACTTTGCTGTACTGTGGAACACAGAGTTTCTCGAAATGGATTCAGACACAGAGCGAG	1900
Db	581	AspPheAlaCysValCysGluTyrGlnSerPheLeuGlnThrValLysAspGlnArgGln	600

QY	1901	TTCTTGAGGAAGTTGAACGAATGGATGTGGCAACCTTCAGATTAGCAAGGGGATGCT	1960
Db	601	LeuLeuValGluValGluHisIleValCysAlaIleProIeuGlnMetArgGlyMetPro	620
QY	1961	GTGCTGAGATTG--AATATCACCTGTCCAAATGATATAGACCAATCATTTGGTGTGTCGGTC	2017
Db	621	ValLeuGluIpheAsnAlaIatIlnCysGlnHisIleSerIysThrIleValGluGlySerVal	640
QY	2018	CTCAGTGTGCTTGTATGTATCTGTGTGTAAGCAATTCTGGCTGTAAAGTTCTATATTTTCACCTG	2077
Db	641	PheSerIleLeuMetValSerValIleAlaValLeuValIlyTrpLysPheItyrPheHisLeu	660
QY	2078	ATGCTTTCTTCTGGCTGCTSCATAAAGTANGTGTAAGAGTGAATAAACAATCTATGATGCTTTGTT	2137
Db	661	MetLeuLeuAlaGlyCysLysLysValGlyAlaGlyGlyIleItyrAspAlaPheVal	680
QY	2138	ATCTATCCAAAGCCAGATAGAGACTGGGTAAAGGAATAGCATTAGTAAGATTATTAAGAA	2197
Db	681	IleItyrSerSerGlnAspGlnAspIleTrpValAlaArgAsnIleuValIlyAsnIleGlnGlu	700
QY	2198	GGGGTGCTCCATTTTCAAGCTCTGGCTTCACTAACAGACCTTTATTTCCGGTGTGGCCATT	2257
Db	701	GlyValProProPheGlnLeuCysLeuHisItyrAlaArgSerPheIleProGlyValAlaIle	720
QY	2258	GCTGCCCAACATCATCCATGAAAGTTTCTCATAAAAAGCCGGAAGGTGATTTGTTGGTGTCC	2317
Db	721	AlaAlaAsnIleIleGlnGluGlyPheHisLysSerItyrGlyValIleValIleValSer	740
QY	2318	CAGCACTTCATCCAGACCGCTGGTGTATCTTTGAATATGATGATGCTCGACCTGGCCAG	2377
Db	741	GlnHisPheIleGlnSerArgItyrCysIlePheGluItyrGluIleAlaGlnIlnTrpGln	760
QY	2378	TTTCTGAGCAGTGGTGTGATCATCTTTGATTTCTCTGTCGAGAAAGGTGAGAAACCTTG	2437
Db	761	PheLeuSerSerArgAlaGlyIleIleIlePheIleValLeuHisItyrLysLeuGlnLysSerLeu	780
QY	2438	CTCAGGAGACAGAGGTGAGAGCTGTACCGCTTCTCAGCAGGAACATTACTCTGAGTGGGAG	2497
Db	781	LeuArgGlnGlnIlnValGluLeuItyrArgIleuLeuAsnArgAsnThrItyrLeuGlnIlyTrpGln	800
QY	2498	GACAGTGTCTCTGGGGGGCGGCACATCTTCTGTGAGAGCACTCAGAAAGCGCTGTGAGATGT	2557
Db	801	AspSerValLeuGluItyrArgHisIleIlePheTrpArgItyrLeuArgLysAlaIleuLeuAspGly	820
QY	2558	AAATCATGGAATCCAGAAAGGAGACA 2581	
Db	821	LysProIlyPheSerProAlaGlyIlnr 828	
RESULT 7			
TLR4_BOVIN	TLR4_BOVIN	STANDARD;	PRT; 841 AA.
AC	09GLF5;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Toll-like receptor 4 precursor.		
GN	Name=TLR4;		
OS	Bos taurus (Bovine).		
OC	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euteleia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovinae; Bos;		
OX	NCBI_TaxID=9913;		
RN	[1]		
RA	SEQUENCE FROM N.A.		
RP	Guionaud C.T., Dubey C., Jungi T.W.;		
RT	"Bovine Toll-like receptor 4 (TLR4).";		
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate		
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via		
CC	MYD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine		
CC	secretion and the inflammatory response (By similarity).		
CC	-1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a		
CC	multi-protein complex containing at least CD14, LY96 and TLR4.		

QY 944 TGCATTTGACATTTGAGATTCGATTTAGCATTTAGTCTGATGATATT 1003
 Db 281 Cysahneuthrilegulinphearglilealatyreumsplyspheaserglyasp 300
 QY 1004 ATTGATTTATTTATTTGTCACAAATGTTTCTTCATTTTCCCTGGAGTGATCTATT 1063
 Db 301 ThraspneubheancysleuallaaenvaliseralliserleuleuSerlleSerleu 320
 QY 1064 GAAAGGTAAGAAGCTTTCTTATTAATTGCGATGCGAATTTAGATTTAGTTAACTGT 1123
 Db 321 GlySerleuGlnlaleuleuLysaspPheargtrpGlnhlsleuGlnlileleasCys 340
 QY 1124 AAATTTGACAGTTTCCACATTTGAAATCTGCAAAAGCTTACTTACTTCACTTCC 1183
 Db 341 AspPheaspPlyspheProalaleuLysleuSerleuLysPheValPheThrAsp 360
 QY 1184 AACAAAGTGGAATGCTTTTTCAGAAATGATTCACAAAGCTTGATTTGATGATCTC 1243
 Db 361 AsnLysaspLleSerThrPheThrGlnPheGlnleuProSerleuGlnLysleuAspLeu 380
 QY 1244 AGTAAAGATGCTTGATTTCAAGGTTGCTGTTTCAAGTATTTTGGAGCAACGAC 1303
 Db 381 LysArgaspnhlsleuSerPheLysglyCysCysSerhlsThrAspPheGlyThrThrAsn 400
 QY 1304 CTAAAGTATTTAGATCTGAGCTTCAATGATGTTATTACATGAGTTCAAACTTCTGGG 1363
 Db 401 LeuLysHhlsleuaspLeuSerPhehAspValilleThrleuGlySerhAspPheMetGly 420
 QY 1364 TTGAACAACATAGAACATCTGATTTTCACATTTCCAAATTTGAACAATGATGATTT 1423
 Db 421 LeuGlnGlnleuGlnHhlsleuAspPheGlnHhlsSerThrleuLysGlnlleAsnAlaPhe 440
 QY 1424 TCAGTATTTCTATCACTCAGAAACCTGATTTACTTACATTTCTCACTCAGACCA 1483
 Db 441 SerAlaPheleuSerleuArgaspLeuLysArgLysleuAspLleSerLysThrAsnIleArg 460
 QY 1484 GTTGCTTTCAATGAGCTTTCATGAGCTTTCGACGTTGCGAAGCTGAAATGGCTGGC 1543
 Db 461 IleValPheHhlsGlyllePheThrGlyLeuValSerleuGlnHhlsleuLysPheAlaGly 480
 QY 1544 AATTTCTTCCAGGAAAACTTCTCCAGATATCTTCCAGAGCTGAGAACTTGACCTTC 1603
 Db 481 AsnSerPheGlnAsnAsnleuLeuProaspLlePheThrGlnleuThrAsnleuThrVal 500
 QY 1604 CTGAGACTCTCTAGGTCACTGAGAGCACTGTCTCCAAAGCATTTAACTCACTCTCC 1663
 Db 501 LeuAspLeuSerLysCysGlnleuGlnValAlaGlnThrAlaPheHhlsSerleuSer 520
 QY 1664 AGTCTTCAGGTACAAATATAGACCAACAACATTTCTTTCAGTATGTTTCTTAT 1723
 Db 521 SerleuGlnValleuAsnMetSerHhlsAsnLysleuLeuSerleuAspThrPheLeuLys 540
 QY 1724 AAGTGTCTGAACCTCCCTCCAGGTTCTTGATTACAGTCTCAATGACATTAATGACTCCAA 1783
 Db 541 GlnProleuHhlsSerleuArgLileuAspCysSerPhehAsnArgLileMetAlaSerLys 560
 QY 1784 AAACAGGAAGTACAGCATTTTCCAGTACGTCTGCTTTTAAATCTTACTCAGATGAC 1843
 Db 561 GlnGlnGlnleuGlnAsnleuProArgSerleuThrTrpLeuAsnleuThrGlnAsnAla 580
 QY 1844 TTGCTGTGATCTTGTAACACAGAGGTTCTGCAATGATGATGACGAGGAGGAGCTC 1903
 Db 581 PheAlaCysValCysGlnHhlsGlnSerPheleuGlnThrPallYsaspGlnArgGlnleu 600
 QY 1904 TTGGTGAAAGTGAACGAATGATGTAACACTTCAATGATGACGAGGAGGAGCTGTG 1963
 Db 601 LeuValGlyAlaGlnGlnMetMetCysAlaGlnProleuAspMetGlnAspMetProVal 620
 QY 1964 CTGAGTTTG--AATATCACTGTCAATGAATAAAGCAATCACTGTTGTGTGGTCTC 2020
 Db 621 LeuSerPheArgaspnhlsThrCysGlnleuSerLysThrIleleSerValSerValVal 640

QY 2021 AGTGTCTGTACTATCTGTGTGTAGCACTTGTGCTCTATAGTTCTATTTTCACTGATG 2080
 Db 641 ThrValleuLeuValSerValValGlyValleuValLysThrLysPheThrPheHhlsleuMet 660
 QY 2081 CTCTTGTGCTGGCTGCATTAAGTATGGTATGAGGTGAAACATCTATGATGCTTTGTATC 2140
 Db 661 LeuLeuAlaGlyCysLysLysTrpGlyArgGlyGlnSerLleLysAspAlaPheValIle 680
 QY 2141 TACTCAAGCAGATAGAGACCTGGGTAGGAATGAGACTGTGTAAGAATTTAGAAAGAGG 2200
 Db 681 TyrSerSerGlnAspGlnAspTrpValArgAsnGlnleuValLysAsnleuGlnGlnGly 700
 QY 2201 GTGCTTCATTTGAGCTGCTGCTTCACTACAGAGACTTTATTCGCGTGTGGCATTTGCT 2260
 Db 701 ValProProPheGlnleuCysleuHhlsTrpArgAspPheIleProGlyValAlaIleAla 720
 QY 2261 GCCAATCATTCATAGAGTTTCCATTAAGCCGAAAGGTGATTTGTTGTGTGCTCCAG 2320
 Db 721 AlaAsnIlelleGlnGlnGlyPheHhlsLysSerArgLysValIleValValSerGln 740
 QY 2321 CACTTCATCAAGAGCGGCTGGTGTATCTTGAATATGAGATGCTGACCTGGCAGTTT 2380
 Db 741 HlsPheIleGlnSerArgtrpCysIlePheGlyTrpGlnIleAlaGlnThrTrpGlnPhe 760
 QY 2381 CTGAGCAGTGTGCTGCTGATTCATCTTCTGCTCAGAGAGTGAGAGACCTGCTC 2440
 Db 761 LeuSerSerArgAlaGlyllellePheIleValleuGlnLysleuLysSerleuLeu 780
 QY 2441 AGGCACAGGTGAGCTGTACCGCTTCTCAAGCAGGAACATTTACTGAGTGGAGAGAC 2500
 Db 781 ArgGlnGlnValGlnleuLysTrpArgleuLeuSerArgAsnThrLysleuGlnTrpGlnAsp 800
 QY 2501 AGTGTCTGTGGGGGAGCACTTCTTGAGACCACTGAGAAAGCCCTGCTGATGGTAAA 2560
 Db 801 SerValleuGlyArgHhlsValIlePheTrpArgArgleuArgLysAlaLeuLeuAlaGlyLys 820
 QY 2561 TCATGGAATCCAGAAAGAACAGTGGGTACAGATGCAATTTGACGAGAGCAACATCT 2617
 Db 821 ProGlnSerProGlnGlyThrAlaAspAlaGlnThrAsnProGlnGlnAlaThrThr 839

RESULT 8
 Q88055 PRELIMINARY; PRT; 841 AA.
 AC Q88055;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RL Ito T., Morimatsu M.,
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB056444; BAB86840.1; -.
 DR HSSP; 060603; 1077.
 DR GO; GO:0046696; G.Lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F.Lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F.Tranmembrane receptor activity; ISS.
 DR GO; GO:0007250; P.Activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P.detection of fungi; ISS.
 DR GO; GO:0003998; P.detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P.macrophage activation; ISS.
 DR GO; GO:0045576; P.mast cell activation; ISS.
 DR GO; GO:0045671; P.negative regulation of osteoclast different. . .; ISS.
 DR GO; GO:0045362; P.negative regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045084; P.positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0045368; P.positive regulation of interleukin-13 biosyn. . .; ISS.

QY 1904 TTGGTGAAGTTGAACCAATGATGCAACCTTCAGATTAAGCAGGGCCTGCTG 1963
 Db 601 LeuValIglValIgluInMetMeCyAlIgluProIeuAspMetGluAspMetProVal 620
 QY 1964 CTGAGTTG---AATATCAGCTGTGACAGATTAAGCAATCATTTGGTGTGCTGCTC 2020
 Db 621 LeuSerPheArgAsnIatInrCyGlnLeuSerIyThrIleIleSerValIserValI 640
 QY 2021 AGTGTGCTGAGATGCTGTTGTGACGTTCTGCTATAGTCTTATTTTTCACCTGATG 2080
 Db 641 ThrValLeuLeuValIserValIValGlyValLeuValIyTrIySpheIyPheHISLeuMet 660
 QY 2081 CTTCCTGCTGCTGATTAAGATATGATGAGGTGAGGTAACATCTATGATGCTTGTATTC 2140
 Db 661 LeuLeuValIglCySylSylSylSylSylSylSylSylSylSylSylSylSylSylSyl 680
 QY 2141 TACTCAAGCCAGATGAGAGCTGGGTAAAGATGAGCTAGTAAAGAAATTTAGAGAGG 2200
 Db 681 TySerSerGlnAspGluAspTrpValArgAsnGluLeuValIySaenLeuGluGluGly 700
 QY 2201 GTGCTTCATTTTCAAGCTCTGCTGCTTCACTACAGAGACTTTTATCCCGGTGGCATTGCT 2260
 Db 701 ValProPheGlnLeuCySylLeuHISyTrArgAspPheIleProGlyValAlaIleAla 720
 QY 2261 GCCAATCATTCATGAAAGTTTTCATTAAGCCGAAGGATTTGTTGGTGTCCAG 2320
 Db 721 AlaAsnIleIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 740
 QY 2321 CACTTCATCCAGAGCCGCTGGTGTATTTTGAATATGATGCTGCTGACCTGGCAGTTT 2380
 Db 741 HisPheIleGlnSerArgTrpCySylPheGlnIyTrGlnIleAlaGlnIyTrPheGlnPhe 760
 QY 2381 CTGAGCAGTGTGTGTGTATCATTTTATTTGCTGCTGAGAGGTGAGAGACCTGCTC 2440
 Db 761 LeuSerSerArgIleGlnIleIlePheIleValLeuGlnIySylSylSylSylSylSyl 780
 QY 2441 AGCAGAGAGGTGAGCTGTACCGCTTCTGAGCAGAGAACATTAAGCTGAGTGGAGAGAC 2500
 Db 781 ArgGlnIleValIgluLeuTrArgLeuLeuSerArgAsnThrIyLeuGlnIyTrPheGlnAsp 800
 QY 2501 AGTGTCTGTGGCGGAGCATTTTCTGAGAGCAGTCAAGAAAGCCCTGCTGATGTGTA 2560
 Db 801 SerValLeuGlnIyArgHISValIlePheTrpArgArgLeuArgIySylAlaLeuValIglIyS 820
 QY 2561 TCATGCAATCCAGAGAGAGAGTGGGTACAGAGATGCATTTGGCAGAGAGCAATCT 2617
 Db 821 ProGlnSerProGlnIyThrAlaAspAlaGlnIyThrAsnProGlnIyAlaIleThr 839

RESULT 9
 O6MCD5 PRELIMINARY; PRT; 841 AA.
 AC O6MCD5; 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.13339571100;
 RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Momack J.B.;
 RT "Haplotype variation in bovine Toll-like receptor 4 and computational
 prediction of a positively selected ligand-binding domain."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
 DR EMBL; AY297040; AA062700.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.

DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003885; LRR_cysc.
 DR InterPro; IPR003591; LRR_typ.
 DR InterPro; IPR00157; LRR_typ.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF05560; LRR_1; 12.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00365; LRR_SD2; 6.
 DR SMART; SM00369; LRR_TYP; 13.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS5104; TIR; 1.
 KW Receptor.
 SQ SEQUENCE 841 AA; 96014 MW; 603936A17B834735 CRC64;

Alignment Scores:
 Pred. No.: 2,18e-239 Length: 841
 Score: 3316.50 Matches: 638
 Percent Similarity: 86.29% Conservative: 86
 Best Local Similarity: 76.04% Mismatches: 114
 Query Match: 38.66% Indels: 1
 DB: 2 Gaps: 1

US-09-396-985b-1 (1-4868) x O6MCD5 (1-841)

QY 104 ATATGTCTGCTGCTGCGGCTGGTGGAGCTGTATCCAGCCATGCGCTTCTCTGCTC 163
 Db 1 MetMetAlaArgAlaArgLeuAlaAlaAlaLeuIleProAlaThrAlaIleLeuSerCyS 20
 QY 164 GTGAGCCAGAAAGCTGGAGCGCCGTGGAGGTGCTTATTTATTTATTTATTTATTTATTT 223
 Db 21 LeuArgThrGlnIySerTrpAspProCySylGlnValIyProAsnIleSerIyGlnCyS 40
 QY 224 ATGAGCTGAAATTTTCAAAATCCCGCAACCTCCCTTCAACCAAGAACTGGAC 283
 Db 41 MetGlnLeuAsnLeuTrIySylIleProAsnIleProIleSerThrIySylMetLeuAsp 60
 QY 284 CTGAGCTTATATCCCTGAGGCACTTTAGGCACTATAGCTTCTTCACTTTCCAGAACTG 343
 Db 61 LeuSerPheAsnIyTrLeuArgIleGlnIySerHISAspPheSerPheProGlnLeu 80
 QY 344 CAGTGTGATTTATCCAGGTGTGAATCCAGAAATGAATGAATGGGCAATTCAGAGC 403
 Db 81 GlnValLeuAspLeuSerTrgCySylIleIySylIleGlnIySylPheIleIySylPheGlnIy 100
 QY 404 CTAGCCACCTCTCTAATTTATTTAGAGAGAAACCCATCCAGATTAGCCCTGGGA 463
 Db 101 LeuAsnHISLeuSerThrIleuIleuThrIyAsnProIleIleuIleuAlaIyTrpGly 120
 QY 464 GCTTTTCTGAGTATCAAGATTATTCAGAAAGCTGGTGGAGCAAAATTTAGCAATCT 523
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnIySylLeuValAlaValGlnIyThrAsnLeuValIser 140
 QY 524 CTAGAAACTTCCCATTTGAGACATCTCAAAACTTTGAAGAATTATAGTGGTCCAAAT 583
 Db 141 LeuAsnAspPheProIleGlyHISLeuIySylAsnLeuIySylLeuAsnValAlaHISAsn 160
 QY 584 CTATCAATCTTTCAATTTACTGAGTATTTTCTAATCTGACCAATTTAGAGCACTTG 643
 Db 161 PheIleHISerPheIySylLeuProGlnIyTrPheSerAsnLeuProAsnLeuGlnIySyl 180
 QY 644 GACCTTTCAGCAAGAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 703
 Db 181 AspLeuSerAsnAsnIySylIleGlnAsnIleIyTrGlyAspValIyValIleuHISGln 200
 QY 704 ATGCGCTTCTCAATCTTTAGACCTGCTCCCTGAATCCATTAAGAACTTTATTTATTTAT 763
 Db 201 MetProLeuAsnLeuSerLeuAspLeuSerLeuAsnProIleuAspPheIleGlnIyPro 220
 QY 764 GGTGATTTAAAGAAATTTAGGCTTCAATAGCTGATTAAGAAATTTATTTATTTATTTAT 823

[illegible][illegible]

Db 261 G1yG1uPhelysAngluArgeAnleuG1yArpheaSplySerlleuengluG1yLeu 280
 QY 944 TGGAAATTGACATGGAAGAAATCCGATTAGACATGACATACCTCGATGATATT 1003
 Db 281 CysAsnleu1le1legluYsPheArg1leAlarYrPheAspYsPheSerGluAspAla 300
 QY 1004 ATTGACTTATTATTATTGTTGACAAATGTTCTTCAATTTTCCCTGGTAGTGACTATT 1063
 Db 301 IleAspSerPheAnCySleuAlaAnValSerThrIleSerleuValIleSleuYrPhe 320
 QY 1064 GAAAGGTTAAACATTTTCTTATTATTGGATGGACATTTAGATTAGTTAACTGT 1123
 Db 321 LySg1LeuYsG1nleuProlYsAsnleuG1YrTg1nArgleuG1uLeuValaAnCyS 340
 QY 1124 AAATTGGACAGTTCCCATGTAAGAACTCAATCTCTCAAAAGGCTTACTTCACTTCC 1183
 Db 341 GluPheGluGlnPheProThrTrpYsleuAspProlleuYsGluLeuValPheSerAla 360
 QY 1184 AACAAAGTGGGAATGCTTTTTCAGAAATGATCTACCAAGCCTTGATTTCTAGATCTC 1243
 Db 361 AsnGluValArgAsnAlaPheThrGlnValLyLeuGlnSerleuGlnPheLeuAspLeu 380
 QY 1244 AGTAGAAATGGCTTGAGTTCAAAGGTTGCTGTTCTCAAGATGATTTGGACACACG 1303
 Db 381 SerArgAsnAspPheSerleuYsSerCySserG1nArgAspLeuG1YrThrArg 400
 QY 1304 CTAAGGATTTAGATCGAGCTTCAATGCTGTTATTACCATGATGATTTCAAACTTCTGGG 1363
 Db 401 LeuYsH1sIleuAspPheSerPheAsnAlaIleThrIleSerSerAsnPheLeuG1Y 420
 QY 1364 TTGAACAATAGACATCGATGATTTTCACATTTCCAACTTGAACAAATAGTGAATT 1423
 Db 421 LeuGlnGlnleuG1nYrleuAspPheGlnH1sSerSerleuYsGlnValSerAspPhe 440
 QY 1424 TCGATTTCTTATCACTGACAAACCTGATTTACTTGACATTTCTCATCTACACACGA 1483
 Db 441 SerValPheleuProlleuYsAsnleuArgYrleuAspIleSerYrThrH1sThrGln 460
 QY 1484 GTTGCTTTCAATGAGCATCTTCAATGGCTTGTCCAGTGTGAGAGCTTGAATGGCTGGC 1543
 Db 461 ValAlaPheH1sG1Y1lePheAsnG1YleuIleSerleuGlnIleleuYsMetAlaG1Y 480
 QY 1544 AATTTCTTCCAGAAAACTTCTCCAGATATCTTCCAGAGCTGAGAACTTGACCTTC 1603
 Db 481 AsnSerPheGlnAspAsnPheleuProlAsnIlePheMetGluLeuThrAsnleuThrIle 500
 QY 1604 CTGACCTCTCTCACTGATCACTGAGACAGTTGTCTCAACAGCATTTAACTCACTCTCC 1663
 Db 501 LeuAspLeuSerAspCySglnleuGlnValSerGlnValAlaPheAsnSerleuPro 520
 QY 1664 AGTCTTCAAGTAAATATAGACACACACATCTTTTCAATGATGATGTTCTCTTAT 1723
 Db 521 LySleuGlnleuLeuAsnMetSerH1sAsnH1sleuLeuSerleuAspThrLeuProlYr 540
 QY 1724 AAGTGTGAAGTCCCTCCAGGTTCTTGATTAAGTCAATGATCAATGATGACTCCAA 1783
 Db 541 GluProlleuH1sSerleuGlnThrleuAspCySerPheAsnArgIleValAlaSerLyS 560
 QY 1784 AAACAGAACTACAGCATTTTCCAGATGATCTTCAATCTTCAATCTTACTCAAGATGAC 1843
 Db 561 G1uGlnGlnleuArgH1sPheProSerAsnleuSerSerleuAsnleuThrArgAsnAsp 580
 QY 1844 TTGGTGTGACTGTTGACACACAGATTTCTGCAATGATGACAAAGACGACGACGCTC 1903
 Db 581 PheAlaCySValCySglnH1sGlnSerPheleuGlnTrpValLySAspGlnArgGlnleu 600
 QY 1904 TTGGTGAAGTTGAACGAATGATGTCACAACTTCAATTAAGACGACGACGACGCTCTG 1963
 Db 601 LeuValGlnValG1uGlnMetValCyAlaIlySerProlleuAspMetGlnGlyMetPromet 620
 QY 1964 CTGAGATTG---AATATCACTGTCAATGAATTAAGACATCATTTGTTGTGTGCTCTC 2020
 Db 621 LeuAsnPheArgAsnAlaThrCySglnValArgYsThrIleIleThrGlySerValPhe 640

QY 2021 AGTGTGCTGTAGTATCTGTTGTAGACAGTTCTGTCTTAAGTTCTATTATTTGACCTGATG 2080
 Db 641 ThrValleuLeuValPheleuValValValleuValYrlySPhetYrPheH1sleuMet 660
 QY 2081 CTTTCTTGTGCTGTCATAAAGTATGATGAGGTGAAAACATGATGATGCTTTGTATT 2140
 Db 661 LeuLeuAlaG1YCylySerYrSerArgG1YGlnSerThrYrAspAlaPheValIle 680
 QY 2141 TACTAAGCAGAGTAGAGGATGGATGAAGATGAGTATGATGAAGATTTAGAGAGGG 2200
 Db 681 TyrSerSerGlnAspGlnAspTrpValArgAsnGlnleuValLyAsnleuGlnG1Y 700
 QY 2201 GTGCTTCATTTCACTGCTGCTTCACTACAGACATTTATTCGSGTGTGCTGCTGCT 2260
 Db 701 ValProPheGlnleuCySleuH1sYrArgAspPheIleProG1YAlaIleAla 720
 QY 2261 GCCAATCATCATGAAAGTTTCCATAAAGCCGAAAGGTATGTTGTGTGCTCCAG 2320
 Db 721 AlaAsnIleIleGlnGlnG1YpHeH1YsSerArgYsValIleValValSerGln 740
 QY 2321 CACTTCATCAGAGCGCGTGTGATCTTTGAATGAGATTGCTCAGACCTGGAGTT 2380
 Db 741 H1sPheIleGlnSerArgTrpCyS1lePheG1YrG1Y1leAlaGlnThrTrpGlnPhe 760
 QY 2381 CTGAGAGTCGTGCTGTATCATCTTCAATTTGCTTGCAGAAAGTGGAGAGACCTGCTC 2440
 Db 761 LeuSerSerArgAlaG1YleIlePheIleValleuGlnlySleuG1uYsSerleuLeu 780
 QY 2441 AGCAGACAGTGAAGCTGTACCGCTTCTCAGCAGGAAACATTTACTGAGTGGAGAC 2500
 Db 781 ArgGlnGlnValG1uLeuYrArgleuLeuAsnArgAsnThrYrleuG1uYrG1uAsp 800
 QY 2501 AGTGTCCGTGGCGGACATCTTCTGAGAGACATCAGAAAGCCCTGTGATGGTTAA 2560
 Db 801 SerValleuG1YArgH1sIlePheTrpArgArgleuValG1YAlaLeuLeuAspG1Ylys 820
 QY 2561 TCATGGAATCCAGAAAGA 2578
 Db 821 ProArgCyPProGlnG1Y 826

RESULT 11
 Q6MCD4 PRELIMINARY; PRT; 841 AA.
 ID Q6MCD4;
 AC Q6MCD4;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE Toll-1ike receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.1333957100;
 RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.E.;
 RT "Haploype variation in bovine Toll-1ike receptor 4 and computational
 prediction of a positively selected ligand-binding domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
 DR EMBL: AY297043; AAO62701.1; -.
 DR EMBL: AY297041; AAO62701.1; JOINED.
 DR EMBL: AY297042; AAO62701.1; JOINED.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR001611; IRR.
 DR InterPro; IPR000483; IRR_Cterm.
 DR InterPro; IPR003885; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Cyst.
 DR InterPro; IPR00157; TIR.
 DR Pfam; PF01463; LRRCT; 1.

DR Pfam; PF00560; LRR_1; 12.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRECT; 1.
 DR SMART; SM00365; LRR_SD22; 6.
 DR SMART; SM00365; LRR_TYP; 13.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 DR Receptor.
 SO SEQUENCE 841 AA; 95954 MW; AD6D06ACEF44CC91 CRC64;

Alignment Scores:

Pred. No.:	1.03e-238	Length:	841
Score:	3307.50	Matches:	637
Best Local Similarity:	86.17%	Conservative:	86
Query Match:	75.92%	Mismatches:	115
DB:	38.55%	Indels:	1
	2	Gaps:	1

US-09-396-985b-1 (1-4868) x Q6WCD4 (1-841)

QY 104 ATGATGTCGCTCGGCGCTGGGACTGTGATCCAGCCATGCGCTTCTCTCTGC 163
 |||||:::|||||
 Db 1 MetMetAlaArgAlaArgLeuAlaAlaLeuIleProAlaThrAlaIleLeuSerCys 20
 164 GTGAGCAAGAGCTGGAGCGCTGCTGGAGGTGCTTCTAATATTAATTAATCAATGC 223
 |||||:::|||||
 Db 21 LeuArgThrIleuSerThrPaeProCysValGlnAlaValProAlaIleSerTyGlnCys 40
 QY 224 ATGAGCTGAATTTCTCAAAATCCCGACAACTCCCTTCTCAACCAAGAACTGGAC 283
 |||||:::|||||
 Db 41 MetGlnLeuAlaSerIleuTyIleProAlaSerIleProIleSerThrIleuMetLeuAsp 60
 QY 284 CTGAGCTTAAATCCCTGAGGCAATTAAGCACTTAAGCTTTCAGTTTCCAGAACTG 343
 |||||:::|||||
 Db 61 LeuSerPheAlaSerIleuArgGlnIleuGlySerHisAlaSerPheProGlnLeu 80
 QY 344 CAGGTGCTGATTTATTCAGGTGGAATCCAGCAATGGAAGTGGGCAATATCCAGAC 403
 |||||:::|||||
 Db 81 GlnAlaLeuAlaSerIleuSerArgCysGlnIleuValIleGlnAlaSerPheGlnGly 100
 QY 404 CTAGAGCACTCTCTCACTTAATTAATTAAGCAAGAAACCCATCCAGATTTAGCCCTGGGA 463
 |||||:::|||||
 Db 101 LeuAlaSerIleuSerThrIleuIleLeuThrGlyAlaSerProIleGlnSerIleuAlaIleProGly 120
 QY 464 GCGTTTCTGACTATCAAGTTTACAGAGCTGGCTGTGGAGACAAATTTAGCATCT 523
 |||||:::|||||
 Db 121 AlaPheSerGlyLeuSerSerIleuGlnIleuValAlaValGlnThrAlaSerValSer 140
 QY 524 CTAGAGCACTCTCCCATTTGACATCTCAAAACTTGAAGAACTTAATTTGGCTGCACAA 583
 |||||:::|||||
 Db 141 LeuAlaSerPheProIleGlyAlaIleuValAlaSerIleuValAlaAlaSer 160
 QY 584 CTATCCAACTCTCAATTAATTAATTAATTTCTATCTGACCAATTTAGAGCACTTG 643
 |||||:::|||||
 Db 161 PheIleHisSerPheIleuPro****PheSerAlaSerProAlaSerIleuGlnIleu 180
 QY 644 GACCTTTTCAGCAACAAGATTCAGATTAATTTATTTGACAGACTTGGCGGTTTCAATCAA 703
 |||||:::|||||
 Db 181 AspLeuSerAlaSerAlaIleGlnAlaSerIleuTyIleGlnAlaSerValIleuHisGln 200
 QY 704 ATGCGCTTACTCAATCTCTCTTTAGACCTGCTGCTGAACTCTATGAATTTATTCACCA 763
 |||||:::|||||
 Db 201 MetProIleuAlaSerIleuSerIleuAlaSerIleuAlaSerIleuAlaSerIleuAla 220
 QY 764 GGTGCTTTTAAAGAAATTAAGCTTCAATGAAGTGAATTAATTAATTTATTTAGATTTA 823
 |||||:::|||||
 Db 221 GlnThrPheIleuSerGlnIleuValAlaSerIleuThrIleuArgSerAlaSerIleuSer 240
 QY 824 AATGTAATGAAGAACTTTATTCAGAGCTGCTGCTGTTTGAAGTCAATCGTTGGTTCTG 883
 |||||:::|||||
 Db 241 HisValMetIleuSerCysIleGlnGlyLeuAlaGlyLeuIleuSerThrAlaSerValIleu 260

QY 884 GGAGAAATTTAGAAATGAAGAAATTTGAAAGATTTGACAAATCTGCTAGAGGCTG 943
 |||||:::|||||
 Db 261 GlnGlnPheIleuAlaSerGlnIleuValAlaSerPheAlaSerPheIleuGlnGlyLeu 280
 QY 944 TGGCAATTTGACCAATTTGAAAGATTTGCAATTTGCAATTTGCAATTTGCAATTTG 1003
 |||||:::|||||
 Db 281 CysAlaSerIleuThrIleGlnIleuPheArgIleAlaTyIleuAlaSerPheSerGlyAlaSer 300
 QY 1004 ATTTGACTTATTTAATGTTTGAACAAATTTTCTCAATTTTCCCTGCTGAGTGAATTT 1063
 |||||:::|||||
 Db 301 ThrAlaSerPheAlaSerIleuAlaSerValIleSerIleuSerIleuSerIleu 320
 QY 1064 GAAAGGTAAGAACTTTTCTTAATTAATTTGCAATGCAATTTGAAATTAATTAATTT 1123
 |||||:::|||||
 Db 321 GlySerIleuGlnAlaIleuLeuIleuAlaSerPheAlaGlyThrGlnIleuGlnIleuAlaSer 340
 QY 1124 AATTTGCAACAGTTTCCCAATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTT 1183
 |||||:::|||||
 Db 341 AspPheAlaSerPheProAlaIleuIleuSerIleuSerIleuValIlePheThrAsp 360
 QY 1184 AACAAAGTGGGAAATCTTTTCAAGATTTGATCCAAAGCTTGAAGTTTCTAGATCTC 1243
 |||||:::|||||
 Db 361 AsnIleuAlaSerIleuThrPheThrGlnPheGlnIleuProSerIleuGlnIleuAlaSer 380
 QY 1244 AGTAGAAATGAGCTTGAATTTCAAGGTTGCTGTTCTCAAGTGAATTTTGGGCAACAGC 1303
 |||||:::|||||
 Db 381 LysAlaGlnAlaIleuSerPheIleuSerGlyCysCysSerHisThrAlaSerPheGlnIleuThrAsp 400
 QY 1304 CTAAAGATTTTGAATGATGATGATTTCAATTTGATTTATTTCAATGATTTCAATTTGATG 1363
 |||||:::|||||
 Db 401 LeuIleuAlaIleuAlaSerPheAlaSerValIleThrIleuGlySerAlaSerPheMetGly 420
 QY 1364 TTAGAAATTTGAAATGATGATTTGCAATTTGCAATTTGCAATTTGCAATTTGCAATTTG 1423
 |||||:::|||||
 Db 421 LeuGlnIleuGlnIleuIleuAlaSerPheGlnIleuSerIleuIleuAlaSerIleuAlaSer 440
 QY 1424 TCAGATTTCTTCACTCAAGAACTCATTTCACTTTGCAATTTTCTGATTTGCAATTTGCA 1483
 |||||:::|||||
 Db 441 SerAlaPheLeuSerIleuAlaSerIleuAlaSerIleuAlaSerIleuAlaSerIleuAla 460
 QY 1484 GTTGCTTTCAATGAGCACTTTCAATTTGCTTGCAGTCTGCAAGTCTTGAATGCTTGC 1543
 |||||:::|||||
 Db 461 IleValPheHisGlyIlePheThrGlyLeuValIleSerIleuGlnIleuThrIleuSerIleuAla 480
 QY 1544 AATTTCTTCCAGGAAATCTTCTCCAGATTTCTTCAAGAGCTGAGGAAATTTGATCTTC 1603
 |||||:::|||||
 Db 481 AsnSerPheGlnAlaSerIleuAlaSerIleuProAlaIlePheThrGlnIleuThrAlaSerIleuVal 500
 QY 1604 CTGAGCTCTCTCAAGTCAAGTCAAGTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTCTCC 1663
 |||||:::|||||
 Db 501 LeuAlaSerIleuSerIleuSerIleuGlnIleuValAlaGlnIleuAlaPheHisSerIleuSer 520
 QY 1664 AGTCTTCAAGTCAATTAATTAAGCAACAATTTCTTTTCAATTTGATTAAGTTTCTTAT 1723
 |||||:::|||||
 Db 521 SerIleuGlnIleuAlaSerIleuAlaSerIleuAlaSerIleuAlaSerIleuAlaSerIleu 540
 QY 1724 AAGTCTGCACTCTCCATGAGTTCTTGAATTTGATTAAGTCAATTAAGTCAATTAAGT 1783
 |||||:::|||||
 Db 541 GluProIleuHisSerIleuAlaGlyIleuAlaSerPheAlaSerPheAlaSerIleuAlaSerIleu 560
 QY 1784 AAACAGAACTCAAGCAATTTTCAAGTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCAAG 1843
 |||||:::|||||
 Db 561 GlnGlnIleuAlaSerIleuAlaSerIleuAlaSerIleuAlaSerIleuAlaSerIleuAla 580
 QY 1844 TTGCTTTGATCTTGAACACCAAGATTTCTGCAATTTGATTAAGTCAAGGCAAGGCACTTC 1903
 |||||:::|||||
 Db 581 PheAlaCysValCysGlnIleuSerIleuAlaSerPheIleuGlnIleuValIleAlaSerPheGlnIleu 600
 QY 1904 TTGCTGAAATTTGAAATGATTTGCAATTTGCAACCTTCAAGATTTGAGAGGCAAGGCACTTC 1963
 |||||:::|||||
 Db 601 LeuValGlnAlaGlnIleuMetCysAlaGlnProIleuAlaSerPheIleuAlaSerPheProVal 620
 QY 1964 CTGAGTTTGT---AATATCACTGTGCAATGAATTAAGACCATGATTTGTTGTTGCTCTTC 2020

```

|||||
Db      621 LeuSerPheArgSerAlaThrCysGlnLeuSerIleThrIleLeuSerValSerVal1 640
QY      2021 AGAGTGGTTCAGTATCTGTTGAGACGCTGCTGCTATAGTTCATTTTTCACCGAG 2080
Db      641 ThrValLeuLeuValSerValValGlyValLeuValTyrIleGlySerPheHisLeuMet 660
QY      2081 CTCTTGTGCTGCGCATAAAGTATGAGTGAAGTGAACATCATGATGCTTGTATG 2140
Db      661 LeuLeuAlaGlyCysIleValTyrGlyArgGlyGlnSerIleTyrAspAlaPheValIle 680
QY      2141 TACTCAAGCCAGATGAGACCTGGGTAAAGATGAGTATGATTAAGATTTAAAGAGG 2200
Db      681 TyrSerSerGlnAspGlnAspTyrValArgAsnGlnLeuValIleAsnLeuGlnGly 700
QY      2201 GTCGCTCCATTTTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2260
Db      701 ValProProPheGlnLeuValCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 720
QY      2261 GCCAATCATCATCATGAGGTTTCCATTAAGCCGAAAGGATGATGTTGTTGTTGCTCCAG 2320
Db      721 AlaAsnIleIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 740
QY      2321 CACTTCATCCAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2380
Db      741 HisPheIleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGlnIleThrTyrGlnPhe 760
QY      2381 CTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2440
Db      761 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIleValLeuGlnIleValLeu 780
QY      2441 AGCAGCAGCTGAGTGAAGTGTACCGCTTCTGAGAGCACTTACCTGAGTGGAGAGAC 2500
Db      781 ArgGlnGlnAlaGlnLeuValTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnLeu 800
QY      2501 AGTGTCTGGGGGCGCATCTTCTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGTAA 2560
Db      801 SerValLeuGlyArgIleValPheTyrArgArgLeuArgIleValLeuAlaGlyIle 820
QY      2561 TCATGAAATCCAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTG 2617
Db      821 ProGlnSerProGlnGlyThrAlaAspAlaGlnThrAsnProGlnGlnAlaThrThr 839

RESULT 12
TLR4_PIG
ID      TLR4_PIG      STANDARD;      PRT;      841 AA.
AC      Q68Y56;
DT      25-OCT-2004 (Rel. 45, Created)
DT      25-OCT-2004 (Rel. 45, Last sequence update)
DT      25-OCT-2004 (Rel. 45, Last annotation update)
DE      Toll-like receptor 4 precursor.
GN      Name=TLR4;
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX      NCBI_TaxID=9823;
RN      [1]
RP      SOURCE FROM N.A.
RC      TISSUE=Alveolus;
RA      Shinkai H.;
RT      "The function of porcine TLR4 gene."
RL      Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC      immune response to bacterial lipopolysaccharide (LPS). Acts via
CC      MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC      secretion and the inflammatory response (By similarity).
CC      -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC      multi-protein complex containing at least CD14, LY96 and TLR4.
CC      Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
CC      their respective TIR domains (By similarity).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC      -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC      -1- SIMILARITY: Contains 1 leucine-rich (LRR) repeats.

```

```

CC      -1- SIMILARITY: Contains 1 TIR domain.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
-----
DR      EMBL; AB188301; BMD36843.1; -.
DR      PROSITE; PS50104; TIR; 1.
KW      Glycoprotein; Immune response; Inflammatory response;
KW      Leucine-rich repeat; Receptor; Signal; Transmembrane.
FT      SIGNAL      1      23
FT      CHAIN      24      841
FT      DOMAIN      24      632
FT      TRANSMEM      633      653
FT      DOMAIN      654      841
FT      REPEAT      53      76
FT      REPEAT      77      100
FT      REPEAT      102      124
FT      REPEAT      149      173
FT      REPEAT      174      197
FT      REPEAT      203      225
FT      REPEAT      277      300
FT      REPEAT      310      334
FT      REPEAT      350      372
FT      REPEAT      373      398
FT      REPEAT      400      421
FT      REPEAT      422      445
FT      REPEAT      446      469
FT      REPEAT      471      494
FT      REPEAT      495      518
FT      REPEAT      520      542
FT      REPEAT      544      566
FT      REPEAT      568      592
FT      DOMAIN      673      819
FT      CARBOHYD      35      35
FT      CARBOHYD      205      205
FT      CARBOHYD      238      238
FT      CARBOHYD      282      282
FT      CARBOHYD      309      309
FT      CARBOHYD      526      526
FT      CARBOHYD      575      575
FT      CARBOHYD      625      625
SQ      SEQUENCE      841 AA; 96308 MW; C52B2622D1C0E253 CRC64;

Alignment Scores:
Pred. No.:      1,79e-230
Score:      3197.50
Percent Similarity:      84.03%
Best Local Similarity:      73.06%
Query Match:      37.27%
DB:      1
Gaps:      1

US-09-396-985b-1 (1-4868) x TLR4_PIG (1-841)
QY      104 ATGATGTCGCTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 163
Db      1 MetIleProArgIleArgLeuAlaValAlaThrIleProAlaMetValPheLeuSerCys 20
QY      164 GAGAGCAGGAAGCTGGAGCGCTGCGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 223
Db      21 LeuArgSerGlnSerTyrPheProCysValGlnValValProAsnIleSerTyrGlnCys 40
QY      224 ATGAGCTGAATTTTACAAATCCCGCAACTCCCTTCTCAACCAAGAACTGAGC 283
Db      41 MetGlnLeuAsnPheTyrIleProAspAsnIleProThrSerValIleLeuAsp 60
QY      284 CTGAGCTTAAATCCCTGAGCACTTATGAGCACTTATGCTTTCAGTTCCAGAACTG 343
Db      61 LeuSerPheAsnTyrLeuSerHisLeuAspSerAsnSerPheSerPheProGlnLeu 80

```

QY	344	CAGGCGTCGAGATTTCACAGGTCGTGAATTCGAGAAATTCAGAGGGGACATTCAGAGC	403
Db	81	GlnValIleuAspLeuSerArgCysGluIleGlnTrpIleAspAspAlaTrpIleIle	100
QY	404	CTAAGCCACCTCTCTACCTTATATATGACAGAGAAACCCATCCAGAGTTTATAGCCCTGGGA	463
Db	101	LeuAsenryrIleuSerThrIleuIleIleuThrGlnAsnProIleGlnSerIleuAlaIleuGly	120
QY	464	GCCTTTTCTGGACTATTCAGATTACAGAAAGCTGGCTGGTGAGACAAATCTAGACATCT	523
Db	121	AlaPheSerGlyLeuProSerIleuGlnIleuValAlaValGlnThrAsnIleuAlaSer	140
QY	524	CTAGAGACTTCCCATTCGGAGCATCTCAAAAATTGGAAGAACTTAATGTGGCTCACAT	583
Db	141	LeuGluAspPheProIleGlyrHisIleuysrThrIleuAsnGluIleuAsnValAlaHisAsn	160
QY	584	CTTATCCAACTCTTCAAAATTACCTGAGTATTTTCTAATCTGACCAATCTAGAGCATTTG	643
Db	161	HisIleIleSerPheIleuProGluTrpPheSerAsnLeuProAsnIleuGluHisIleu	180
QY	644	GACCTTCCAGACAAGAATTCAAAGTTTATTTGACAGACCTTGCGGGTCTCATATAA	703
Db	181	AspLeuSerIleuAsnIleuIleGluAsnIleuTrpHisIleuHisIleuGlnValIleuHisIleu	200
QY	704	ATGCCCCCTACCAATCTCTCTTTAAACCTGTGCCCAATCCATAGACCTTATCCACCA	763
Db	201	ValProIleuHisAsnIleuSerIleuAsnProIleuAsnProIleuAsnPheIleuIleuPro	220
QY	764	GGTCGATTAAAGAAATTAGCTTCATAGCTGACTTTTAAAGAAATTAATTGATAGTTTA	823
Db	221	GlyAlaPheAsnIleuIleArgIleuAsnGlyIleuTrpIleuAlaGserAsnPheAsnSerIleu	240
QY	824	AATGTAATGAAAACCTTGATTCAGAGCTCGGCTGGTGTATAGAAAGTCATCGTATGGTTCG	883
Db	241	AspValIleuIleuTrpCysIleGlnIleuAlaGlySerIleuValAsnGlnIleuValIleu	260
QY	884	GGAGATTTAGAAATGAAGAAACTTGGAAAAGTTTGACAAAATCTGCTCTAGAGGGCCTG	943
Db	261	GlyGluPheIleuAsnGluAlaArgAsnIleuGluSerPheAspIleuSerValIleuGluIleuLeu	280
QY	944	TGCATTTGGACATTTGAAGAAATTCGGATTAGATACCTTAGACTACTACCTGATGATATT	1003
Db	281	CysAsnIleuTrpIleuGlnIleuPheArgIleuAlaHisIleuGlyGluPheProAspAspAla	300
QY	1004	ATTGACTAATTTAATGTGTGTCACAAATGTTCTCTATTTCCCTGGTAGAGTGACTATT	1063
Db	301	SerAspIleuPheAsnCysIleuAlaAsnValIleSerValIleSerIleuLeuSerIleuAsnIleu	320
QY	1064	GAAAGGGTAAAGACTTTTCTTAAATATTCCGATGGCAACATTTTGAATTAGTTAACTGT	1123
Db	321	HisGlyIleuGluAlaIleuProAsnAspPheArgTrpGlnHisIleuGluValValAsnGly	340
QY	1124	AAATTTGGACAGTTTCCACATTTGAATGAACCTCAAAATCTCAAAAGGCTTACTTCACTTCC	1183
Db	341	LysIleuGlnIleuPheProAlaIleuLysPheAsnSerIleuLysIleuPheValPheLysAsp	360
QY	1184	AACAAAGGTGGAGATGCTTTTTCAGAGATTGATCTTCAAGAGCTTGAGCTTCTAGATCTC	1243
Db	361	AsnIleuHisIleuHisIleuThrPheThrGluIleuAsnLeuProIleuGlnIleuPheAsnIleu	380
QY	1244	AGTAAATATGCTTAGTTCACAAAGGTGCTGTTCACAAAGCATTTTGGACAAACCGAC	1303
Db	381	SerGlyAsnHisIleuSerPheLysGlyCysCysSerHisAsnGluPheIleuTrpThrIleu	400
QY	1304	CTAAAGTATTTAGATCTGAGCTTCAATGGTGTTTATTTACATGATAGTTTCAATCTTGGGC	1363
Db	401	LeuIleuHisIleuAspLeuSerPheAsnGlnIleuIleIleuTrpMetIleuSerAsnIleuGly	420
QY	1364	TTAGAAACAATCGAACATCTGGATTTTCCAGCACTTCCAAATTTGAACAATAAGTGAATTT	1423
Db	421	LeuGlnGlnIleuGlnTrpIleuAspPheGlnHisIleuSerIleuLysGlnAlaAsnAspPhe	440

QY	1424	TCAGATATCCCATGACAGAAACCTGATTTACTGTGACATTTCTCATGACACACAGA	1483
DB	441	SerLeuPheLeuSerLeuValArgAsnLeuIleTyrLeuAspIleSerTyrTrpAsnIleHis	460
QY	1484	GTTGCTTTCAATGGCATCTTCTCAAAAGGCTGTGGCCAGTGTCCAGACAGCTTGAAATGGCTGGC	1543
DB	461	ValValPheArgGlyIlePheAlaGlyLeuValSerLeuGlnTrpLeuIleuPheAlaGly	480
QY	1544	AATTCCTTCCAGAGAAAATTCCTTCCAGATATCTTCCACAGAGCTGAGAACTTGACCTTC	1603
DB	481	AsnSerPheGlnAsnAsnLeuLeuProAspValPheThrAspLeuThrAsnLeuIleLeu	500
QY	1604	CTGGACCTCTCTCAGTGTCAACTGGACAGCTGTGTCTCCACACAGATTTAACTACTCTCC	1663
DB	501	LeuAspLeuSerTyrCysGlnLeuGlnGlnValSerGlnArgAlaPheHisSerLeuPro	520
QY	1664	AGCTCTCAGGATCTAAATATATGAGCCACAAACAATCTTTTCATTTAGATAGCTTCCCTAT	1723
DB	521	ArgLeuGlnValLeuAsnMetSerHisAsnArgLeuLeuPheLeuAspTrpLeuProTyr	540
QY	1724	AAGTGTCTGAACCTCCCTCCAGAGTTCTTGATTTACAGTCACTCAATATGACTTCCAA	1783
DB	541	LysProLeuHisSerLeuArgIleLeuAspCysSerTyrAsnLeuIleValAlaSerTyr	560
QY	1784	AAACAGAACTACACGCACTTTTCCAGATGCTAGCTTTCTTAAATCTTACTCAGAAATGAC	1843
DB	561	GlnGlnGlnLeuGlnHisLeuProArgSerLeuAlaPheLeuAsnLeuThrTyrAsnAsp	580
QY	1844	TTTGCTGTATCTTGTGAACACCAAGTTCTCTGAAATGATACAGACACAGGACACTCTG	1903
DB	581	PheSerCysAlaCysGlnHisGlnThrPheLeuGlnTrpValLysAspGlnLysGlnLeu	600
QY	1904	TTGGTGGAAAGTTGAAACAAATGAATGTGCACAACCTTCAGATTAAGACGGAGCACTGTG	1963
DB	601	LeuValGlyAlaGlnGlnMetValCysThrGlnProLeuGlnMetGlnAspLeuProVal	620
QY	1964	CTGAGATTGG--AATATCACTGTCCAGATGAATTAAGACCATCATGTGTTGTGCTCTC	2020
DB	621	LeuSerPheArgAsnAlaThrCysGlnIleSerGlnAlaValIleSerAlaSerValLeu	640
QY	2021	AGTGTGCTGTAGATATGTGTGTGAGACAGTTCTGTCTATATAGTTCTATTTTACCTGATG	2080
DB	641	ThrPheLeuLeuValSerValAlaGlyIleLeuValTyrLysPheTyrPheHisLeuLeu	660
QY	2081	CTTCTGTGCTGGCTCATATAAGTATGATAGAGAGTGAACCACTTATGATGCTTGTGTATC	2140
DB	661	LeuPheValGlyCysLysLysTyrGlyAlaGlyLysSerThrTyrAspAlaPheValIle	680
QY	2141	TACTCAAGCCAGATGAGAGCTGGGTAAAGGAATGAGTAAAGAAATTTAGAAAGAGG	2200
DB	681	TyrSerSerGlnAspGlnAspTrpValArgAsnIleLeuValLysAsnLeuGlnGlnGly	700
QY	2201	GTCGCTTCATTTCAAGCTCTGCTTCATCTACACAGACTTTATCCCGGTGGGCATTTGCT	2260
DB	701	ValProProPheHisLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla	720
QY	2261	GCCAAACATCATCCTGAAGGTTTCCATATAAAGCCGGAAGGATTTGTGTGGTGTCCAG	2320
DB	721	AlaAsnIleIleGlnGlnGlnLysPheHisLysSerArgLysValIleValValSerGln	740
QY	2321	CACCTTCATCCAGAGCCGCTGGTGTATCTTTGAATATAGATGTGCTCAGACCTGGCAGTTT	2380
DB	741	HisPheIleGlnSerArgTrpCysIlePheGlyTyrGlnIleAlaGlnTrpGlnPhe	760
QY	2381	CTGAGCAGCTGCTGCTGTATCATTTTCAATGTTCTCTGAGAAAGTGGAGAAAGCCCTGCTC	2440
DB	761	LeuArgSerHisAlaGlyIleIlePheIleValLeuGlnLysLeuGlnLysSerLeuLeu	780
QY	2441	AGGAGCAGCGGTGAGCTGTACCGGCTTCTCAGCAGAAACAATTACTCTGAGTGGAGAGAC	2500
DB	781	ArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTrpGlnAsp	800
QY	2501	AGTGTCTCGGGCGGCAATCTTCTTGAGAGCACTCGAAGAAAGCCCTGCTGATGTATA	2560

```

Db      801 SerValleuGLyRghIstIlePheTrpArgLeuLysAlaLeuLeuAbpGIyLys 820
QY      2561 TCATGGAATCCAGAAAGACAGTGGTACAGATGCATTTGGACAGACAACTCT 2617
Db      821 ProTrpSerProGIuLgIlyThrgIuApsSerGIuApsnIhIAspThrIrrAla 839

RESULT 13
Q8MIQ2 PRELIMINARY; PRT; 839 AA.
ID      Q8MIQ2
AC      Q8MIQ2;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Toll-like receptor 4.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kajikawa O., Frevert C.W., Goodman R.B., Wong V.A., Martin T.R.;
RL      Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ101394; AAM50060.1; -.
DR      HSSP; O60603; 1077.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR      InterPro; IPR001611; IRR.
DR      InterPro; IPR000483; IRR_Cterm.
DR      InterPro; IPR003591; IRR_Typ.
DR      Pfam; PF00560; LRR_1; 11.
DR      Pfam; PF01582; TIR_1.
DR      PRINTS; PR00019; LEURICHRPT.
DR      SMART; SM00082; LRCT_1.
DR      SMART; SM00369; LRR_Typ; 1.
DR      SMART; SM00255; TIR_1.
DR      PROSITE; PSS0104; TIR; 1.
KM      Receptor.
SQ      SEQUENCE 839 AA; 96338 MW; 09F7D401EC1456A CRC64;

Alignment Scores:
Pred. No.: 2,336-223 Length: 839
Score: 3102.50 Matches: 611
Percent Similarity: 82.64% Conservative: 84
Best Local Similarity: 72.65% Mismatches: 141
Query Match: 36.16% Indels: 5
DB: 2 Gaps: 3

US-09-396-985b-1 (1-4868) x Q8MIQ2 (1-839)
QY      104 ATATATGTCTCCCTGGCCCTGGCTGGGACTCTGATCCCAAGCATGGCTTCTCTCTGC 163
Db      1 MetMeProAArgLeuArgLeuAlaGIyThrLeuValProAlaMetAlaPheLeuSerTyr 20
QY      164 GTGAGACCAAGAACTGGAGCCCTGGCTGGAGGTGTTCTTAATTTACTTATCATATGC 223
Db      21 LeuArgProGIuLgIlyThrgIuApsSerGIuApsnIhIAspThrIrrAla 40
QY      224 ATGAGCTGAATTTCTAACAATATCCCGACAACTCCCTTCTCAACCAAGAACTGGAC 283
Db      41 MetGIuLysnLeuTyrLysIleProAspAsnIleProPheSerThrLysAsnLeuAsp 60
QY      284 CTGAGCTTTAATCCCTGAGGCACTTTAGGCACTATAGCTTCTTCAAGTTCCCAAGACTG 343
Db      61 LeuSerPheAsnLeuLeuGIuLgIlySerHisSerPheLeuHisValSerGIuLeu 80
QY      344 CAGGTGTGATTTATTCAGGTGGAATCAGCAATTCAGCAATTTGAGGTGGATTCAGAGC 403
Db      81 HisPheLeuAspLeuSerArgCysLysIleHisThrIleGIuLysnIleAspAlaTyrGIuLg 100
QY      404 CTAAAGCACTCTCTAATTAATTTAGACAGAAACCCATTCAGAGTTTAAAGCTTGGAG 463

```

```

Db      101 LeuLysAsnLeuSerThrLeuIleLeuThrgIuApsnProIleGlnSerLeuSerProGln 120
QY      464 GCCTTTTCGACTATCAAGTTTACAGAGCTGGTGGTGGAGCAAACTCTACATCT 523
Db      121 AlaPheSerGIuLysnSerAsnLeuGIuLysnValAlaValGIuThrHisLeuThrSer 140
QY      524 CTAGAGAACTTCCCATTCGACATCTCAAACTTTGAAAGAACTTAATGTGCTCACAAT 583
Db      141 LeuGIuLysnPheProIleGIyHisLeuSerThrLeuLysGIuLysnValAlaHisAsn 160
QY      584 CTATTCATCTTTCTCAATTTACCTGAGTATTTTCTAATTCAGCAATTCAGCACTTG 643
Db      161 LeuIleHisSerPheSerIleProAspTyrPheSerAsnLeuSerSerLeuGIuLysn 180
QY      644 GACCTTTCAGCAACAAAGTTCAAGTATTTTTCAGACAGCTGGGGTCTTACATCA 703
Db      181 AspLeuSerAsnAsnLysIleGlnSerIleTyrHisLysAspLeuArgValLeuHisGln 200
QY      704 ATGCCCTTACCTCAATCTCTCTTTAGACCTGTCCCTGAACTCTTGAACCTTTATCCAA 763
Db      201 MetProLeuGIyThrLeuSerLeuAspLeuAlaLeuAsnProIleAspPheIleProPro 220
QY      764 GGTGCAATTAAGAAATTTAGCTTCAATTAAGCTTCAATTAAGAAATTTTGAATGTTTA 823
Db      221 GIyAlaPheGIuLgIlyLeuArgLeuHisGIuLeuIleLeuLysSerAsnPheLysSerThr 240
QY      824 AATGTAATAAAACTGTGTTCAGGTCTGGCTGGTTTGAAGTGCATGCTTGTGTTGT 883
Db      241 AsnIleMetLysIleLysIleGlnGIuLysnSerGIyLeuGIuLysnHisArgLeuValLeu 260
QY      884 GGAGAAATTTAGAAATGAAAGAACTTGGAAAGTTTGAACAAATCTGCTTAGAGGGCTG 943
Db      261 GIyGIuLysnLysnAsnGIuLysnLysnMetLysAsnPheAspLysSerAlaLeuGIuLysn 280
QY      944 TGCATTTTCACTTGAAGAAATTCGATTTAGCACTTACTTACTTCACTCATGATATT 1003
Db      281 CysAsnLeuAlaIleGIuLysnLysnArgLeuAlaTyrIleAspAspLeuGIuLysnIle 300
QY      1004 ATTTGACTTATTAATTTGTTTGAACAAATGTTTCTTCAATTTCCCTGGTGGAGTACTATT 1063
Db      301 ThrAspLeuPheAspLysnLeuGIuLysnValSerValMetAlaLeuValHisMetTyrIle 320
QY      1064 GAAAGGTTAAAGACTTTTCTTAATTTTCGAGTGGCACTTTGAATTTAGTTAACTGT 1123
Db      321 AsnAsnGIuLysnIlePheProLysAspPheSerTyrLysSerLeuGIuLysnHisCys 340
QY      1124 AAATTTGACAG---TTTCCCACTTGAACCTCAAACTCTTCAAAAAGCTTACTTCACT 1180
Db      341 GIuPheSerGIuLysnIlePhePheLeuLysLeuSerSerLeuArgArgLeuIlePheThr 360
QY      1181 TCCAAACAAAGTGGGAATGCTTTTTCAGAAAGTTGATCTCAAGCTTGAAGTTTCTAGAT 1240
Db      361 AlaAsnLysGIyAlaArgThrPheProGIuLysnAsnThrProSerLeuGIuLysnLeuAsp 380
QY      1241 CTCAGTAGAAATGGCTTGAATTTCAAGGTTCTGTCTCAAAAGTATTTGGACAAAC 1300
Db      381 IleSerAsnAsnGIuLysnSerLeuGIuLysnSerCysSerValAsnSerLeuArgLeuThr 400
QY      1301 AGCTTAAGTATTTAGATTTGAGCTTCAATGGTGTATTATTCAGTGAAGTTCAAACTTCTTG 1360
Db      401 GlnLeuLysnIleLeuAsnLeuSerPheAsnGIyAlaIleThrMetThrSerAsnPheVal 420
QY      1361 GGCTTGAACAACTGAACATGCTGATTTCCAGCAANTTCAATTTGAACAAATGAAGTGG 1420
Db      421 GIyLeuGIuLysnLeuGIuLysnLysnThrPheGlnHisSerAsnLeuArgAsnIleAsnGln 440
QY      1421 TTTTCAGTATCTTCACTCACTCAAAACCTCAATTTACTTGAATTTCTCACTCAACC 1480
Db      441 PheSerIlePheLeuSerLeuAsnAsnLeuLysnLeuLysnIleSerTyrThrHisIle 460
QY      1481 AGAGTGTCTTTCAATGCACTTCAATGGCTTGTCCAGTCTGCAAGCTTTGAATAGCT 1540
Db      461 ArgValAlaPheArgGIyIlePheAspGIyLeuTyrSerLeuArgValLeuLysMetAla 480

```

QY	1541	GGCAATCTTTCCAGAAACCTTCCTCCATGATCTTCACAGAGCTGAAAGTTC	1600
Db	481	Glyseraldehyde1nAspAsnArgLeuLeuAsn1IlePheThrGluMetThrSerLeuThr	500
QY	1601	TTCTGACCTCTCTCAGTGTCAACTGGAGCAGTTGTCTCCAAACGACATTTAACTCACTC	1660
Db	501	ThreonineAspLeuSerSerCysGlnLeuGlnValTyrGlnGlnValAlaPheGlnSerLeu	520
QY	1661	TCCAGTCTTCAGAGTAATAATATAGCGCAACAACTTCCTTTCATTTGGAATGACTTCCT	1720
Db	521	ProArgLeuGlnSerLeuAsnMetSerHisAsnAsnLeuLeuValLeuAspThrLeuThr	540
QY	1721	TATAAGTGTCCGAACCTCCCTCCAGGTTCTTATATACAGTCTCAATTCACATATGACTTCC	1780
Db	541	TyrosCysLeuTyrSerLeuGlnValLeuAspLeuSerPheAsnHisIleGlyAsnIle	560
QY	1781	AAAAAACGAGACTACAGACTTTTCCAGTACGTCTAGTCTTTTAACTCTTACTCAGAT	1840
Db	561	ThrluProGlnGlnGlnHisPheProSerAsnLeuThrLeuLeuHisIleLeuThrLysAsn	580
QY	1841	GACTTTGCTGTACTGTGGAACACCAAGATTTCCTCGCAATGATCAAGACCAAGAGAG	1900
Db	581	AlaPheValCysAspCysGlnHisGlnIlePheMetGlnTrpIleLysAspGlnArg	600
QY	1901	CTCTTGGTGAGAGTGAACGAGTAATGTCGCAACCTTCAGATTAAGCAGGAGCATGCT	1960
Db	601	LeuLeuValGlnValGlnGlnMetValCysIleThrProProAsn-----MetPro	617
QY	1961	GTGTGTGAGTTG---AATATCACTGTTCAGATGAATAAGACATCATTTGCTGTGCTGCT	2017
Db	618	ValLeuSerPheThrAsnAlaThrCysGlnIleSerLysThrIleIleSerValSerVal	637
QY	2018	CTCAGTGTGCTTGTAGTATCTGTTGTGACGACTTCTGCTGTAAATCTATATTTCACTG	2077
Db	638	PheSerValLeuValValSerPheAlaValValLeuValTyrLysPheTyrPheProLeu	657
QY	2078	ATGCTTTCTGCTGCTGCATAAAGTATGTAAGAGTGAAACATCATATGATGCTTTGTT	2137
Db	658	MetLeuLeuValGlyArgArgLysTyrGlyArgLysSerValTyrAspAlaPheVal	677
QY	2138	ATTATCTCAACCCAGAGATGAGAGCTGGGTAGGAATGACATGTAAGAAATTTGAAGA	2197
Db	678	IleTyrSerSerGlnAspGlnAspTrpValAlaArgAsnGlnLeuValLysAsnGlnGln	697
QY	2198	GGGGTGCCTTCATTCAAGCTGTGCCTTCACTACAGAGACTTATATCCGGTGTGGCAAT	2257
Db	698	GlyValProProPheArgLeuCysLeuHisIleTyrArgAspPheIleProGlyValAlaIle	717
QY	2258	GCTGCCAATCATATCCATGAAGGTTTCCATAAAGCCGAAGGATGTTGTGTGTCTCC	2317
Db	718	AlaIaAsnIleIleGlnGlnGlyPheHisLysSerArgLysValIleValAlaValSer	737
QY	2318	CAGACATTCATCCAGAGCCGTGTGTATCTTAAATATGAGATTGTCCAGACTGGGAG	2377
Db	738	GlnHisPheIleGlnSerArgTrpCysIlePheGluTyrGlnIleAlaGlnThrTrpGln	757
QY	2378	TTTCTGACGAGTGTGTGTATCATCTTCAATGCTCTCGAAGAGTGAGAAACCTG	2437
Db	758	PheLeuSerSerHisAlaGlyIleIlePheIleValLeuGlnLysValGlnLysSerLeu	777
QY	2438	CTCAGGACGAGGTGAGAGCTGTACCGCTTCTCAGAGGAACAATTACCTGAGTGGAG	2497
Db	778	LeuArgGlnArgValGlnLeuTyrArgLeuLeuSerArgAsnTrpTyrLeuGlnTrpLys	797
QY	2498	GACAGTGTCTGTGGGGCGGACATCTTTCGAGACGACTCAGAAAAAGCCTGTGATGCT	2557
Db	798	AspThrValLeuGlnGlyArgHisIleIlePheThrArgTrpLeuArgLysAlaLeuLeuAspGly	817
QY	2558	AAATCATGAGATCCAGAGAAAGCAAGTGGGTACAGATTCGATTTGGAGGAAGCAACATCT	2617
Db	818	LysThrLeuSerProGlnGlyMetAlaArgAlaGlnAsnAsnGlnGlnValMetThr	837

Oy	2618	ATC 2620
Dd	:	:
	838	Lcu 838
<hr/>		
RESULT 14		
ID	TLR4_CRIGR	STANDARD; PRT; 838 AA.
AC	OSWV82;	
DT	28-FEB-2003 (Rel. 41, Created)	
DT	28-FEB-2003 (Rel. 41, Last sequence update)	
DT	05-JUL-2004 (Rel. 44, Last annotation update)	
DE	Toll-like receptor 4 precursor.	
GN	Name:TLR4;	
OS	Cricetulus griseus (Chinese hamster).	
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;	
CC	Cricetulus.	
RN	NCBI_TaxID=10029;	
XX	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Macrophage;	
FX	MEDLINE=20148868; PubMed=10683379;	
RA	Lien E., Means T.K., Heine H., Yoshimura A., Kusumoto S., Fukase K.,	
RA	Fenton M.J., Oikawa M., Qureshi N., Monks B., Finberg R.W.,	
RA	Ingalls R.R., Goldenbock D.T.;	
RT	"Toll"-like receptor 4 impacts ligand-specific recognition of bacterial	
RL	lipopolysaccharide.";	
J.	J. Clin. Invest. 105:497-504(2000).	
-I-	FUNCTION: Cooperates with LY96 and CD14 to mediate the innate	
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via	
CC	MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine	
CC	secretion and the inflammatory response (By similarity).	
CC	-I- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a	
CC	multi-protein complex containing at least CD14, LY96 and TIR4.	
CC	Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via	
CC	their respective TIR domains.	
-I-	SUBCELLULAR LOCATION: Type I membrane protein (By similarity).	
CC	-I- TISSUE SPECIFICITY: Detected in macrophages and the Chinese	
CC	hamster ovary fibroblast cell line.	
CC	-I- SIMILARITY: Belongs to the Toll-like receptor family.	
CC	-I- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.	
CC	-I- SIMILARITY: Contains 1 TIR domain.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outpost -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
CC	modified and this statement is not removed. Usage by and for commercial	
CC	entities requires a license agreement (See http://www.isdb.ch/announce/	
CC	or send an email to license@isdb-sib.ch).	
CC	-----	
DR	EMBL; AF153676; AAP41891.1; -.	
DR	HSSP; Q15399; IFV.	
DR	InterPro; IPRO01611; LRR.	
DR	InterPro; IPRO00483; LRR_Cterm.	
DR	InterPro; IPRO03591; LRR_TYP.	
DR	InterPro; IPRO00157; TIR.	
DR	Pfam; PF00560; LRR; 8.	
DR	Pfam; PF01582; TIR; 1.	
DR	PRINTS; PR00019; LEORICHRPT.	
DR	SMART; SM00082; LRRT; 1.	
DR	SMART; SM00369; LRR_TYP; 1.	
DR	SMART; SM00255; TIR; 1.	
DR	PROSITE; PS50104; TIR; 1.	
KM	Glycoprotein. Immune response; Inflammatory response;	
KM	Leucine-rich repeat; Receptor; Signal; Transmembrane.	
FT	SIGNAL	1..25
FT	CHAIN	26..838
FT	DOMAIN	26..629
FT	TRANSMEM	630..650
FT	DOMAIN	651..838
FT	REPEAT	31..52
FT	REPEAT	53..75
FT	REPEAT	LRR 1.
FT	REPEAT	LRR 2.

```

FT REPEAT 76 99 LRR 3.
FT REPEAT 100 123 LRR 4.
FT REPEAT 127 148 LRR 5.
FT REPEAT 149 172 LRR 6.
FT REPEAT 173 196 LRR 7.
FT REPEAT 200 224 LRR 8.
FT REPEAT 227 251 LRR 9.
FT REPEAT 305 330 LRR 10.
FT REPEAT 351 370 LRR 11.
FT REPEAT 371 393 LRR 12.
FT REPEAT 396 419 LRR 13.
FT REPEAT 420 443 LRR 14.
FT REPEAT 468 492 LRR 15.
FT REPEAT 494 516 LRR 16.
FT REPEAT 517 538 LRR 17.
FT REPEAT 541 563 LRR 18.
FT REPEAT 565 589 LRR 19.
FT DOMAIN 670 816 TIR.
FT CARBOHYD 34 34 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 115 115 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 237 237 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 307 307 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 492 492 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 524 524 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 572 572 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 622 622 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 838 AA; 96277 MW; 129B3596E908B48 CRC64;

```

Alignment Scores:

```

Pred. No.: 5,9e-217 Length: 838
Score: 3017.00 Matches: 581
Percent Similarity: 82.60% Conservative: 112
Best Local Similarity: 69.25% Mismatches: 142
Query Match: 35.17% Indels: 4
DB: 1 Gaps: 4

```

US-09-396-985b-1 (1-4868) x TLR4_CRIGR (1-838)

```

QY 104 ATGATGTGCTGCGCGCTGGCTGGAGCTCTGATCCAGCCATGGCCCTTCCTCCTGC 163
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1 MetMetProSerPheCysIleuAlaGlyThrIleuMetMetAlaLeu--PheLeuSerSer 19

QY 164 GTGAGACCAAGAGCTGGAGCCCTGGCTGGAGGCTTCTAATATTACTTATCAATGC 223
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 20 LeuArgProGlnSerIleuAspProCysValGluValAspSerAsnThrSerTyrGlnCys 39

QY 224 ATGAGCTGAATTTCTCAAAATCCCGCAACACTCCCTTCACACCAAGAACTGGAG 283
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 40 MetAspArgAsnIleuAsnIleuProAspAsnIleProSerSerValIleuValAsp 59

QY 284 CTGAGCTTAAATCCCTGAGCATTTAGGAGCTATAGCTTCTTCACTTCCAGAACTG 343
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 60 LeuSerPheAsnProIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 79

QY 344 CAGGTGCTGATTTATCCAGCTGTGAATCCAGACATTTGAAGATGGGCGATATCGAGC 403
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 80 LysLeuIleuAspIleuSerArgCysGlnIleuThrIleuIleuAspIleuValIleuIleu 99

QY 404 CTAGAGCACTCTCTAATCTTAATATTGACAGAAACCCATCCAGATTTAGGCGCTGGG 463
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 100 LeuHisGlnIleuThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 119

QY 464 GCGTTTCTGAGCTATCAAGATTACAGAGCTGGCTGGCTGTGAGACAAATCTGACATCT 523
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 120 ThrPheSerGlyLeuAlaIleuGlnAsnLeuValAlaValGlnIleuIleuValAsp 139

QY 524 CTAGAGCACTTCCCATTTGACATCTCAAACTTTGAAAGAACTTAAATGGGCTCACAAT 583
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 140 LeuAspSerIleuProIleuGlyHisIleuValThrIleuIleuIleuValAlaHisAsn 159

```

```

QY 584 CTATCCAACTTTGCAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTG 643
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 160 LeuIleHisSerPheIleuIleuProGluIleuIleuIleuIleuIleuIleuIleuIleuIleu 179

QY 644 GACCTTTCCAGACAAAGATTGAAAGTATTTATGACAGACTTGGCGGCTTCTACATCA 703
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 180 AspIleSerAsnAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 199

QY 704 ATGCCCTCACTCAATCTCTCTTGAACCTGGCTGGCTGCAATCTTGAAGCTTTTCCAGCA 763
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 200 AsnProGlnIleuAsnIleuSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 219

QY 764 GGTGCAATTTAAAGAAATTAAGCTTCAAGCTGATGACTTAAAGAAATTAATTTGATAGTTTA 823
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 220 GlyAlaPheGlnGlyIleuArgLeuHisGlnIleuIleuIleuIleuIleuIleuIleuIleuIleu 239

QY 824 AATGTATTAAGAAACTTTGATTTCAAGGTCTGGCTGGTTTGAAGTCCATGTTGGTCTCG 883
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 240 AsnValMetIleuThrCysIleHisAsnIleuAspGlyLeuGlnValHisArgIleuIleu 259

QY 884 GGAGAAATTTAAGAAAGAAAGAACTTGAAGAAAGTTTGAACAATTCGCTTAGAGGGCGTCG 943
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 260 GlyIleuPheLysAsnGlnLysArgAsnValGluArgPheAspArgTyrValIleuGlnGlyLeu 279

QY 944 TCGAATTTGACCATTTGAAGAAATTCGATTAAGCATTTAGACTTACTACTCGATGATATT 1003
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 280 CysLysValThrIleuGlnIleuPheArgPheThrTyrAlaAsnGlnIleuPheSerGlnIleu 299

QY 1004 ATTGACTTATTTAATGTTTGAACAAATGTTTCTTCAATTTCCCTGGTGAAGTGTACTATT 1063
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 300 ThrAsp---PheAspCysLeuAlaAsnValSerAlaMetSerIleuAlaAsnValTyrLeu 318

QY 1064 GAAAGGTAAGAAAGACTTTTCTTATATATTTGCGAGTGAACATTTGAATTAATCTGT 1123
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 319 LysArgLeuGlnIleuAspIleuProLysTyrPheLysTyrGlnThrLeuAlaValIleuArgCys 338

QY 1124 AATTTGACAGTTTCCCATTTGAAGTGAACATTCATCTTCAAGGCTTACTTCACTTCC 1183
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 339 GlnLeuIleuGlnIleuPheProIleuGlnIleuProPheIleuIleuIleuIleuIleuIleu 358

QY 1184 AACAAAGTGGAGAACTTTTTCAGAGTTGATCTACAAAGCTTGAAGTTTCTAGATCTTC 1243
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 359 AsnLysGlyAlaThrSerPheProGlnValAsnLeuProSerIleuThrPheIleuAspLeu 378

QY 1244 AGTAAGAAATGCGTGAAGTTTCAAGGCTGCTGCTCAAGATTTTGGCAACACCAAC 1303
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 379 SerGlyAsnGlyMetSerPheArgGlyCysSerTyrThrAspLeuIleuAlaArgSer 398

QY 1304 CTAAAGTATTTAGATCTGACTTCAATGCTGTTATTAACCATGATGTTCAAACTTCTTGGGC 1363
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 399 LeuIleuHisIleuAspIleuSerPheAsnGlyValIleuSerMetSerGlnAsnIleuMetGly 418

QY 1364 TTGAAACAATGAACATCTGATTTCCAGCAATTCCAATTTGAAACAATGAGTGAAGTTT 1423
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 419 LeuGlnIleuGlnIleuIleuAspPheGlnHisSerThrLeuIleuLysValaThrGluPhe 438

QY 1424 TCAGATTTCTTCACTCAAGAAACCTCAATTTCACTTCACTTCACTTCACTCAACACCA 1483
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 439 SerMetPheLeuProIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 458

QY 1484 GTTGCTTTCAATGAGCATTTCTCAATGAGCTTGTCCAGCTTGAAGTCTTGAAGAAATGGCTGCG 1543
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 459 IleAspPheAsnGlyIlePhePheGlyLeuThrIleuIleuIleuIleuIleuIleuIleuIleu 478

QY 1544 AATTTCTTCCAGGAAATCTTCTTCCAGATATCTTCAACAGCTGAGAAATTTGACCTTTC 1603
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 479 AsnSerPheLysAspAsnIleuIleuSerAsnValIleuThrAsnThrThrAsnIleuThrPhe 498

QY 1604 CTGAGACTCTCAAGTCAACTGAGAGCGCTGTGCTCCAAAGCAAGCATTTAATCACTCTGC 1663
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 499 LeuAspIleuSerLysGlnIleuGlnValIleuIleuIleuIleuIleuIleuIleuIleuIleu 518

QY 1664 AGTCTTCAGGTAATAATATGAGCCACAACAATCTTTTCAATGGATGACGTTTCTTAT 1723

```

Dd		ArgLeuGIleuLeuAsnMetSerHisAsnIleuLeuAspLeuPheHisLysTr	538
Oy	1724	AAGTGTCTGAACCTCCCTCGAGGTTCTTAATTAAGTTCATACATAAATGACTTCAAA	1783
Dd	539	LysGIleuHisSerLeuLysThrLeuAspCysSerPheAsnHisIleGIuThrSer---	557
Oy	1784	AAAAGAACAATACAGCATTTTCCAAAGTAGTCTAGCTTTCTTAATCTTACTCACAAATGAC	1843
Dd	558	LysGIuIleMetGINHisPheProLysSerLeuAlaPheLeuAsnLeuThrAsnAsnPro	577
Oy	1844	TTTGCTGTACTGTGGAAACACAGAGATTTCCTGCAGATGATCAAGAACGACAGGAGCTC	1903
Dd	578	PheAlaCysIleCysGIuHisIleGINAsnPheLeuGINtrPValLysAspGIuArgLeuPhe	597
Oy	1904	TTGTGTGAAGTTGAAACGAATGGAATGTCACAACCTTCAGATACGACGGCATGCTGTG	1963
Dd	598	LeuValLysTrINgIuGINMetThrCysAlaThrProValGIuMetLysAspSerLeuVal	617
Oy	1964	CTGAGCTTG---AATATACCTGTGCATGAAATAAAGAACCATCATGCTGTGTGGCTCTC	2020
Dd	618	LeuAspPheArgAsnAlaThrCysLysValGINLysThrIleIleSerValSerValIle	637
Oy	2021	AGTGGCTGTAGTATCTGTGTGAAGACATTCGCTGTAACTTAAGTCTATTTCACTGATG	2080
Dd	638	SerValLeuValSerThrIleAlaPheLeuValLysLysPheTyPheHisLeuIle	657
Oy	2081	CTTCTGTGCTGCTGCATGAAGATGATGGTAGAGGTGAAAAACATGATGACCTTTGTTATC	2140
Dd	658	LeuIleAlaGIuCysLysLysLysSerArgGIuGlnSerIleTyRAspAlaPheValIle	677
Oy	2141	TACTACAGCCAGATGAGACTGGGTAAAGAAATGACTAGTAAAGAAATTGAAGAAGGG	2200
Dd	678	TyrSerSerGINAspGIuAspLTPValArgAsnGIuLeuValLysAsnLeuGIuGINLys	697
Oy	2201	GMGCTCCATTTACGCTCGCTGCCCTTACACACAGAGCTTATTCGCGGTGGCAATGCT	2260
Dd	698	ValProProPheGINLeuCysLeuHisLysTyRArgAspPheIleProGIuValAlaIleAla	717
Oy	2261	GCSAAACATCATCCATGAAGATTTCATATAAACCCGAAAGATGATTGTGTGGTCCAG	2320
Dd	718	AlaAsnIleIleGINLysLysPheHisLysSerArgLysValIleValValValSerArg	737
Oy	2321	CATTTCATCCAGAGCCGCTGGTGTATCTTTAATATGATATGAGATGCTCAGACCTGGCACTT	2380
Dd	738	HisPheIleGINSerArgTrpCysIlePheGINLysGIuIleAlaGINThrTrpGINPhe	757
Oy	2381	CTGAGCAATCGCTGCTGATATCTTATCTTATGCTTCGCGAAGGTGGAGAAACCCTGCTC	2440
Dd	758	LeuSerSerHisSerGIuIleIlePheIleValLeuGINLysValGINLysSerLeuLeu	777
Oy	2441	AGGAGAGAGGTGAGACTGATCCGCTTTCACAGAGAAACATTGCTGAGTGGAGAGAC	2500
Dd	778	LysGINLysValGIuLeuTyRArgLeuLeuSerArgAsnTrpTyRLeuGINTrpGIuAsp	797
Oy	2501	AGTGTCTGGAGCGGACATCTTCTGAGAGSAGTACAGAAAAAGCCTTGCTGATGTGAA	2560
Dd	798	AsnAlaLeuGIuArgHisIlePheThrTrpArgTrpLeuLysLysAlaLeuLeuAspGIuArg	817
Oy	2561	TCATGGAATCCAGAAAGAAACAGTGGGTACAGAGTSCAATTGGCAGAAAGCAAACTCT	2617
Dd	818	AlaTrpAsnProGINLysAlaThrGIuAlaGINLysAsnGINLysGINLysThrThr	836

OC	Eumetazoa; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN	NCSI_faxID=10116;
RP	SEQUENCE FROM N.A.
RC	STRAIN=Sprague-Dawley; TISSUE=Heart;
RX	MEDLINE=99362487; PubMed=10430608;
RA	Prantz S., Kobzik L., Kim Y.-D., Fukazawa R., Medzhitov R., Lee R.T.,
RT	Kelly R.A.;
RL	"Toll4 (TLR4) expression in cardiac myocytes in normal and failing
RT	mocardium.";
CC	J. Clin. Invest. 104:271-280(1999).
CC	-I- FUNCTION: Cooperates with LY6E and CD14 to mediate the innate
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via
CC	MyD88, TRAP and TRAFs, leading to NF-kappa-B activation, cytokine
CC	secretion and the inflammatory response (By similarity).
CC	-I- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC	multi-protein complex containing at least CD14, LY6E and TLR4.
CC	Binds LY6E via the extracellular domain. Binds MyD88 and TRAP via
CC	their respective TIR domains (By similarity).
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	-I- SIMILARITY: Belongs to the Toll-like receptor family.
CC	-I- SIMILARITY: Contains 17 leucine-rich (LRR) repeats.
CC	-I- SIMILARITY: Contains 1 TIR domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF057025; AAC13313.1; .
DR	HSSP; Q15399; IFV.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000483; LRR_Cterm.
DR	InterPro; IPR000157; TIR.
DR	Pfam; PF00560; LRR_10.
DR	Pfam; PF01582; TIR; 1.
DR	PRINTS; PRO0019; LEURICRPT.
DR	SMART; SM00082; LRRCt; 1.
DR	SMART; SM00255; TIR; 1.
DR	PROSITE; PS50104; TIR; 1.
KW	Glycoprotein; Immune response; Inflammatory response;
KW	Leucine-rich repeat; Receptor; Signal; Transmembrane.
FT	SIGNAL 1 25
FT	CHAIN 26 835
FT	DOMAIN 26 638 Extracellular (Potential).
FT	TRANSMEM 639 659 Potential.
FT	DOMAIN 660 835 Cytoplasmic (Potential).
REPEAT	REPEAT 32 52 LRR 1.
REPEAT	REPEAT 53 75 LRR 2.
REPEAT	REPEAT 76 99 LRR 3.
REPEAT	REPEAT 100 123 LRR 4.
REPEAT	REPEAT 148 172 LRR 5.
REPEAT	REPEAT 173 196 LRR 6.
REPEAT	REPEAT 201 224 LRR 7.
REPEAT	REPEAT 227 251 LRR 8.
REPEAT	REPEAT 305 330 LRR 9.
REPEAT	REPEAT 370 393 LRR 10.
REPEAT	REPEAT 396 419 LRR 11.
REPEAT	REPEAT 420 443 LRR 12.
REPEAT	REPEAT 468 492 LRR 13.
REPEAT	REPEAT 493 516 LRR 14.
REPEAT	REPEAT 518 540 LRR 15.
REPEAT	REPEAT 542 563 LRR 16.
REPEAT	REPEAT 565 589 LRR 17.
DOMAIN	TIR. 670 816
CARBOHYD	34 N-linked (GlcNAc...) (Potential).
CARBOHYD	43 N-linked (GlcNAc...) (Potential).
CARBOHYD	75 N-linked (GlcNAc...) (Potential).
CARBOHYD	172 N-linked (GlcNAc...) (Potential).


```
QY 1964 CTGAGTTG---AATATCACCTGTGCAGATGAATAGACCATCATGTGTCGGCTC 2020
Db 618 LeuAspPheThrAsnSerThrCysTrpIleTyrIleSerValSerValVal 637
QY 2021 AGTGTGCTTGAGTATCTGTTGTAGACAGTTCTGGCTATAAGTTCTATTTCACCTGATG 2080
Db 638 SerValIleuValIleAlaThrValAlaPheIleuIleTyrHisPheTyrPheHisIleuIle 657
QY 2081 CTTGTGCTGAGCTGATTAAGTATAGTGTAGAAACATCATATGATGACCTTGTATC 2140
Db 658 LeuIleAlaGlyCysLysLysTyrSerArgLysIleTyrAspAlaPheValIle 677
QY 2141 TACTCAAGCCAGATGAGAGCTGGGTAAAGATGAGTAAAGATTAAGAAAGAGG 2200
Db 678 TyrSerSerGlnAsnGlnAspTrpValArgAsnGlnIleuValLysAsnIleuGlnIle 697
QY 2201 GTGCTTCATTTCAGCTTGCCTTCACTAACAGACTTATTCCTGGTGGCCATTGCT 2260
Db 698 ValProArgPheGlnIleuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 717
QY 2261 GCCAACAATCATCCATGAAGTTTCCATTAAGCCGAAAGGTGATTTGTTGTGTCAG 2320
Db 718 AlaAsnIleIleGlnGlnGlyPheHisLysSerArgLysValIleValValSerArg 737
QY 2321 CACTTCATCCAGAGCCGCTGTATCTTTGAATATGAGATTGCTCAGACCTGGCAGTT 2380
Db 738 HisPheIleGlnSerArgTrpCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPhe 757
QY 2381 CTGAGCAGTCGTGCTGTATCATCTTCAATTGTCTGAGAAAGTGGAGAAAGCCCTGCTC 2440
Db 758 LeuSerSerArgSerGlyIleIlePheIleValIleuGlnLysValGlnLysSerLeuIleu 777
QY 2441 AGGAGAGAGGTGAGCTGTACCGCTCTCGACGAGAAACACTTACTGAGTGGAGAGAC 2500
Db 778 ArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTrpGlnAsp 797
QY 2501 AGTGTCTGGGGCGGACATCTTCTGGAGACGACTCAGAAAAGCCCTGTGATGTAA 2560
Db 798 AsnAlaIleuGlnArgHisIlePheTrpArgArgLeuLysLysAlaLeuLeuAspGlyLys 817
QY 2561 TCATGAAATCCAGAAAGAACAGTGGGTACAGGATGCAATTGGCAGAAAGCAACATCATC 2620
Db 818 AlaLeuAsnProAsp-----GlnThrSerGlnGlnGlnGlnIleAlaThrThrLeu 834
```

Search completed: March 29, 2005, 17:27:00
Job time : 350.083 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 09:56:53 ; Search time 163.22 Seconds

(without alignments)
18050.838 Million cell updates/sec

Title: US-09-396-985B-3
Perfect score: 6724
Sequence: 1 aacggggccactgctgtcacc.....tctcactgacagagagacta 3811

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+np.model -DEV=xlh
-Q/cgnt.1/USPTO.spool/US09396985/runat.28032005.155742.21135/app.query.fasta_1.85098
-DB=A.Geneseq.16Dec04 -QPMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09396985 @CGN_1_1_4007 @runat.28032005.155742.21135 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: A.Geneseq.16Dec04:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	4325	64.3	839	6	ABU04773	Abu04773 Human exp
2	4325	64.3	839	6	ABU04774	Abu04774 Human exp
3	4325	64.3	839	6	ABU04775	Abu04775 Human exp
4	4325	64.3	839	7	ADCA7885	Adc7885 Human PRO
5	4325	64.3	839	7	ADCA8826	Adc8826 Human PRO
6	4315.5	64.2	837	2	AAW86361	Aaw86361 Human DNA
7	4315.5	64.2	837	5	AAE16102	Aae16102 Human DNA
8	4308.5	64.1	837	6	ABU04776	Abu04776 Human exp
9	4308.5	64.1	837	5	AAE16116	Aae16116 Human DNA
10	4178	62.1	808	8	AD057782	Ad057782 Chimpanze

11	4167	62.0	808	8	AD057785	Ad057785 Gorilla t
12	4164	61.9	808	8	AD057803	Ad057803 Chimpanze
13	4141	61.6	799	2	AAW86352	Aaw86352 Human DNA
14	4141	61.6	799	5	AAE16093	Aae16093 Human DNA
15	4141	61.6	799	5	ABE83162	Abb83162 Human TOI
16	4141	61.6	799	6	ABR42963	Abt42963 Human TOI
17	4141	61.6	799	7	ADB39121	Adb39121 Human TOI
18	4141	61.6	799	8	ADP56656	Adp56656 Human TOI
19	4141	61.6	799	8	ADP48597	Adp48597 Human TOI
20	4040	60.1	801	8	AD057788	Ad057788 Gibbon to
21	3918	58.3	795	8	AD057791	Ad057791 Rhesus mo
22	3892	57.9	795	8	AD057800	Ad057800 Hamadryas
23	3819	56.8	801	8	AD057797	Ad057797 Squirrel
24	3794	56.4	738	8	ADP29455	Adp29455 Human sec
25	3501	52.1	745	8	AD057794	Ad057794 White-fac
26	1090	16.2	208	3	AAH88059	Aay88059 Human TOI
27	919	13.7	178	8	ADN12270	Adn12270 IL-1R/TLR
28	785	11.7	179	7	ADC42707	Adc42707 Murine To
29	619.5	9.2	661	2	AAW28510	Aaw28510 Product o
30	619.5	9.2	661	2	AAW87556	Aaw87556 B cell su
31	619.5	9.2	661	7	ADC38652	Adc38652 Human sec
32	619.5	9.2	661	7	ADP69098	Adp69098 Human MP5
33	618.5	9.2	650	3	AAH82527	Aay82527 Human RPI
34	605.5	9.0	661	2	AAW47274	Aaw47274 Human B-c
35	603.5	9.0	784	2	AAW86350	Aaw86350 Human DNA
36	603.5	9.0	784	5	AAE16091	Aae16091 Human DNA
37	603.5	9.0	784	5	ABE83161	Abb83161 Human TOI
38	603.5	9.0	784	8	ADN02005	Adn02005 Human int
39	602.5	9.0	784	2	AAV05869	Aay05869 Human TOI
40	602.5	9.0	784	6	ABU61956	Abu61956 Human TOI
41	602.5	9.0	784	7	ADL15005	Adl15005 Human TOI
42	602.5	9.0	784	8	ADP56652	Adp56652 Human TOI
43	602.5	9.0	784	8	ADP48593	Adp48593 Human TOI
44	602.5	9.0	784	8	ADP23787	Adp23787 PEO polyp
45	602.5	9.0	784	8	ADQ39727	Adq39727 Human myo

ALIGNMENTS

RESULT 1	ABU04773	standard; protein; 839 AA.
ABU04773	ABU04773	
AC	ABU04773;	
XX		
XX	29-JAN-2003	(first entry)
DT		
DE	Human expressed protein tag (EPT) #1439.	
XX		
KW	Translational profiling; expressed protein tag; EPT, kinase; phosphatase;	
KW	protease; protease inhibitor; transporter; cytoskeletal protein;	
KW	receptor; transcription factor; cancer; MHC;	
KW	major histocompatibility complex; myeloma; colon cancer; gastric cancer;	
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200278524-A2.	
XX		
PD	10-OCT-2002.	
XX		
PF	28-MAR-2002; 2002WO-US009671.	
XX		
PR	28-MAR-2001; 2001US-0279495P.	
XX		
PR	21-MAY-2001; 2001US-0292544P.	
XX		
PR	08-AUG-2001; 2001US-0310801P.	
XX		
PR	01-OCT-2001; 2001US-0326370P.	
XX		
PR	04-DEC-2001; 2001US-0336780P.	
XX		
PR	20-FEB-2002; 2002US-0358985P.	
XX		
PA	(ZYCO-) ZYCOS INC.	
XX		
PI	Chicz RM, Tomlinson AJ, Urban RG;	

```
XX WPI; 2003-040607/03.
DR
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
PS Example 2; SEQ ID NO 1439; 134pp; English.
XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 839 AA;

Alignment Scores:
Pred. No.: 0 Length: 839
Score: 4325.00 Matches: 839
Percent Similarity: 95.45% Conservative: 0
Best Local Similarity: 95.45% Mismatches: 0
Query Match: 64.32% Indels: 40
DB: Gaps: 1

US-09-396-985b-3 (1-3811) x ABU04773 (1-839)

QY 45 ATGATGTCGCTCGCCCTGGCTGGAGACTTGATCCAGCAATGCGCTCTCTCTCTC 104
DB 1 MetMeSerIaSerAglLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 105 GTGAGACAGAAAGCTGGAGCCCTGGCTGGAGACTTGAGCCCTAAACACAGAGAGAGC 164
DB 21 ValArgProGluSerTrpGluProCysVal----- 30
QY 165 TGGCATGAAACCCAGAGCTTTCAGACTCCGAGGCTCAGCCCTTACCCCGATTCATTG 224
DB 30 ----- 30
QY 225 CTTCCTGCTAAAGTCGCGCTTTTATCAGAGAGTGCTTCCTAATATTACTTATCAATGC 284
DB 31 -----GluValValProAlaIleThrIlyrGlnCys 40
QY 285 ATGAGAGTGAATTTCTACAAATCCCGAGAACCTCCCTTCACCAAGAACCTGGAGC 344
DB 41 MetGluLeuAsnProPheTrpIlyrSileProAspAsnLeuProPheSerThrIlyrAsnLeuAsp 60
QY 345 CTGAGCTTTAATCCCTCGAGAGCAATTTAGGAGCTATAGCTTCTTCAGTTTCCGAGACTG 404
DB 61 LeuSerPheAsnProLeuAlaGlnLeuGlySerTrpSerPhePheSerPheProGluLeu 80
QY 405 CAGGTGCTGATTTATTCAGAGTGTGAATTCAGACAAATTGAAGATGGGGCATATCAGAGC 464
DB 81 GluValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaIlyrGlnSer 100
QY 465 CTAAAGCACTCTCTACTTAAATTTAGACAGAAACCCCATCCAGATTTAGCCCTGGAGC 524
DB 101 LeuSerIleLeuSerThrIleuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
QY 525 GCCTTTCTGAGACTATCAAGATTTCAGAGAGCTGGTGTGAGAGCAAAATCTAGCATCT 584
```

```
DB 121 AlaPheSerGlyLeuSerSerLeuGlnIlyrLeuValAlaValGluThrAsnLeuAlaSer 140
QY 585 CTAGAGAACTTCCCATTTGGACATCTCAAAACTTTGAAAGAACTTAATGCTGCATCAT 644
DB 141 LeuGluAsnProPheProIleGlyIleuIlyrThrLeuIlyrGluLeuAsnAlaIleAsn 160
QY 645 CTATTCGAATCTTTCAAATTAATTCAGATTTTCTTAATCTTGAACCAATCTTAGAGCACTTG 704
DB 161 IleIleGlnSerPheIlyrLeuProGluTrpPheSerAsnLeuThrAsnLeuIlyrIleu 180
QY 705 GACCTTTCCAGACACAGATTCAGAAATTTATTCACAGACTTGGGGCTTTCATCAATCA 764
DB 181 AspLeuSerSerAsnIlyrIleGlnSerIleTrpCysThrAspLeuArgValIleuIleGln 200
QY 765 ATGCCCTCTCAATCTCTCTTAAACCTGTCGCCCTGAAACCCCTTAGAATTTTCCAAACA 824
DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
QY 825 GGTGATTTAAAGAAATTAAGCTTCATAGCTGACTTAAAGAAATTAATTTGATAGTTTA 884
DB 221 GlyAlaPheIlyrGluIleArgLeuIlyrIlyrLeuThrIleuArgAsnAsnPheAspSerLeu 240
QY 885 AATGTATGAAAACTTGATTCAGAGTCTGGCTGTTAGAAATCCATGCTTGTCTG 944
DB 241 AsnValMetIlyrThrCysIleGlnIlyrLeuAlaGlyLeuGluValIleArgLeuValLeu 260
QY 945 GAGAGATTTTAAAGAAATGAAGAAACCTTGAAGAAAGTTGACAAATCTGCTTAAAGGCCCTG 1004
DB 261 GlyGluProPheArgAsnIleuIlyrAsnLeuGluIlyrPheAspIlyrSerIleuGluGlyLeu 280
QY 1005 TGCATTTTACCATTTGAAGAAATTCGATTAAGACTTCTAGACTTCTCATCTCATGATATT 1064
DB 281 CysAsnLeuThrIleGlnIlyrPheArgLeuAlaIlyrLeuAspTrpIlyrIleuAspIle 300
QY 1065 ATTGACTTATTAATTTGTTTGAACAAATGTTTCTTCAATTTCCCTGGTGAAGTGTACTATT 1124
DB 301 IleAspLeuPheAsnIlyrLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
QY 1125 GAAAGGTTAAAGACTTTCTTATTAATTTGGATGGCAACATTTGAATTAATTAATCTG 1184
DB 321 GluArgValIlyrAspPheSerIlyrAsnPheGlyTrpGlnIleLeuGluLeuValAsnCys 340
QY 1185 AAATTTGACAGATTTCCCATTTGAACCTCAATCTCTCAAAAGGCTTACTTCTTCACTTCC 1244
DB 341 IlyrPheGlyGlnPheProThrIleuIlyrLeuIlyrSerLeuIlyrArgLeuThrIleThrSer 360
QY 1245 AACAAAGGTGGGAATGCTTTTTCAGAAAGTTGATCTTCAAGCTTGAAGTTTCTAGATCTC 1304
DB 361 AsnIlyrGlyGlyAsnAlaPheSerGluValAspLeuProSerIleuGluPheLeuAspLeu 380
QY 1305 AGTAGAAATGCTTGATTTCAAGAGTTTCTGCTTCACAAAGATTTTGGGCAACACAGC 1364
DB 381 SerArgAsnGlyLeuSerPheIlyrGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
QY 1365 CTAAAGTATTTAGATGATGAGCTTCAATGAGTGTATTAACCATGAGTTCAAACTTCTGGGC 1424
DB 401 LeuIlyrIlyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1425 TTAGAACCACTGAACATCTGATTTTCAGACTTCCAAATTTGAAACAAATGAGTGAATT 1484
DB 421 LeuGluGlnLeuGlnIlyrIleuAspPheGlnIleSerAsnLeuIlyrIleMetSerGluPhe 440
QY 1485 TCGATTTCTTATCATCTGAGAAACCTCATTTTACCTTGAATTTCTCATCTCATCACACAA 1544
DB 441 SerValPheLeuSerIleuArgAsnLeuIlyrIlyrLeuAspIleSerIleThrIlyrIlyrArg 460
QY 1545 GTTGCTTTCAATGGCATCTTCAATGAGCTTGTCAAGCTTGAAGTCTTGAAGAAATGAGCTGC 1604
DB 461 ValAlaPheAsnIlyrIlePheAsnGlyLeuSerSerLeuGluValIleuIlyrIleAlaGly 480
QY 1605 AATTTCTTCCAGGAAACTTCTTCCAGATATCTTTCAGAGAGTGAAGAACTTGAACCTTTC 1664
```

Db	481	AmserPheGlnGluAsnPheLeuProAspIlePheThrGluLeuAlaArgAsnLeuThrPhe	500
QY	1665	CTGGAACCTCTCTCACTGTCAACTGGAGCAATTGTCTCCAAACAGCAATTAACCTACTCTCC	1724
Db	501	LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer	520
QY	1725	AGCTTCAGGTAATTAAATATGAGCCACAACAATCTTTTCAATTGGAAATAGCTTCCATT	1784
Db	521	SerLeuGlnValLeuAsnMetSerIleAsnAsnPhePheSerLeuAspThrPheProIyr	540
QY	1785	AAGTGTCTGAACCTCCCTCAGAGTTCCTTATTAATACAGTCCAAATCAATATATACATCCAAA	1844
Db	541	LysCysLeuAsnSerLeuGlnValLeuAspIyrSerLeuAsnHisIleMetThrSerIys	560
QY	1845	AAACAGGAACATACAGCAATTTTCCAAAGATGCTTAACTTTTAACTTAACTCAAGATGAC	1904
Db	561	LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp	580
QY	1965	TTTGCTTTTACTGTGGAACACCAAGGTTTCCCGAATGAGATCAAGACCAAGGAGAGCTC	1964
Db	581	PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu	600
QY	1965	TTGGTGAAGTTGAACGAATGAATGCTCAACAACCTTCAAGATTAAGCAGGCAATGCTGTG	2024
Db	601	LeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnIleMetProVal	620
QY	2025	CTGAGTTTGAATATACCTGTCCAGATGAATGAACCATCATGCTGTGTGCTGCTCTCAGT	2084
Db	621	LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlnValSerValLeuSer	640
QY	2085	GTGCTTGAATATATCTGTGTGTAGCACTTCTGCTCTTAAGTTCTATTTCACTGATGCTT	2144
Db	641	ValLeuValValSerValAlaValLeuValLysPheLysPheHisLeuMetLeu	660
QY	2145	CTTGCTGCTGCAATTAAGATGATGCTGTAGAGGTGAACCATCTAATGAGCTTTGTTATCTAC	2204
Db	661	LeuAlaGlyCysIleLysIyrGlyArgGlyGluAsnIleLysAspAlaPheValIleLys	680
QY	2205	TCAAGCCAGATGAGAGACTGGGTTAAGGAATGAGCTATGAAGAAATTTAGAAAGAGGCTG	2264
Db	681	SerSerGlnAspGlnAspTrpValAlaArgAsnGluLeuValLysAsnLeuGlnGlnVal	700
QY	2265	CCTCATTTCAAGCTTGTGCTTCACTACAGAGACTTATTTCCCGGTGTGGCAATGTGCTGCC	2324
Db	701	ProProPheGlnLeuCysLeuHisIleLysArgAspPheIleProGlyValAlaIleAlaIa	720
QY	2325	AACATCATCCATGAAGTTTCCATTAAGCCGGAAGAGATGTTGTGTGTCCTCCAGAC	2384
Db	721	AsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValValSerGlnHis	740
QY	2385	TTTCATCCAGACCGCTGGTGTATCTTTGAATATGATGTGCTCAGACCTGCGAGTTTCTG	2444
Db	741	PheIleGlnSerArgTrpCysIlePheHisIyrGlnIleAlaGlnThrTrpGlnPheLeu	760
QY	2445	AGCAGTGTGCTGTGATCATCTTCAATTGTCTCGAAGAGTGGAGAGAACCTGTGCTCAGG	2504
Db	761	SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg	780
QY	2505	CAGCAGGTGGAGCTGTACCGCTTCTCGACAGGAACAATTACCTGAGGTGGAGAGACAGT	2564
Db	781	GlnGlnValGlnLeuLysArgLeuLeuSerArgAsnTrpLysGlnTrpGlnAspSer	800
QY	2565	GTCTGTGAGGCGGACATCTTCTGTGAGAGAGACTCAGAAAGCCCTGCTGATGTAAATCA	2624
Db	801	ValLeuGlnLysArgHisIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer	820
QY	2625	TGGAAATCCAGAAAGAACAGTGGGTATCAGAGATGCAATTTGGCAGAAAGCAACATCTATC	2681
Db	821	TrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle	839

XX ABU04774;
 AC XX
 DT 29-JAN-2003 (first entry)
 XX XX
 DE Human expressed protein tag (EPT) #1440.
 XX XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX XX
 OS Homo sapiens.
 XX XX
 PN WO200278524-A2.
 PD 10-OCT-2002.
 XX XX
 PF 28-MAR-2002; 2002MO-US009671.
 XX XX
 PR 28-MAR-2001; 2001US-0279495P.
 XX XX
 PR 21-MAY-2001; 2001US-0292544P.
 XX XX
 PR 08-AUG-2001; 2001US-0310801P.
 XX XX
 PR 01-OCT-2001; 2001US-0326370P.
 XX XX
 PR 04-DEC-2001; 2001US-0336780P.
 XX XX
 PR 20-FEB-2002; 2002US-0358985P.
 XX XX
 PA (ZYCO-) ZYCOS INC.
 XX XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX XX
 DR WPI; 2003-040607/03.
 XX XX
 PT New polypeptide (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.
 XX XX
 PT
 XX XX
 PS Example 2; SEQ ID NO 1440; 134pp; English.
 XX XX
 CC The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned disease. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at [ftp.wipo.int/publ/published_pct_sequences](http://wipo.int/publ/published_pct_sequences)

Db 1 MetMetSerAlaSerArGleuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 105 GTGAGACCAAGAAAGCTGGAGGCCCTGTGCTGAGAACTTGGCCCTTAACACACAGAAAGAGC 164
Db 21 ValArgProIleuSerThrGluProCysVal----- 30
QY 165 TGGCATTGAACCAAGAGCTTTCAGACTCCGAGAGCTTCAGCCCTTACCCCGATTCCATTG 224
Db 30 ----- 30
QY 225 CTTCCTGCTAAATGCTGCCGTTTATCAACGAGGTGGTTCCTAATAATTACTTATCAATGC 284
Db 31 -----GluValValProAlaIleThrTyrGlnCys 40
QY 285 ATGAGAGCTGAATTTCTACAAATATCCCGACAACTCCCTTCTCAACCAAGAACTGGAGC 344
Db 41 MetGluLeuAlaPheThrTyrLysIleProAlaPheLeuProPheSerThrLysAlaLeuAsp 60
QY 345 CTGAGCTTTAATCCCGTGAAGCAATTTAGAGGCTATGCTTTCAGTTTCCGAGAACTG 404
Db 61 LeuSerPheAlaProLeuAlaArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 80
QY 405 CAGGTGCTGATTTATTCAGAGTGTGAATCCAGAACTTGAAGATGGGCGATATCAAGAC 464
Db 81 GluValLeuAlaPheLeuSerArGysGluIleGlnThrIleGluAlaPheGlyAlaTyrGlnSer 100
QY 465 CTTAAGCCACTCTCTACCTTAATATTTGACAGAAACCCCATCCAGAGTTTACGCTGGGA 524
Db 101 LeuSerHisIleLeuSerThrLeuIleLeuThrGlyAlaSerProIleGlnSerLeuAlaLeuGly 120
QY 525 GCCTTTCTGACTATCAAGTTTACAGAGCTGTGCTGTGGAGACAAATCTAGACTC 584
Db 121 AlaPheSerIleLeuSerSerLeuGlnLysLeuValAlaValGluThrAlaLeuAlaSer 140
QY 585 CTAGAGAACTTCCCATTTGACACTTCAAAAATTGGAAGAACTTAAATGTGCTCACAAT 644
Db 141 LeuGluAlaPheSerProIleGlyHisLeuLysThrLeuLysGluLeuAlaValAlaHisAsn 160
QY 645 CTATATCCAACTTTTCAAAATTAACCTGAGATTTTCTAATCTGACCAATCTAGAGCACTTG 704
Db 161 LeuIleGlnSerPheLysLeuProGluTyrPheSerAlaLeuThrAlaLeuGluHisLeu 180
QY 705 GACCTTCCAGCAACAAGATTCAAAAGTATTATTTGACAGACTTGGCGGTTTCAATCAA 764
Db 181 AspLeuSerSerAlaHisIleGlnSerIleTyrCysThrAspLeuAlaGlyValIleuHisGln 200
QY 765 ATGCCCTTACTCAATCTCTCTTATGACCTGTCCCTGAACCTTATGAACCTTATCCAA 824
Db 201 MetProLeuLeuAlaLeuSerLeuAspLeuSerLeuAlaSerProMetAlaPheIleGlnPro 220
QY 825 GGTGCATTTAAAGAAATTAAGCTTCAATAGCTGACTTAAAGAAATATTTTGTATGTTTA 884
Db 221 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAlaPheAspSerLeu 240
QY 885 AATGTAATGAAGAACTTGTATTCAGAGTCTGCTGGTGTGAAGGTCATCTTGGTCTTG 944
Db 241 AsnValMetLysThrTyrCysIleGlnGlyLeuAlaGlyLeuGluValHisAlaGlyLeuVal 260
QY 945 GGAAGATTTGAAGAAAGAACTTGAAGAAAGTTTGAACAAATCTGCTTATGAGAGGCTG 1004
Db 261 GlyGluPheArgAlaGlnGlyAlaLeuGlnIleLysPheAspLysSerAlaLeuGlnGlyLeu 280
QY 1005 TGCATTTTGAACATTAAGAAATTCGATTAAGCAATCTTACATCTACCTCGATGATTA 1064
Db 281 CysAlaSerLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 300
QY 1065 ATTAGACTTATTTAATGTTTGAACAATGTTTCTCATTTTCCCGTGAAGGTGATCAATT 1124
Db 301 IleAspLeuPheAlaSerLeuThrAlaSerValSerSerPheSerLeuValSerValThrIle 320
QY 1125 GAAAGGTAAGAAAGCTTTTCTTATTAATTTGAGATGGACAACTTTGAATTAAGTAACTGT 1184
Db 321 GluArgValLysAspPheSerTyrAlaPheGlyTyrGlnHisLeuGluLeuValAlaAsnCys 340

QY 1185 AAAATTTGACAGATTTCCCAATTTGAAGCTCAAAATCTTCAAAAAGGCTTACTTCACTTCC 1244
Db 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
QY 1245 AACAAAGGTGGAAATGCTTTTTCAGAAAGTGAATCTTACAAAGCTTGTGAGTTTGTAGATCTC 1304
Db 361 AsnLysGlyLysAlaAlaPheSerGluValAlaPheLysProSerLeuGluPheLeuAlaPhe 380
QY 1305 AGTAGAAATGGCTTGAATTTCAAAGTGTCTGTCTTCAAAAGTATTTTGGGCAACACGAC 1364
Db 381 SerArgAlaGlnLysLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
QY 1365 CTAAAGTATTTAGATCTGAGCTTCAATGGTGTATTAACATGATGTTCAAACTTCTTGAGC 1424
Db 401 LeuLysTyrLeuAspLeuSerPheAlaGlyValIleThrMetSerSerAlaPheLeuGly 420
QY 1425 TTGAACAACATGAAATCTGATTTCCAGACTTCCAAATTTGAAACAAATGAGTGAATT 1484
Db 421 LeuGlnGlnLeuGlnHisLeuAlaPheGlnHisSerAlaPheLeuLysGlnMetSerGluPhe 440
QY 1485 TCAGTATTTCTTATCACTCAAGAAACCTCATTTACCTTGAATTTTCTATCTCAACACAGA 1544
Db 441 SerValPheLeuSerLeuAlaArgAlaLeuIleTyrLeuAspIleSerHisThrHisArg 460
QY 1545 GTTGCCTTCAATGGCACTTCAATGGCTTGTCCAGTCTGAGAGTCTTGAATAATGGCTGGC 1604
Db 461 ValAlaPheAlaGlnGlyIlePheAlaGlnLysLeuSerSerLeuGluValLeuLysPheAlaGly 480
QY 1605 AATTCCTTTCAGAGAAACCTTCCCTCCAGATATCTTCAAGAGCTGAGAAACTTGAACCTTC 1664
Db 481 AsnSerPheGlnGluAlaPheAlaPheLeuProAlaIlePheThrGluLeuArgAlaLeuThrPhe 500
QY 1665 CTGGACCTTCTTCAAGTGTCAACTGAGAGCAAGTTGTCTTCAACAGCATTTAACTCACTTCC 1724
Db 501 LeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAlaSerLeuSer 520
QY 1725 AGTCTTCAAGTACTAAATATGAGCCACAGCAACTTCTTTCATTTGAGTACGTTTCTTAT 1784
Db 521 SerLeuGlnValLeuAlaPheAlaPheSerHisAlaAlaPhePheSerLeuAlaPheProTyr 540
QY 1785 AAGTGTCTGAATCTCCCTCCAGGTTCTTGATTAAGTCTCAATCACTAATGAATGAACCTTCA 1844
Db 541 LysCysLeuAlaSerLeuGlnValLeuAlaPheTyrSerLeuAlaHisIleMetThrSerLys 560
QY 1845 AAAAGAGAACTTACAGATTTTCCAAATAGTCTTATGCTTTTAAATTTTCTACAGATGAC 1904
Db 561 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAlaSerLeuThrGlnAlaSer 580
QY 1905 TTTGCTGTATCTTGTGAACACAGAGTTTCCGTGCAATGGATCAAGACCAAGGACAGCTC 1964
Db 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrrIleLysAlaPheGlnArgGlnLeu 600
QY 1965 TTGGTGAAGTTGAAGAAATGGAATGTGCAACACTTCAGATTAAGCAGGCGACTGTG 2024
Db 601 LeuValGluValGluArgMetGluCysAlaIleThrProSerAspLysGlnGlyMetProVal 620
QY 2025 CTGAGTTTGAATATCACTCTGTCAAGATGAATGAACATATGATGTGTGTGCGCTCAAT 2084
Db 621 LeuSerLeuAlaSerHisIleThrCysGlnMetAlaLysThrIleIleGlyValSerValLeuSer 640
QY 2085 GTGCTGTGATATCTGTGTGAGAGATTCTGATATTAAGTCTAATTTTCAACCTGATGCTT 2144
Db 641 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeu 660
QY 2145 CTTCGTGCTGCATTAAGTATGATGATGAGGTGAAGAAATCTATGATGCTTGTGTATCTAC 2204
Db 661 LeuAlaGlyCysIleLysTyrGlyArgGlyAlaSerHisIleTyrAspAlaPheValIleTyr 680
QY 2205 TCAAGCCAGATGAGAGCTGGGTTAAGAAATGAGCTTGTAAAGAAATTTAAGAAAGGGGTG 2264
Db 681 SerSerGlnAspGluAspTrrValAlaArgAlaGlnLeuValLysAlaSerLeuGlnGlyVal 700

QY	2245	CCTGCATTTCAGAGCTGCTGGCTTCACATACAGACAGACTTATTCCTCCGGTGGCCATTGCTGCC	2324
Db	701	ProProPheGlnLeuCySLeuHisIryrArgAspPheIleProGlyValAlaIleAlaIa	720
QY	2325	AACATCATCCATGAAAGTTTCCATTAAGCCGAAAGAGTGATGTGTGTGTGTCCAGAC	2384
Db	721	AsnIleIleHisGlnGlyPheHisGlySerArgIysValIleValIleValSerGlnHis	740
QY	2385	TTTCATCCAGAGCCCTGGTGTATCTTTGAAATATGAGATGTGCTCAGACCTGGCACTTCTG	2444
Db	741	PheIleGlnSerArgTrpCysIlePheGlnIyrGlnIleAlaGlnThrTrpGlnPheIleu	760
QY	2445	AGCAGCTGCTGGTGGATCATCTTTCATTCCTCTCGAGAAAGGTGGAGAAAGCCCTCTCAG	2504
Db	761	SerSerArgAlaGlyIleIlePheIleValLeuGlnIysValIleGlyIysThrLeuLeuArg	780
QY	2505	CAGCAGGTGAGAGCTGTACCGGCTTCTCGACGAGAAACCTTACCTGGATGGAGAGACAGT	2564
Db	781	GlnGlnValIleGlnLeuIyrArgLeuLeuSerArgAsnThrIyrLeuGlnTrpGlnAspSer	800
QY	2565	GTCCTGGGGCGGCAACATCTTCTGAGACAGACTCGAAGAAAGCCCTGCTGATGTAAATCA	2624
Db	801	ValleuGlyArgHisIlePheTrpArgArgLeuArgIysAlaLeuLeuAspGlyLysSer	820
QY	2625	TGGAAATCCAGAAAGAACAGTGGGTTCAGAGATGCATTTGGCAGAGAACACATCTATC	2681
Db	821	TrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnIleAlaThrSerIle	839

RESULT 3

ABU04775

ID ABU04775 standard; protein, 839 AA.

XX AC ABU04775;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1441.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.

XX KW Homo sapiens.

XX OS

XX EN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX XX 28-MAR-2001; 2001US-0279495P.

XX ER 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCO5 INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX WP1; 2003-040607/03.

XX XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.

XX XX Example 2; SEQ ID NO 1441; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a

fragment of a kinase, phosphatase, protease, protease inhibitor, CC transmembrane, cytoskeletal protein, receptor or transcription factor. The CC polypeptide is useful as an immunogenic composition for eliciting in a CC mammal an immunogenic response directed against any of the purified CC polypeptide, the purified polypeptide, or the antibody that binds to this CC polypeptide, is useful for treating cancer. The polypeptide is also CC useful for identifying compounds that binds to a naturally processed CC class I or class II MHC-binding polypeptide. The polypeptides and CC polynucleotides are particularly useful for treating or preventing CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, CC lymphoma or leukemia. These are also useful for screening agents for CC treating the above mentioned diseases. This sequence represents an CC expressed protein tag (BPT) isolated from human tissue for translational CC profiling. Note: This sequence does not appear in the printed CC specification but was obtained in electronic format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences

Alignment Scores:

Alignment Scores:

Pred. No.:	0	Length:	839
Score:	4325.00	Matches:	839
Percent Similarity:	95.45%	Conservative:	0
Best Local Similarity:	95.45%	Mismatches:	0
Query Match:	64.32%	Indels:	40

US-09-396-985B-3 (1-3811) X ABU04775 (1-839)

45 ATGATGTCCTGCCCTCGCGCCTGGCTGGACTCTGATCCAGCCATGGCCTTCTCTCTGC 104

Db 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20

105 GTGAGACCAGAAAGCTGGGAGCCCTGCGTGGAGACTTGGCCCTAAACCACACAGAAGAGC 164

```

21 ValArgProcInSerTmgInProcVvaVal----- 30

```

165 TGGCATGAAACCCAGAGCTTTCAGACTCCGAGCCCTACAGCCCTTTCACCCCGATTCCATTGG 224

30

295 294

[illegible]

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

27

01 0111VADPCEWAB7PUCU8C6IAHJ9CY801UULCEVIMIIIIIILECEIWEAB7PCEIYAHDAIYL01INBCEI 100

463 CTAAGCCACCTCTACCTTAATAATGACAGAAATCCCACTCAGAGTAAATCCCTGGAA 324

DB 101 LeuserH1BleuserInrlreu1LeuUInrglyAvnPro1LegInserUua1aLeugly 120

525 GCCCTTCTCGACTATCAAGTTTACGAGAGCTGGTGGCTGTGGAGACAATCTAGCATCT 584

D6 121 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSer 140

585 CTAGAGAACTTCCCATTTGGACATCTCAAAACTTTGAAGAACTTAATGTGGCTCACAAT 644

Db 141 LeuGluAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 160

645 CTATCCAACTTTCAATTACCTGAGTATTTCTAATCTGACCAATCTAGAGCACTTG 704

Db 161 LeuIleGlnSerPheIysLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu 180

QY 705 GACCTTTCAGACAAGATTCAGATATTTATTCAGACAGACTGGGGCTTACATCAA 764
Db 181 AapLeuSerSerAanLysIleGlnSerIleTyCysThrAspLeuArgValLeuHisGln 200
QY 765 ATGCCCTTACTCAATCTCTCTTTAGACCTGTGCTCCGTAACCTTATGAACTTTATCCACCA 824
Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
QY 825 GGTGCATTTAAAGAAATTTAGGCTTCATAGCTGACTTTAAGAAATPAAATTTGATAGTTTA 884
Db 221 GlyAlaPheLysGlnIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu 240
QY 885 AATGTAATGAAAATTGTAATTCAGAGTCTGGCTGGTTTGAAGTCCATCGTTGGTCTG 944
Db 241 AasnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeu 260
QY 945 GGAGAAATTTAGAAATGAAAGAAAATTGGAAAAGTTTGACAAATCTGCTCTAAGAGGCTTG 1004
Db 261 GlyGluPheArgAsnGlnIleAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 280
QY 1005 TGCATTTTGACATTCAGAAATTCGATTTAGCATTTAGTACTGACTACCTCGATGATATT 1064
Db 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyLeuAspTyTyTyLeuAspPheIle 300
QY 1065 ATTTGACTTATTTAATTTGTTGACAAATGTTTCTTCATTTCCCTGGTGAAGTGAATATT 1124
Db 301 IleAspLeuPheAsnLysLeuThrAsnValSerSerPheSerLeuValSerAlaThrIle 320
QY 1125 GAAAGGGTAAAGACTTTTCTTATTAATTTCCGATGGCAACTTTAGAAATTTAGTTAACTGT 1184
Db 321 GluArgValLysAspPheSerTyArgAsnPheGlyTyArgHisIleLeuGlnLeuValLancys 340
QY 1185 AAATTTGACAGATTTCCCATTTGAAATCTCAAAATCTCTCAAAAAGCTTCTTCACTTCC 1244
Db 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
QY 1245 AACAAAGGTGGAAATGCTTTTTCAGAAATGATCTACCAAGCTTGAGTTCTAGATCTC 1304
Db 361 AasnLysGlyLysAsnAlaPheSerGlnValAlaPheLeuProSerLeuGlnIlePheLeuAspLeu 380
QY 1305 AGTAGAAATGGCTTGAGTTTCAAAAGTGTGCTGTTCAAAAGTATTTTGGAGAACCCAGC 1364
Db 381 SerArgAsnGlyLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrThrSer 400
QY 1365 CTAAAGATATTTAGATCGAGCTTCATATGGTGTTATTAACCATGAGTCAAACTTCTTGAGC 1424
Db 401 LeuLysTyLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1425 TTAGAACAACTGAAACATCTGATTTTCAGACATTTCCAAATTTGAAACAAATGAGTGAATT 1484
Db 421 LeuGlnGlnLeuGlnHisIleLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPhe 440
QY 1485 TCAGATATTCCTATCACTCAGAAACCTCATTTTACCTTGACATTTCTATATCTCACACCAG 1544
Db 441 SerValPheLeuSerLeuArgAsnLeuIleTyLeuAspIleSerHisThrHisThrArg 460
QY 1545 GTTTCCTTAAATGGCACTTTCATATGGCTTCCAGATCTGCAAGTCTTGAATATGGCTGGC 1604
Db 461 ValAlaPheAsnGlyLysPheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly 480
QY 1605 AATTTCTTTCAGAGAAACTTCTTCAGATATCTTCAGAGCTGAGAAACTTGACCTTC 1664
Db 481 AsnSerPheGlnGlnLysAsnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPhe 500
QY 1665 CTGAGACTCTCTCAAGTGTCACTGAGACAGTGTCTTCAACAGACATTTAACTCATCTTCC 1724
Db 501 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 520
QY 1725 AGCTTCAGAGTCTAAATATGAGCCACAACTTCTTTTCAATGATAGTTCGTTCTTAT 1784
Db 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTy 540
QY 1785 AAGTGTCTGAACCTCCCTCCAGGTTCTTGATTAAGTCTCAATGACATTAATGACTTCCAA 1844

Db 541 LysCysLeuAsnSerLeuGlnValLeuAspTySerSerLeuAsnHisIleMetThrSerLys 560
QY 1845 AAACAGAAACTACAGACATTTTCCAGATGATGCTAGCTTCTTAAATCTTACTCAGAAATGC 1904
Db 561 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1905 TTTGCTTGACTTTTGAAACACAGAGTTTCTTCGAATGATATCAAGACACAGAGCAGCTC 1964
Db 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeu 600
QY 1965 TTGTTGAAAGTTGAACGAATGGAAATGTGCACACCTTCAGATTAACAGAGGCTGCTTG 2024
Db 601 LeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProVal 620
QY 2025 CTGAGTTTGAATATCACCTGTGACAGTGAATGAATGAACATCATGATGGTGGTCCGCTCAGT 2084
Db 621 LeuSerLeuAsnThrCysGlnMetCysAsnLysThrIleGlyValSerValLeuSer 640
QY 2085 GTGCTTGATGATCTGTTGTAGCAGTTCTGCTATTAAGTTCTATTTTCACTGATGCTT 2144
Db 641 ValLeuValValSerValValAlaValLeuValTyTyLysPheTyPheHisIleuMetLeu 660
QY 2145 CTTCGTGCTGCATAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2204
Db 661 LeuAlaGlyCysIleLysTyGlyArgGlyGlnAsnIleTyArgAspAlaPheValIleTy 680
QY 2205 TCAAGCCAGAGAGAGAGCTGGGTAGAGATGAGCTAGTAAAGAAATTTGAAACAGAGGGG 2264
Db 681 SerSerGlnAspGlnAspTrpValArgAsnGlyLeuValLysAsnLeuGlnGlyVal 700
QY 2265 CCTGCATTTACAGCTGTGCTTCACTACAGAGACTTATTTCCGCTGGCCATTCGTGCTGC 2324
Db 701 ProProPheGlnLeuCysLeuHisTyTyArgAspPheIleProGlyValAlaIleAlaIle 720
QY 2325 AACATCATTCATGAAGTTTCCATTAAGCCGAAAGGTGATTTGTGTGCTCCAGAC 2384
Db 721 AsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValValSerGlnHis 740
QY 2385 TTTCATCCAGAGCGGCTGGGTATCTTTGAATGATGATTTGCTCAGACCGGAGATTTCTG 2444
Db 741 PheIleGlnSerArgTrpCysIlePheGlnTyGlnIleAlaGlnThrTrpGlnPheLeu 760
QY 2445 AGCAGTGTGCTGTATCATCTTCATTTGCTTCGCAAGAGGTGAGAGACCTGTCTCAG 2504
Db 761 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg 780
QY 2505 CAGCAGGTGAGCTGTACCGCTTCTCAGCAGAAACATTTACCTGAGTGGAGAGACGT 2564
Db 781 GlnGlnValGlnLeuTyArgLeuLeuSerArgAsnThrTyLeuGlnTyTrpGlnAspSer 800
QY 2565 GTTCGTGGGCGGACATCTTCGAGAGAGACTCAAGAAAGCCCTGAGTGGTAAATCA 2624
Db 801 ValLeuGlyArgHisIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 820
QY 2625 TGGAAATCCAGAGAAAGAGTGGGTACAGGATGCAATTTGGCAGAGAAACATCTATC 2681
Db 821 TrpAsnProGlnGlyThrValGlyTyThrGlyCysAsnTrpGlnGlnAlaThrSerIle 839

RESULT 4
ADCT8785
ID ADCT8785 standard; protein; 839 AA.
XX
AC ADCT8785;
XX
XX 01-JAN-2004 (first entry)
DT XX
XX
DE Human PRO protein #7.
KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
KW Crohn's disease.
XX
OS Homo sapiens.

XX WO2003034984-A2.
 XX PD 01-MAY-2003.
 XX PF 15-OCT-2002; 2002WO-US033070.
 XX PR 19-OCT-2001; 2001US-0340083P.
 XX (GETH) GENENTECH INC.
 XX PI Goddard A, Gurney AL;
 XX DR WPI; 2003-481990/45.
 XX N-PSDB; ADC78784.
 XX PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
 XX PT medicament for diagnosing or treating cancer or inflammatory bowel
 XX PT disorder e.g., ulcerative colitis or Crohn's disease.
 XX PS Claim 12; SEQ ID NO 14; 327pp; English.
 CC The invention comprises the amino acid and coding sequences of human PRO
 CC proteins. The DNA and protein sequences of the invention are useful for
 CC the diagnosis and treatment of cancer and inflammatory bowel disease
 CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
 CC sequence represents a human PRO protein of the invention.
 XX SQ Sequence 839 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 839
 Score: 4325.00 Matches: 839
 Percent Similarity: 95.45% Conservative: 0
 Best Local Similarity: 95.45% Mismatches: 0
 Query Match: 64.32% Indels: 40
 DB: 7 Gaps: 1
 US-09-396-985B-3 (1-3811) x ADC78785 (1-839)

DB 121 AlpheSerGlyLeuSerSerLeuGlnLeuValAlaValGluThrAsnLeuAlaSer 140
 QY 585 CTAGAGAACTTCCCAATCTGACATCTCAAAACTTTGAAAGAACTTAATGTGGCTGCACAT 644
 DB 141 LeuGluAsnPhleProIleGlyAsnLeuYsthrLeuYsGluLeuAsnValAlaAsn 160
 QY 645 CTTATCCAACTCTTCAAAATTAACCTGAGTATTTTCTTAATCTGACCAATCTAGAGCACTG 704
 DB 161 LeuIleGlnSerPheLeuSerProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeu 180
 QY 705 GACCTTTCAGACACAGAAATTCAAAGTATTTATTCACAGACTTGGCGGCTTTCACATCAA 764
 DB 181 AspleuSerSerAsnLeuYsthrIleGlnSerIleTyrCysThrAspLeuAspValLeuHisGln 200
 QY 765 ATGCCCTTCTCAATCTCTCTTAAGACCTGTGCTCCGACACCTTATGAACTTTATCCACCA 824
 DB 201 MetProLeuLeuAsnLeuSerLeuAsnProMetAsnPhleIleGlnPro 220
 QY 825 GGTGCAATTTAAGAAATTAAGCTTCATTAAGCTTGAAGTATTAAGTATTAAGTATTA 884
 DB 221 GlyAlaPheLeuYsGluIleArgLeuHisValLeuThrLeuAsnAsnPhleAspSerLeu 240
 QY 885 AATGTATGAAATCTTGTATTCAGAGCTGCTGCTGCTTGAAGTCCATGCTTGGTTCG 944
 DB 241 AsnValMetLeuYsthrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 260
 QY 945 GGAGAAATTTAAGAAATTAAGAGAACTTGGAAAAGTTTGACAAATCTGCTTGAAGGCTCG 1004
 DB 261 GlyGluPheArgAsnGluGlyAsnLeuGluYsPheAspYsSerAlaLeuGluGluYsLeu 280
 QY 1005 TGCATTTGACATTTGAAGAAATTCGATTAAGTACTTGAATCTGATGATGAT 1064
 DB 281 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspPhe 300
 QY 1065 ATTGACTTATTAATTTGTTTGAACAATGTTTCTTCAATTTCCCTGGTAGTGTACTAT 1124
 DB 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerAlaThrIle 320
 QY 1125 GAAAGGTTAAAGACTTTCTTATTAATTCGATGCGCAACATTGAAATTAAGTATCTG 1184
 DB 321 GluArgValYsAspPheSerTyrAsnPhleGlyTyrGlnHisLeuGluLeuValAsnCys 340
 QY 1185 AATTTGACAGTTTCCCACTTGAATCTCAAACTCTCAAAAGCTTCACTTCCCTTCC 1244
 DB 341 LysPheGlyGlnPheProThrLeuYsLeuYsSerLeuYsArgLeuThrPheThrSer 360
 QY 1245 AACAAAGGTGGAAATGCTTTTCAAGATTTGATCTTACCAAGCTTGAATTTAGATCTC 1304
 DB 361 AsnLysGlyGlyAsnAlaPheSerGluValAlaAspLeuProSerLeuGluPheLeuAspLeu 380
 QY 1305 AGTAGAATGCTTGAATTTCAAGGTGCTGTTCTCAAGATTTTGGACCAACACAC 1364
 DB 381 SerArgAsnGlyLeuSerPheLeuYsGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1365 CTAAAGTATTTGATCTGAGCTTCAATGCTTATTAACATGATTTCAAACTTTTGGGC 1424
 DB 401 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
 QY 1425 TTAGAACTTGAACATCTGATTTCCAGATTTCCAAATTTGAAACAAATGAGTAGT 1484
 DB 421 LeuGluGlnLeuGluHisIleuAspPheGlnHisSerAsnLeuYsGluMetSerGluPhe 440
 QY 1485 TCAATATCTTATCTACAGAACTCATTTACCTTGAATTTCTCATCTCACACACAGA 1544
 DB 441 SerValPheLeuSerLeuAsnGlnLeuIleTyrLeuAspIleSerHisThrHisThrArg 460
 QY 1545 GTTGCTTTCAATGAGCATCTTCAATGCTTGTGCTTCAATCTGCAAGTCTTGAATGCTGCG 1604
 DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuYsMetAlaGly 480
 QY 1605 AATTTCTTTCAGAGAAACTTCTTCCAGATATCTTCAAGAGCTGAGAAACTTGAACCTTC 1664

Db 481 AenSerPheGlnGluAenPheLeuProAapIlePheThrGluLeuArgAenLeuThrPhe 500
 QY 1665 CTGACCTCTCTCAAGTGTCAACTGAGCAGATTGTCTCAACAGCATTTTAAGTCACTCTCC 1724
 Db 501 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAenSerLeuSer 520
 QY 1725 AGTCTTGAGGTACTAAATATAGCCCAACAACCTTTCTTTTCAATGATAGTTTCTTAT 1784
 Db 521 SerLeuGlnValLeuAenMetSerHisAenAenPhePheSerLeuAspThrPheProIyr 540
 QY 1785 AAGTGTCAAGTCCCTCCAGAGTCTTGATTAACGTCATCAATCAATTAATGACTTCCAAA 1844
 Db 541 LysCysLeuAenSerLeuGlnValLeuAspIyrSerLeuAenHisIleMetThrSerLys 560
 QY 1845 AAACAGAACTACAGACATTTTCCAAAGTACTAGCTTTCTTAAATCTTCTCAGAAATGAC 1904
 Db 561 LysGlnGlnLeuGlnHisPheProSerSerLeuHisPheLeuAenLeuThrGlnAenAsp 580
 QY 1905 TTTGCTTGACTTGTTGTAACAACAAGATTTCTGCAATGATCAAGACCAAGACAGCTTC 1964
 Db 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu 600
 QY 1965 TTGTTGGAAGTGAAGAATGGAATGGAATGGAACCTTCAATGAGAGGAGGAGCTGTG 2024
 Db 601 LeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProVal 620
 QY 2025 CTGAGTTGAATATCACTGTCAAGATGATGAATGAACCATCATGTTGTTGCTGCTCACT 2084
 Db 621 LeuSerLeuAenHisLeuThrCysGlnMetAenLysThrIleIleGlyValSerValLeuSer 640
 QY 2085 GTGCTTGATGATCTGTGTGAGACAGTTGCTGTATTAAGTTCTATTTTCACTGATGCTT 2144
 Db 641 ValLeuValValSerValValAlaValLeuValLysPheThrPheHisLeuMetLeu 660
 QY 2145 CTTCGCGGTGCTAATAAGTATGTTAGAGTGAAGAAATATGATATGCTTGTATCTAC 2204
 Db 661 LeuAlaGlyCysIleLysIyrGlyArgGlyGlnAenLysIyrAspAlaPheValIleIyr 680
 QY 2205 TCAGACGAGATGAGGACTGGTGAAGATGAGCTGTGAAGATTTAGAAAGAGGGGTG 2264
 Db 681 SerSerGlnAspGlnAspTrpValAlaArgAenGlnLeuValLysAenLeuGlnGlyVal 700
 QY 2265 CCTCATTTCAAGTCTGCTCTTCACTACAGAGACTTTATTCCTGCTGCTGCTGCTGCT 2324
 Db 701 ProProPheGlnLeuGlnCysLeuHisIyrArgAspPheIleProGlyAlaIleAlaIle 720
 QY 2325 AACATATCAATGAAGTTCATTAAGCCGAAAGCTGATGTTGTTGCTGCCGACAC 2384
 Db 721 AsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValSerGlnHis 740
 QY 2385 TTCATCCAGAGCCGCTGTGTATCTTTGAATATGAGATGCTCAGACCTGCGAGTTCTG 2444
 Db 741 PheIleGlnSerArgIyrCysIlePheGlnIyrGlnIleAlaGlnThrTrpGlnPheLeu 760
 QY 2445 AGCAGTGTGCTGTGATCATTTCTATTTCTGTCAGAGAGTGAAGAACCTGCTCAGG 2504
 Db 761 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg 780
 QY 2505 CAGCGGTGAGAGTGAACGCTTCTCAGACAGAAACATTAAGTGAAGTGAAGAGCACT 2564
 Db 781 GlnGlnValGlnLeuLysArgLeuLeuSerArgAspThrIyrLeuGlnLysPheSer 800
 QY 2565 GTCTGTGGGCGGACATCTTCTGAGAGACACTCAGAAAGCCCTGTGATGGTAAATCA 2624
 Db 801 ValLeuGlyArgHisIlePheTrpArgAlaGlnArgLysAlaLeuLeuAspGlyLysSer 820
 QY 2625 TGGATTCAGAAAGAACAGTGGGTACAGATGCAATTTGACAGAGCAACATCTATC 2681
 Db 821 TrpAenProGlnGlyThrValGlyThrGlyCysAenTrpGlnGlnLysThrSerIle 839

RESULT 5
 ADD48826
 ID ADD48826 standard; protein; 839 AA.

XX AC ADD48826;
 XX 02-DEC-2004 (revised)
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein AAF05316, SEQ ID NO 14536.
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNR; Chung.
 OS Homo sapiens.
 OS Unidentified.
 PN MO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0335347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR GENBANK; AAF05316.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Example 1; Page; 1017pp; English.
 XX
 The invention discloses a composition comprising two or more isolated rat
 or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNR)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 839 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 839
 Score: 4325.00 Matches: 839
 Percent Similarity: 95.45% Conservative: 0
 Best Local Similarity: 95.45% Mismatches: 0

Query Match: 64.32% Indels: 40
 DB: 7 Gaps: 1
 US-09-396-985b-3 (1-3811) x ADD48826 (1-839)

QY 45 ATATATGTCCTCGGCGCTGGCTGGACCTGTGATCCAGCAATGGCTTCTCTCTGC 104
 DB 1 MetMetSerLaserLysleuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 105 GTGAGACCGAAGAGCTGGAGCGCCTGGCTGGAGACTTGGCCCTTAACCAACACAGAAAGC 164
 DB 21 ValArgProGluSerThrGluProCysVal----- 30
 QY 165 TGGCATGAAACCGAGACTTTCAGACTCCGAGCCTCAGCCCTTCAACCCGATTCCATTG 224
 DB 30 ----- 30
 QY 225 CTTCTGTAAATGCTGCGCTTTTATCAAGAGGTGGTTCCTAATATTACTTATCAATGC 284
 DB 31 -----GluValValProAsnIleThrTyrgInCys 40
 QY 285 ATGAGACTGAATTTCTACAAATATCCCGAACAACCTCCCTTTCACACCAAGAACTGGAC 344
 DB 41 MetGluLeuAsnPhetYrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 60
 QY 345 CTGAGCTTAAATCCCTGAGGACATTAGGCACTATAGCTTCTTCAGTTTCCAGAACTG 404
 DB 61 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 80
 QY 405 CAGTCTGATTTATTCAGAGTGTGAATTCAGACAAATTGAGATGGGCAATTCAGAGC 464
 DB 81 GluValLeuAspLeuSerArgCysGluIleGlnThrIleGluLeuAspGlyAlaTyrgInSer 100
 QY 465 CTAAAGCACTCTCTACCTTAATATGACAGAAACCCCTCCAGAGTTTGAAGCCCTGGGA 524
 DB 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
 QY 525 GCCTTTTCTGACATATCAAGTTTACAGAAAGCTGTGGCTGTGGAGCAAACTTACAGACT 584
 DB 121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGluThrAsnLeuAlaSer 140
 QY 585 CTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAGAACTTAATGTGCTCACAAT 644
 DB 141 LeuGluAsnPheProIleGlyHisLeuLysThrLeuIleGluLeuAsnValAlaHisAsn 160
 QY 645 CTTATCCAACTCTTCAATTAACCTGAGTATTTTCTAATTCACCAATCTAGAGCACTTG 704
 DB 161 LeuIleGlnSerPheLysLeuProGluTyPheSerAsnLeuThrAsnLeuGluHisLeu 180
 QY 705 GACCTTTCAGAAACAAGATTCAAGATTTATTTGACAGACTTGGGGGTTCTACATCA 764
 DB 181 AspLeuSerSerAsnLysIleGlnSerIleTyrcysThrAspLeuArgAlaLeuHisGln 200
 QY 765 ATGCCCTCACTCAATCTCTTTTGAACCTGTCCCTGACCTTAAGCACTTATTCACACA 824
 DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 825 GGTGCACTTAAAGAAATTAAGCTTCAATAGCTCACTTAAAGAAATTTTGAATGTTTA 884
 DB 221 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu 240
 QY 885 AATGTATGAAAACTGTATTTCAAGGCTGGCTGGTGGTTTGAAGTCCATGGTTGGTTTG 944
 DB 241 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisSerGluValLeu 260
 QY 945 GGAGAAATTTAGAAATGAAGAAACTTGAAGAAATTTGACAAATCTGCTTAGAGGGCTTG 1004
 DB 261 GlyGluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu 280
 QY 1005 TGGAAATTTGACCTTGAAGAAATTCGATTAGCACTTACCTAGCACTTCACTGATTAAT 1064
 DB 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyLeuAspTyTyLeuAspAspIle 300

QY 1065 ATTGACTTAATTAATTTGACAAATGTTTCTTCAATTTCCCTGGTAGGTGACTATT 1124
 DB 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
 QY 1125 GAAAGGTTAAAGACTTTTCTTAATTTTCGGATGGCAACATTAGAAATTTAGTAATGCT 1184
 DB 321 GluArgValLysAspPheSerTyArgAsnGlyTyrgLinhIleuGluLeuValAsnCys 340
 QY 1185 AAATTTGACAGTTTCCCATTTGAACCTCAATCTCTCAAAAAGCTTACTTCACTTCC 1244
 DB 341 LysPheGlyGluPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
 QY 1245 AACAAAGTGGAAATGCTTTTTCAGAAATGATCTTACAAAGCTTGAGTTTCTAGATCTC 1304
 DB 361 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuIleuPheLeuAspLeu 380
 QY 1305 AGTAGAAATGGCTTGAGTTTCAAGGTTCTGTTCTCAAGATTTTGGAGAACACAGC 1364
 DB 381 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1365 CTAAAGTATTTAGATGAGCTTCAATGAGTGTATTAACATGATGATCAAACTTCTGGGC 1424
 DB 401 LeuLysTyLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
 QY 1425 TTAGAACAACATGACATCTGATTTCCAGACTTCCAAATTTGAAACAAATGAGTAGATT 1484
 DB 421 LeuGluGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 440
 QY 1485 TCAGATTTCTTATCACTCAAGAAACCTCAATTTAACCCTTATCTCATCTACACACAGA 1544
 DB 441 SerValPheLeuSerLeuArgAsnLeuIleTyLeuAspIleSerHisThrHisThrArg 460
 QY 1545 GTTGTCTTGAAGGCACTTCTCAATGCTGTGCTGCAAGTCCGAGTCTTGAAGAAATGGCTGC 1604
 DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly 480
 QY 1605 AATTTCTTTCAGAAACCTTCTCCAGATATCTTCCAGAGCTGAGAAACTTGACCTTC 1664
 DB 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
 QY 1665 CTGAGCTTCTGAGTGTCACTGAGACAGGTTGTCTCAACAGACATTTAACTCATCTGTC 1724
 DB 501 LeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSer 520
 QY 1725 AGCTTTCAGCTACTAAATATGAGCAACAACCTTCTTCAATGGATACGTTCCCTTAT 1784
 DB 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTy 540
 QY 1785 AAGTGTGAACTCCCTCCAGGTTCTTGATTAACGTCAATCACATAATGACTTCCAA 1844
 DB 541 LysCysLeuAsnSerLeuGlnValLeuAspTyrsSerLeuAsnHisIleMetThrSerLys 560
 QY 1845 AAAACAGAACTACAGCAATTTTCAAGTAGCTAGCTTTCTTAAATCTTACAGAAATGAC 1904
 DB 561 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnArg 580
 QY 1905 TTTGCTTGACTTGGAGAACCAAGAGTTTCTCGCAATGATTAAGAACCAAGGACGCTC 1964
 DB 581 PheAlaCysThrCysGluHisGlnSerPheLeuGlnTyPrlLysAspGlnArgGlnLeu 600
 QY 1965 TTGTGTGAAGTTGAAGAAATGAGATGTGCAACACTTCAGATAGACAGAGGAGCTGTG 2024
 DB 601 LeuValGluValGluArgMetGlyCysAlaThrProSerAspLysGlnIleMetProVal 620
 QY 2025 CTGAGTTGAATATCACTGTGAGATGAATGAAGCAATCATGATGGTGTGCTGCTGACT 2084
 DB 621 LeuSerLeuAsnIleThrCysGlnMetCysLysThrIleIleGlyValSerValLeuSer 640
 QY 2085 GTGCTTGAATATCTGTTGATGACATTTCCGCTTAATGTTTCTAATTTTCACTGATGCTT 2144
 DB 641 ValLeuValValSerValValAlaValLeuValTyLysPheTyPheHisLeuMetLeu 660
 QY 2145 CTTGCTGCTGATGAAGATGATGAGTGAAGAAACATCTATGATGCTTTGTATTCTAC 2204

```

Db      661  LeuAlaGlyCysIleIleValSerIleValArgGlyGluAsnIleValAspAlaPheValIleTyr 680
Qy      2205 TCAGCGCAGATATAGAGATCGGGTATAGAGATGAGCTGTAAAGATTTAGAGAGAGGGGTG 2264
Db      681  SerSerGlnAspIleAspIleValArgAsnGluLeuValLysAsnLeuGluGluVal 700
Qy      2265 CCGCCATTCAGCTCGCCCTTCACTACAGAGACTTATTCGCCGGTGGGCATTGTGCTGC 2324
Db      701  ProProPheGlnLeuCysLeuHisIleTyrArgAspPheIleProGlyValAlaIleAla 720
Qy      2325 AACATCATCATGATGAGCTTTCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2384
Db      721  AsnIleIleHisGluGluPheHisIleValSerArgIleValIleValValIleValSerGlnHis 740
Qy      2385 TTGATTCAGAGAGCGCGGTGTATCTTGAATATGAGATTGCTCAGACCTGGCAGTTTCG 2444
Db      741  PheIleGlnSerArgIleTyrCysIlePheGlnIleValGlnIleThrIleTyrGlnPheLeu 760
Qy      2445 AGCAGTCGTGCTGATTCATCTTCATTCCTGCTGAGAGAGAGAGAGAGAGAGAGAGAG 2504
Db      761  SerSerArgAlaIleIleIlePheIleValLeuGlnIleValGluIleValThrLeuLeuArg 780
Qy      2505 CAGCAGGTGAGCTGTACCGCTTCTCAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2564
Db      781  GlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGluIleTyrGlnIleAspSer 800
Qy      2565 GTCTCTGGGGGGGAGACATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2624
Db      801  ValLeuGlnIleArgHisIlePheIleTyrArgLeuArgLysAlaLeuLeuAspGlyLysSer 820
Qy      2625 TGGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2681
Db      821  TrpAsnProGluGlnIleThrValGlyThrGlyCysAsnTrpGlnIleAlaThrSerIle 839

RESULT 6
AAW86361
ID      AAW86361 standard; protein; 837 AA.
XX
AC      AAW86361;
XX
DT      15-MAR-1999 (first entry)
XX
DE      Human DNAX toll-1-like receptor DTLR4.
XX
KM      DNAX toll-1-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW      interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW      modulate inflammatory function; morphological effect;
XX
OS      Homo sapiens.
XX
PN      WO9850547-A2.
XX
PD      12-NOV-1998.
XX
PF      07-MAY-1998; 98WO-US008979.
PR      07-MAY-1997; 97US-0044293P.
PR      22-JAN-1998; 98US-0072212P.
PR      05-MAR-1998; 98US-0076947P.
XX
PA      (SCHE ) SCHERING CORP.
XX
PI      Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
XX
DR      WPI; 1999-059670/05.
XX
DR      N-PSDB; AAW80675.
XX
PT      Human DNAX toll-1-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
XX      metabolism, modulate inflammatory function or innate immunity responses.
XX      Claim 3; Page 147-149; 171pp; English.

```

```

XX      CC The present invention specifically describes human DNAX toll-1-like
CC      receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC      in the present invention. Also described are: (1) a fusion protein
CC      comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC      an antibody or antibody fragment which specifically binds to a DTLR
CC      protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC      ; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC      host cell comprising the vector of (4). The host cell of (5) can be used
CC      to produce the DTLR proteins. The DTLR proteins can be used to alter
CC      phosphate metabolism, to modulate inflammatory function, innate immunity
CC      responses or morphological effects. The DTLR proteins can be used in the
CC      treatment of conditions exhibiting abnormal expression of the receptors
CC      of their ligands. These abnormalities are typically manifested by
CC      immunological disorders
XX
SQ      Sequence 837 AA;
XX
Alignment Scores:
Pred. No.: 0 Length: 837
Score: 4315.50 Matches: 837
Percent Similarity: 95.33% Conservative: 0
Best Local Similarity: 95.33% Mismatches: 0
Query Match: 64.18% Indels: 41
DB: 2 Gaps: 1

US-09-396-985B-3 (1-3811) x AAW86361 (1-837)
Qy      48  ATGTCTGCTGCGCGCTGCTGAGACTGTATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 107
Db      1  MetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCysVal 20
Qy      108  AGACCAAGAAAGTGGGAGGCGCTGCGTGGAGACTTGCGCCTAAACACACAGAGAGAGCTGG 167
Db      21  ArgProGlnSerIleTyrGlnProCysValGln----- 30
Qy      168  CATGAACCCAGAGCTTTCAGACTCCGAGAGCTCAGCCCTTCAGCCCGATTCATTGCTT 227
Db      30  ----- 30
Qy      228  CTTGCTAAATGCTGCCGTTTTCACGAGAGGTGTTCTTAATTAATTACTTAATGACAG 287
Db      31  -----ValProAsnIleThrTyrGlnCysMet 39
Qy      288  GAGCTGAATTTTACAAATCCCGGACACACTCCCTTCTCAACAGAGAGAGAGAGAGAGAGAGAG 347
Db      40  GluLeuAsnPheTyrIleIleProAsnLeuProPheSerThrLysAsnLeuAspLeu 59
Qy      348  AGCTTAAATCCCTGAGGAGATTAGGAGAGCTATAGCTTCTTCAAGTTTCCAGAGAGCTGAG 407
Db      60  SerPheAsnProLeuArgHisIleLeuGlySerTyrSerPhePheSerPheProGluLeuGln 79
Qy      408  GTGCTGGATTATCCAGGTGTGAATCCAGACAAATTGAAGAGGGGCAATATCAGAGCTTA 467
Db      80  ValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaTyrGlnSerLeu 99
Qy      468  AGCCACTCTCTACCTTAATTTGACAGAGAAACCCATCCAGAGTTTACCCCGGAGAGCC 527
Db      100  SerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
Qy      528  TTTTCTGACTATCAAGTTTACAGAGAGCTGTGCTGTGGAGACAAATCTAGACATCTTA 587
Db      120  PheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSerLeu 139
Qy      588  GAGAACTTCCCATTTGAGACTCAAAACTTTGAAGAACTTAATGTGCTCAATCTT 647
Db      140  GluAsnPheProIleGlyHisLeuYsrThrLeuLysGluLeuAsnValAlaHisAsnLeu 159
Qy      648  ATCCATCTTTCAAAATTTACTGAGTATTTTCTAATCTGACCAATCTAGAGACTGGAG 707
Db      160  IleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeuAsp 179
Qy      708  CTTTCAGACAGAGATTCAGATTAATTATTCACAGAGCTTCGCGGTTCTACATCAATG 767

```

Db 180 LeuSerSerAsnIleGlnSerIleYrCysThrAspLeuArgValLeuHISGlnMet 199
 QY 768 CCCCTACTCAATCTCTTAGACCTGTCCTCCGACCTTAGCACTTAATCCAAACGAGT 827
 Db 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnProIleGlnProGly 219
 QY 828 GCATTTAAAGAAATTAAGCTTCAATAGCTGACTTAAGAAATTAATTAATTAATTAAT 887
 Db 220 AlaPheIleGlnIleLeuArgLeuHISlySLeuThrLeuArgAsnAsnPheAspSerLeuAsn 239
 QY 888 GTAATGAAAACCTTGATTCAGAGCTGCTGCTGTTTAGAAGCTCAGCTGTTGTTGGGA 947
 Db 240 ValMetIleThrCysIleGlnIleLeuAlaGlyLeuGlnValHISArgLeuValIleuGly 259
 QY 948 GAATTTAGAAATGAAAGAAACCTTGAAAGCTTGAACAAATCTGCTTAGAGGGCCGTGTC 1007
 Db 260 GluPheArgAsnIleGlnIleLeuGlnIlePheAspIleSerAlaLeuGlnIleuGlyLeuCys 279
 QY 1008 AATTGACCAATGAAAGATCCGATTAGCATACTGACTGACTGACTGACTGACTGACTGAA 1067
 Db 280 AsnLeuThrIleGlnIleGlnIleuPheArgLeuAlaIleuAspIleThrIleuAspAlaIle 299
 QY 1068 GACTTATTTAATGTTTGAACAAATGTTTCTTCAATTTCCCTGCTGAGTGTGACTTATGAA 1127
 Db 300 AspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGln 319
 QY 1128 AGGGTAAAGACTTTTCTTAATATTTGGATGGCAACATTTAATTAATTAATTAATTAAT 1187
 Db 320 ArgValIleAspPheSerIleuAsnPheGlyIleGlnIleuLeuValIleuAsnCysIle 339
 QY 1188 TTGTGACAGTTTCCCATTTGAACCTCAATCTCTCAAAAGGCTTCACTTCACTTCAAC 1247
 Db 340 PheGlyGlnPheProThrLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 359
 QY 1248 AAAGGTGGGAATGCTTTTTCAGAAATGATCTACCAAGCTTGAATTTTGAATCTCAGT 1307
 Db 360 LysGlyGlyAsnAlaPheSerGlnValAspLeuProSerIleuGlnIleuLeuAspLeuSer 379
 QY 1308 AGAAATGGCTTGATTTCAAAAGTGTCTGTTTCAAAAGTATTTGGAGAACCAACGCTTA 1367
 Db 380 ArgAsnGlyIleuSerPheIleuGlyCysCysSerGlnSerAspPheGlyThrIleuSerLeu 399
 QY 1368 AAGTATTTGATGATGAGCTTCAATGAGTGTATTAACATGAGTCAAACTTCTGGGGCTTA 1427
 Db 400 LysIleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419
 QY 1428 GAACTAGTAAATCTGATTTTTCAGATTTCCAAATTTGAAACAAATGAGTGAATTTTCA 1487
 Db 420 GlnGlnIleuGlnIleuIleuAspPheGlnHISerAsnIleuIleuIleuIleuIleuIleu 439
 QY 1488 GATTTCTTATCACTCGAAACCTTCATTTTACCTTGAACATTTCTATCTACACCAAGATT 1547
 Db 440 ValPheLeuSerLeuArgAsnIleuIleuIleuIleuAspIleSerHISThrIleuIleuIleu 459
 QY 1548 GCTTGAATGAGCACTTCAATGAGTGTCTGCAATCTGAGTCTTGAATTAATGCTGCAAT 1607
 Db 460 AlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnIleuValIleuIleuIleuIleuIleu 479
 QY 1608 TCTTTTCAGAAAACCTTCTTCAGATATCTTCAGAGAGCTGAGAACTTGACCTTCTG 1667
 Db 480 SerPheGlnGlnAsnIleuPheProAspIlePheThrGlnIleuArgAsnIleuThrPheLeu 499
 QY 1668 GACCTCTCTCAGTGTCACTGAGACGTTGTCTTCAACAGCATTTAACTCAGCTTCCAGT 1727
 Db 500 AspLeuSerGlnIleuGlnIleuGlnIleuLeuSerProThrAlaPheAsnIleuSerSer 519
 QY 1728 CTTGAGTACTAATTAATGAGCAACAACCTTCTTTCATTTGATGATGCTTCTTCTTAAAG 1787
 Db 520 LeuGlnIleuIleuAsnMetSerHISAsnAsnPhePheSerIleuAspThrPheProIleuIleu 539
 QY 1788 TGTCTGAACCTCCCTCAGAGTCTTGAATACAGTCTCAATCACTTAATGACTTCAAAA 1847

Db 540 CysLeuAsnSerLeuGlnValIleuAspIleuSerLeuAsnHISIleuThrSerIleuIleu 559
 QY 1848 CAGGAATCAAGACATTTTCCAGTAGTCTAGCTTTCTTAATCTTCAAGAAATGACTT 1907
 Db 560 GlnGlnIleuGlnIleuPheProSerSerLeuAlaPheLeuAsnIleuThrGlnAsnAspPhe 579
 QY 1908 GCTTGTACTTGTGAACACCAAGATTCTTCAATGGATCAAGGACCAAGGAGCTCTTG 1967
 Db 580 AlaCysThrCysGlnIleuIleuGlnSerPheLeuGlnIleuIleuIleuAspGlnArgGlnIleu 599
 QY 1968 GTGGAAGTTGAAAGAAATGGAATGTGCAACACTTCAAGATPAAGAGGGCACTGCTGCTG 2027
 Db 600 ValGlnValGlnArgMetGlnCysAlaThrProSerAspIleuGlnIleuIleuIleuIleu 619
 QY 2028 AGTTGAATATCACTGTCAGATGAAATGAACCATCATTTGAGTGGTGTGCGGCTCAGTGTG 2087
 Db 620 SerLeuAsnIleThrCysGlnMetCysAsnIleIleIleGlyAlaSerValIleuSerVal 639
 QY 2088 CTGTGATATCTGTGTGACAGTCTGCTCTAATGCTTCAATTTTCACTGATGCTTCTT 2147
 Db 640 LeuValIleuSerValIleuAlaValIleuValIleuIleuValIleuIleuIleuIleuIleu 659
 QY 2148 GCTGCTGCAATAAGTATGTGTGAGGTGAAACATTATGATGCTTGTGTATCTACTCA 2207
 Db 660 AlaGlyCysIleIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 679
 QY 2208 AGCCAGGATGAGGAGCTGGGTAAAGGATGAGTAAAGATTTTGAAGAGGGGCGCT 2267
 Db 680 SerGlnAspGlnAspIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 699
 QY 2268 CCATTTCACTGCTGCTTCACTACAGAGACTTATTCCTGGTGTGCGCACTTGTGCGCAAC 2327
 Db 700 ProPheGlnIleuCysIleuHISIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 719
 QY 2328 ATCATCATGAAGTTTCCATPAAGCCGAAAGGTGATGTTGTGTGCTCCAGCACTTC 2387
 Db 720 IleIleIleIleGlnGlyPheHISlysSerArgIleuValIleuValIleuIleuIleuIleu 739
 QY 2388 ATCCAGAGCGCTGGGTATCTTTGAATGAGATTTGCTCAGACCTGGGAGTTCTGAGC 2447
 Db 740 IleGlnSerArgIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 759
 QY 2448 AGTCGTGCTGATCATCTTCAATTTGCTGCAAGAGTGAAGAGCACTGCTCAGAGCAG 2507
 Db 760 SerArgAlaGlyIleIlePheIleuValIleuGlnIleuValGlnIleuIleuIleuIleuIleu 779
 QY 2508 CAGGTGAGCTGTACCGCTTCTCAGACAGAAACATTACCTGAGTGGAGAGCAGTGT 2567
 Db 780 GlnValGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 799
 QY 2568 CTGGGCGGACATCTTCTGAGACGATCAGAAAGCCCTGTGATGTTAATGATG 2627
 Db 800 LeuGlyArgHISIlePheThrArgLeuAlaGlyValIleuIleuAspGlyIleuSerIleu 819
 QY 2628 AATCCAGAGAAACAGTGGGTACAGATGCAATTTGGCAGAAACATCTATC 2681
 Db 820 AsnProGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 837

RESULT 7
 AAE16102
 ID AAE16102 standard; protein; 837 AA.
 AC AAE16102;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 XX
 DB Human DNAX Toll like receptor (DTLR) 4 #2.
 XX
 XX Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
 KW Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
 XX
 OS Homo sapiens.
 XX

PN WO200190151-A2.
 XX 29-NOV-2001.
 XX 23-MAY-2001; 2001MO-US016766.
 PF 25-MAY-2000; 2000US-0207558P.
 XX (SCHE) SCHERING CORP.
 XX Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SMK, Liu Y;
 PI WPI; 2002-083085/11.
 DR N-PSDB; AAD26292.
 XX
 XX New DNAX Toll like receptor (DTLR) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 PS
 PS Claim 3; Page 41; 297pp; English.
 XX
 CC The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DNAX Toll like receptor (DTLR) protein and their corresponding
 CC nucleic acids. The DTLR is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTLR is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTLR is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g. capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTLR or its various fragments. The
 CC purified DTLR can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression
 CC libraries for particular expression products. These are useful for
 CC detection or diagnosing various immunological conditions related to
 CC expression of DTLR or cells that express it. The present sequence is
 CC human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
 CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
 CC sequence shown in page 240-243 (AAE16116). However these sequences differ
 CC at several locations
 CC
 XX
 XX Sequence 837 AA;
 SQ
 Alignment Scores:
 Pred. No.: 0 Length: 837
 Score: 4315.50 Matches: 837
 Percent Similarity: 95.33% Conservative: 0
 Best Local Similarity: 95.33% Mismatches: 0
 Query Match: 64.18% Indels: 41
 DB: 5 Gaps: 1
 US-09-396-985B-3 (1-3811) x AAE16102 (1-837)
 QY 48 ATGTCTGCTGGCGCTGGCTGGAGCTGTGATCCAGCCATGCGCTTCTCTCGCGTG 107
 Db |||||
 Db 1 MetSerLaseRArgLeuNlaGlyThrLeuIleProAlaMetValaHeuSerCysVal 20
 QY 108 AAGACCGAAGAGCGGAGCCCTGCGTGAGACTTGGCCCTTAACCAACAGAAAGAGCTGG 167
 Db |||||
 Db 21 ArgProGlnSerThrPgluProCysValGlu----- 30
 QY 168 CATGAACCCAGAGCTTTCAGACTCCGAGAGCTCAGCCCTTCAACCCGATTCATTGCTT 227
 Db ----- 30
 QY 228 CTGTGCTAAATGCTGCCGTTTTCACAGAGTGCTTCTAATATTACTTATCAATGATG 287
 Db |||||
 Db 31 -----ValProAsnIleThrTyrlGlnCysMet 39
 QY 288 GAGCTGAATTTTTCACAAATCCCGCAACACTCCCTTTCACCAAGAACTGGACCTG 347
 Db |||||
 Db 40 GluLeuAsnPherylTyrlleProAspAsnLeuProPheSerThrTyrlAsnLeuAspLeu 59

QY 348 AGCTTTAATCCCTGAGGCACTTAGGACGTATAGCTTCTTCAGTTTCCAGAACTGCAG 407
 Db |||||
 Db 60 SerPheAsnProLeuNlaRghIleuGlySerTyrlSerPhePheSerPheProGluLeuGln 79
 QY 408 GTGCTGGAATTTATCCAGGTGTGAAAATCCAGCAATTAAGATGGGCAATATGAGCCCTA 467
 Db |||||
 Db 80 ValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrlGlnSerLeu 99
 QY 468 AGCCACCTCTCTACCTTATATTTACAGAGAAACCCCATCCAGATTTAGCCCTGGAGCC 527
 Db |||||
 Db 100 SerH1sLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
 QY 528 TTTTTCGAGACTATCAAGTTTACAGAGCGTGCGTGAGAGCAAAATCTAGCATCTCTA 587
 Db |||||
 Db 120 PheSerGlyLeuSerSerLeuGlnIleuValAlaValGluThrAsnLeuAlaSerLeu 139
 QY 588 GAGAACTTCCCATTTGACATCTCAAAACTTTGAAGAATTAATGTGGCTCACAATCTT 647
 Db |||||
 Db 140 GluAsnPherProIleGlyH1sLeuTyrlLeuTyrlGluLeuAsnValAlaH1sAsnLeu 159
 QY 648 ATCCAAATCTTTCAATTTACCTGATATTTTCTAATCTGACCAATCTAGACACTTGGAC 707
 Db |||||
 Db 160 IleGlnSerPheTyrlLeuProGluTyrlPheSerAsnLeuThrAsnLeuGluH1sLeuAsp 179
 QY 708 CTTTCCAGCAACAAAGATTCAAAGTATTTATTCACAGACTTGGGGTTTCTACATCAATG 767
 Db |||||
 Db 180 LeuSerSerAsnIleIleGlnSerIleTyrlCysThrAspLeuArgValLeuH1sGlnMet 199
 QY 768 CCCCTACTCAATCTCTTTAGACCTGTCCCTGAACCTTGAACCTTTATCCAACCAAGT 827
 Db |||||
 Db 200 ProLeuAsnLeuSerSerLeuAspSerLeuAsnProMetAsnPhelIleGlnProGly 219
 QY 828 GATTTTAAAGAAATTAGGCTTTCATAGCTGATCTTAAAGAAATTAATTTGATGTTAAT 887
 Db |||||
 Db 220 AlaPheTyrlGluIleArgLeuH1sTyrlLeuThrLeuAspAsnPhasAspSerLeuAsn 239
 QY 888 GTAAAGAAAACCTTGATTCAGAGCTGGCTGTTTGAAGATCCATCGTTTGTTCGGGA 947
 Db |||||
 Db 240 ValMetTyrlThrCysIleIleGlnTyrlLeuAlaGlyLeuGluValH1sArgLeuValLeuGly 259
 QY 948 GAATTTAGAAATGAAGAAACTTGGAAAATTTGACAAATCTGCTCTAGAGGCGCTGTGC 1007
 Db |||||
 Db 260 GluPheArgAsnGluGlyAsnLeuGluTyrlPheAspTyrlSerAlaLeuGluIleuTyrlCys 279
 QY 1008 AATTTGACCATTTGAAGAAATCCGATTAGCATCTTAGACTACTGATGATATTTATT 1067
 Db |||||
 Db 280 AsnLeuThrIleIleGluGluPheArgLeuAlaTyrlLeuAspTyrlTyrlLeuAspAlleIle 299
 QY 1068 GACTTATTTAATTTGTTGACAAATGTTTCTTCAATTTCCCTGGAGTGAGTCAATTGAA 1127
 Db |||||
 Db 300 AspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGlu 319
 QY 1128 AGGTTAAAGACTTTTCTTATTAATTTGAGTGAACAATTTGAATTAAGTTAACTGTAAA 1187
 Db |||||
 Db 320 ArgValTyrlAspPheSerTyrlAsnPhelGlyTrpGlnH1sLeuGluLeuValAsnTyrlCys 339
 QY 1188 TTTTGAACAGTTTCCCAATTTGAAGTCAAAATCTTCAAAAAGGCTTACTTTCCTCCAC 1247
 Db |||||
 Db 340 PheGlyGlnPheProThrLeuTyrlLeuTyrlSerLeuTyrlValGlyLeuThrPheThrSerAsn 359
 QY 1248 AAAGTGGAATGCTTTTTCAGAAAGTTGATCTACCAAGGCTTGAAGTTTCTTGAATCTCAGT 1307
 Db |||||
 Db 360 TyrlGlyGlyAsnAlaPheSerGluValAspLeuProSerIleGluPheLeuAspLeuSer 379
 QY 1308 AGAAATGGCTTGAGTTTCAAGGTGCTGTTCTCAAGATGATTTTGGAGCAACAGCCTTA 1367
 Db |||||
 Db 380 ArgAsnGlyLeuSerPheTyrlGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu 399
 QY 1368 AAGTATTTAGATCTGAGCTTCAATGCTGTATTTACATGAGATGTTCAAACTTCTGGGCTTA 1427
 Db |||||
 Db 400 TyrlTyrlLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPhelLeuGlyLeu 419

QY 1428 GAAACAAGTGAACATCTGATATTCAGACATTCAGATTTGAACAAATGAGTGGATTCA 1487
 DB 420 G|U|G|I|L|e|u|g|I|u|H|I|s|l|e|u|A|p|h|e|G|I|n|H|I|s|e|r|A|s|n|l|e|u|y|s|g|I|n|e|t|S|e|r|G|l|u|p|S|e|r 439
 QY 1488 G|T|A|T|T|C|C|A|T|C|C|A|G|A|A|C|C|T|T|A|C|T|T|G|A|C|T|T|T|C|A|T|A|C|T|C|A|C|C|A|G|A|G|T 1547
 DB 440 V|A|L|P|h|e|u|s|e|r|l|e|u|A|n|l|e|u|I|e|T|y|L|e|u|A|s|P|I|l|e|S|e|r|H|I|s|T|R|H|I|s|T|R|A|G|V|A|L 459
 QY 1548 G|C|T|T|C|A|A|G|G|A|C|T|T|C|A|A|G|G|G|T|T|C|C|A|G|T|C|C|A|G|T|C|C|A|A|A|T|G|G|G|G|C|C|A|T 1607
 DB 460 A|A|P|h|e|A|n|s|I|l|e|P|h|e|A|n|s|I|l|e|u|S|e|r|S|e|r|l|e|u|I|n|V|A|l|l|e|u|y|S|e|C|H|A|G|I|y|A|s|n 479
 QY 1608 T|C|T|T|C|A|G|G|A|A|A|C|T|T|C|T|C|A|G|A|T|T|C|T|C|A|G|A|G|G|T|G|A|A|A|C|T|T|G|A|C|T|T|C|C|T 1667
 DB 480 S|e|P|h|e|G|I|n|I|u|s|n|P|h|e|u|P|r|o|A|s|P|I|l|e|P|h|e|T|H|I|u|e|u|A|n|l|e|u|I|n|P|h|e|u 499
 QY 1668 G|A|C|C|T|C|T|C|A|G|T|C|A|C|T|G|A|G|C|A|G|T|G|T|C|T|C|A|C|A|C|A|C|A|T|T|T|A|C|T|C|T|C|C|A|G|T 1727
 DB 500 A|s|P|l|e|u|s|e|r|I|n|C|y|s|g|I|n|l|e|u|G|I|n|l|e|u|S|e|r|P|r|o|H|I|A|P|h|e|A|n|s|e|r|l|e|u|S|e|r 519
 QY 1728 C|T|T|C|A|G|T|A|A|A|T|T|G|A|G|C|C|A|C|A|C|A|C|T|T|T|C|T|T|C|A|T|G|A|T|G|G|T|T|C|T|T|A|G 1787
 DB 520 L|e|u|G|I|n|V|A|l|l|e|u|A|n|e|t|S|e|r|H|I|s|A|n|A|n|P|h|e|S|e|r|l|e|u|A|s|P|I|n|P|h|e|P|r|o|T|y|L|y|S 539
 QY 1788 T|G|T|G|A|A|C|T|C|C|T|C|C|A|G|T|T|C|T|T|G|A|T|T|A|G|T|C|T|C|A|T|C|A|A|T|A|G|T|C|C|A|A|A|A 1847
 DB 540 C|y|L|e|u|A|n|s|e|r|l|e|u|G|I|n|V|A|l|l|e|u|A|s|P|I|y|S|e|r|l|e|u|A|n|H|I|s|I|l|e|u|e|t|H|I|s|e|r|I|y|S|y|e 559
 QY 1848 C|A|G|A|A|C|T|A|C|A|G|A|T|T|T|C|C|A|G|A|G|T|C|T|A|G|C|T|T|T|C|T|T|A|A|T|C|T|T|A|C|G|A|A|T|G|A|C|T|T 1907
 DB 560 G|I|n|G|I|l|e|u|G|I|n|H|I|s|P|r|o|S|e|r|S|e|r|l|e|u|A|l|A|P|h|e|u|A|n|l|e|u|I|n|G|I|n|A|n|A|s|P|h|e 579
 QY 1908 G|C|T|T|G|A|C|T|T|G|A|A|C|C|A|G|A|G|T|T|C|C|G|C|A|N|T|G|A|T|C|A|A|G|A|C|C|A|G|A|G|C|C|T|G 1967
 DB 580 A|A|C|y|s|T|H|y|S|g|I|n|H|I|s|I|n|S|e|r|P|h|e|L|e|u|G|I|n|T|P|I|l|e|y|A|s|P|G|I|n|A|G|I|n|l|e|u 599
 QY 1968 G|T|G|A|A|G|T|T|G|A|G|A|T|G|A|T|G|A|G|C|A|C|C|T|C|A|G|A|T|A|G|A|G|G|C|A|T|C|C|T|G|C|T|G 2027
 DB 600 V|A|L|G|I|V|A|G|I|u|A|n|g|e|t|G|I|u|C|y|A|A|A|T|H|P|r|o|S|e|r|A|s|P|I|y|S|g|I|n|G|I|n|P|r|o|V|A|l|l|e|u 619
 QY 2028 A|G|T|T|G|A|T|T|C|A|C|T|G|T|C|A|G|A|T|A|A|C|A|C|A|T|T|G|T|G|T|G|T|C|C|T|C|A|G|T|G 2087
 DB 620 S|e|r|l|e|u|A|n|l|e|H|I|s|C|y|S|I|n|e|t|A|s|n|I|y|T|H|I|l|e|G|I|y|A|S|e|r|V|A|l|l|e|u|S|e|r|V|A|l 639
 QY 2088 C|T|T|G|A|T|C|T|G|T|G|A|G|A|G|T|T|C|G|G|T|A|T|A|G|T|C|A|T|T|T|C|A|T|T|T|C|C|G|A|G|T|T|C|T 2147
 DB 640 L|e|u|V|A|l|S|e|r|V|A|l|A|A|A|V|A|l|l|e|u|V|A|l|y|T|l|y|S|P|h|e|T|y|P|h|e|H|I|S|e|u|e|t|L|e|u 659
 QY 2148 G|C|T|G|G|T|C|A|T|A|A|G|T|G|T|A|G|G|T|G|A|G|G|A|A|C|A|T|C|T|A|T|G|A|T|G|C|T|T|G|T|A|T|C|T|A|C|T|A 2207
 DB 660 A|A|G|I|C|y|S|I|l|e|y|S|T|y|G|I|y|A|G|G|I|y|G|I|u|A|n|l|e|T|y|A|s|P|A|A|P|h|e|V|A|l|l|e|T|y|S|e|r 679
 QY 2208 A|G|C|A|G|A|T|G|A|G|A|C|T|G|G|T|A|G|A|G|A|T|G|A|G|A|T|T|G|A|A|A|T|T|G|A|A|G|A|G|G|G|T|G|C|T 2267
 DB 680 S|e|r|G|I|n|A|s|P|I|u|A|s|P|I|P|V|A|l|A|G|A|n|G|I|u|e|u|V|A|l|l|y|A|s|n|l|e|u|G|I|n|G|I|y|V|A|l|P|r 699
 QY 2268 C|C|A|T|T|T|C|A|G|C|T|G|C|C|T|T|C|T|C|A|C|A|G|A|C|T|T|A|T|T|C|C|G|G|T|G|G|C|A|T|T|G|C|T|G|C|C|A|C 2327
 DB 700 P|r|o|P|h|e|I|n|l|e|u|C|y|S|e|u|H|I|s|T|y|A|G|A|s|P|h|e|I|l|e|P|r|o|I|y|A|A|A|I|e|A|I|e|A|A|A|A|s|n 719
 QY 2328 A|T|C|A|T|C|A|T|G|A|G|T|T|C|A|T|A|A|A|G|C|C|A|A|G|G|T|G|T|T|G|G|T|G|C|C|A|G|A|C|T|T|G 2387
 DB 720 I|l|e|I|l|e|H|I|s|G|I|u|G|I|P|h|e|H|I|s|y|S|e|r|A|G|I|y|V|A|l|l|e|V|A|l|V|A|l|S|e|r|G|I|n|H|I|s|P|h|e 739
 QY 2388 A|T|C|A|A|G|C|G|G|T|G|T|A|T|C|T|T|G|A|T|A|T|G|A|A|T|T|G|C|C|A|G|C|T|G|C|A|G|T|T|G|A|G|C 2447
 DB 740 I|l|e|G|I|S|e|r|A|G|I|P|C|y|S|I|l|e|P|h|e|G|I|u|T|y|G|I|n|l|e|A|I|G|I|n|H|I|s|T|P|G|I|n|P|h|e|u|S|e|r 759
 QY 2448 A|G|C|G|G|C|G|T|G|T|A|T|C|T|T|C|A|T|T|G|C|C|A|A|G|G|T|G|A|A|G|G|A|A|C|C|G|C|C|A|G|G|A|G 2507
 DB 760 S|e|T|A|G|I|A|G|I|y|l|e|I|l|e|P|h|e|I|l|e|V|A|l|l|e|u|G|I|n|V|A|l|G|I|u|y|S|T|H|I|l|e|u|A|V|A|G|I|n 779
 QY 2508 C|A|G|G|T|G|A|G|C|T|G|A|C|C|T|T|C|A|G|A|G|A|C|T|T|A|C|T|G|A|G|G|A|G|A|C|A|G|T|G|T 2567

DB 780 G|I|n|V|A|l|G|I|u|e|T|y|A|G|I|u|e|u|S|e|r|A|G|A|n|H|I|s|T|y|L|e|u|G|I|u|T|P|G|I|u|A|s|P|e|r|V|A|l 799
 QY 2568 C|T|G|G|G|G|G|G|A|C|A|T|C|T|T|G|G|A|G|A|C|C|A|G|A|A|G|C|C|T|G|G|A|T|G|T|A|A|T|C|A|T|G 2627
 DB 800 L|e|u|G|I|y|A|G|I|s|I|l|e|P|h|e|T|P|A|G|I|u|A|G|I|y|S|A|l|e|u|e|u|A|s|P|G|I|y|S|e|r|T|P 819
 QY 2628 A|A|T|C|A|G|A|G|A|A|C|A|G|T|G|G|T|A|C|A|G|A|T|G|C|A|A|T|T|G|C|A|G|A|A|C|A|C|A|T|C|T|A|T|C 2681
 DB 820 A|n|P|r|o|G|I|u|G|I|y|T|H|V|A|l|G|I|y|T|H|I|g|I|y|S|A|n|T|P|G|I|u|A|H|I|s|e|r|I|l|e 837
 RESULT 8
 ABU04776
 ID ABU04776 standard; protein; 837 AA.
 XX
 AC ABU04776;
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1442.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 OS Homo sapiens.
 PN MO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002MO-US009671.
 XX
 XX 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 XX (ZYCO-) ZYCOS INC.
 PA
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1442; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptides. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIP0 at
 CC ftp.wip0.int/pub/published_pct_sequences
 XX

SQ Sequence 837 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 837
 Score: 4315.50 Matches: 837
 Percent Similarity: 95.33% Conservative: 0
 Best Local Similarity: 95.33% Mismatches: 0
 Query Match: 64.18% Indels: 41
 DB: 6 Gaps: 1
 US-09-396-985b-3 (1-3811) x ABU04776 (1-837)
 48 ATGTCTGCTCGGCGCTGGCTGGAGCTGTGATCCAGCCATGCGCTTCTCTCGCTG 107
 1 MeSeSerAlaSerxArgLeuAlaGlyThrLeuIleProAlaMetAlaHeuSerCysVal 20
 108 AGACCGAAAGCTGGAGCCCTGCGTGAGACTTGGCCCTAAACACACAGAAAGCTGG 167
 21 ArgProGluSerTrpGluProCysValGlu----- 30
 168 CATGAAGCCAGAGCTTTGAGACTCGGAGGCTCAGCCCTTACCCCGATTCCATTGCTT 227
 30 ----- 30
 228 CTGTGTAATGCTGCGGTTTTATCAGGAGGTGGTCTTAATATTAATTATCAATGCTAG 287
 31 -----ValProAsnIleThrTyrGlnCysMet 39
 288 GAGCTGAATTTCTACAAATCCCGGCAACCTCCCTTCTCAACGAAAGCTGGACTG 347
 40 GluLeuAsnPheTyrIleProAsnAsnLeuProPheSerThrIleAsnLeuAspLeu 59
 348 AGCTTAATCCCGTGAGGACTTGAAGAGCTATAGCTTCTGAGTTCCAGAACTGACG 407
 60 SerPheAsnProLeuArgIleLeuGlySerTyrSerPhePheSerPheProGluLeuGln 79
 408 GTGCTGATTTATCAGGTGTGAATCCAGACAAATTGAAGATGGGCAATATCAGAGCTTA 467
 80 ValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSerLeu 99
 468 AGGCACCTCTTACCTTAATATTGACAGAAACCCATCCAGAGTTTAAAGCCCTGGAGGC 527
 100 SerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
 528 TTTTTCGACTATCAAGTTTACAGAGCTGTGGCTGTGAGACAAATCTAGACATCTCTA 587
 120 PheSerGlyLeuSerSerLeuGlnIleValAlaValGluThrAsnLeuAlaSerLeu 139
 588 GAGAACTTCCCACTGGACATCTCAAAACTTTGAAGAACTTAATGTGCTCAAACTTT 647
 140 GluAsnPheProIleGlyHisLeuIleThrLeuIleGluLeuAsnValAlaHisAsnLeu 159
 648 ATCCAAATCTTGAATTAATCTGAGATTTTCTTAATCTGACCAATCTGAGCACTTGGAC 707
 160 IleGlnSerPheIleLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeuAsp 179
 708 CTTTCAGCAACAAGATTCAAGATTTATTTGACAGACTTGGGGGTTCTCAATCAAAAG 767
 180 LeuSerSerAsnIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGlnMet 199
 768 CCCCTACTCAATCTCTTTAGACTGTCCCTGAACCTATGAACCTTATCAACAGAGT 827
 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnHeIleGlnProGly 219
 828 GCATTTAAAGAAATTAGGCTTCAATAGCTGACTTTAAGAAATTAATTTGATGATTAAAT 887
 220 AlaPheIleGluIleArgLeuHisIleTyrLeuThrLeuArgAsnAsnPheAspSerLeuAsn 239
 888 GTAATGAAAATCTGTATTCAGAGTCTGGCTGTTTGAAGTTCATGATGTTTGGTTGGGA 947
 240 ValMetIleThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisValArgLeuValLeuGly 259
 948 GAATTTAGAAATGAGGAAACTTGAAGAAAGTTTGACAAATCTGCTTAGAGGCGCTGTGC 1007

260 GluPheArgAsnGluGlyAsnLeuGluIleIleAspLeuAspIleSerAlaLeuGluIleCys 279
 1008 AATTTGACATTTGAAGAAATTCGATTAACATTAATCTAGACTACTGATGATTTTAT 1067
 280 AsnLeuThrIleGlnGluPheArgLeuAlaTyrIleAspTyrTyrIleAsnAspIleIle 299
 1068 GACTTATTTAATTTGTTTGAACAATGTTTCTTCAATTTCCCTGGAGTGTGACTATTGA 1127
 300 AspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGlu 319
 1128 AGGGTAAAGACTTTTCTTAATATTGCGATGGCAACTTTAGAAATTGATTAAGTTTAA 1187
 320 ArgValIleAspPheSerTyrAsnPheGlyTyrGlnHisLeuGlnLeuValAsnCysIle 339
 1188 TTTTGACAGTTTCCCACTTGAAGTCAAAATCTCAAAAGGCTTAATTTCACTTCCAC 1247
 340 PheGlyGlnPheProThrLeuIleIleAspIleIleAspIleIleThrIleThrAsn 359
 1248 AAAGTGGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAAGTTTCTAGATCTCAGT 1307
 360 IlySGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeuSer 379
 1308 AGAAATGCTTGAATTTCAAGGTTGCTGTTCTCAAAGTATTTGGGCAACAGCTTA 1367
 380 ArgAsnGlyLeuSerPheIleGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu 399
 1368 AAGTATTTAGATCTGAGCTTCAATGTTGTTATTAACATGAGTTCAAACTTCTGGGCTTA 1427
 400 LysTyrLeuAspLeuSerPheAsnGlyValIleIleMetSerAsnPheLeuGlyLeu 419
 1428 GAACAACATAAGATCTGATTTCCAGACTTCCAAATTTGAACAATGAGTGAATTTTCA 1487
 420 GluGlnIleGluHisLeuAspPheGlnHisSerAsnLeuIlySGlyMetSerIlePheSer 439
 1488 GTATTCCTATCACTAGAAACCTCAATTAATCTTGAACATTTCTCATCTCAACAGAGTT 1547
 440 ValPheLeuSerLeuArgAsnLeuIleTyrIleAspIleSerHisThrHisArgVal 459
 1548 GCTTTCATGAGCATCTTCAATGCTTTCAGTCTGCAAGTCTTGAAGAAATGCTGGCAAT 1607
 460 AlaPheAsnGlyIlePheAsnGlyLeuSerSerIleGluValLeuIlySGlyMetAlaGlyAsn 479
 1608 TCTTTTCAGGAAGAACTTCCCTTCAGATATCTTCAAGAGCTGAGAACTTGAACCTTCTG 1667
 480 SerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPheLeu 499
 1668 GACCTCTCTCACTGTCAACTGGAGAGCTGTGCTCAACAGATTTAACTCACTTCCAGT 1727
 500 AspLeuSerGlnCysGlnIleGluGlnIleuSerProThrAlaPheAsnSerLeuSerSer 519
 1728 CTTGAGATCTTAATATGAGCCCAACAACCTCTTTTCAATGATACGTTTCTTAATAG 1787
 520 LeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyrIle 539
 1788 TGTCTGAATCCCTCCAGGTTCTTGATTAAGTCAATCAATCAATATGACTTCCAAAAA 1847
 540 CysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerIleIlySG 559
 1848 CAGGAATCAAGACATTTTTCAGATGCTAGCTTTCTTAATCTTAATCTTCAAGATGACTTT 1907
 560 GlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
 1908 GCTTGATCTTGAACAACAGAGTTTCCGCAATGATGATCAAGCAACAGAGGAGCTCTTG 1967
 580 AlaCysThrCysGlnHisGlnSerPheLeuGlnTyrIleIlyAspGlnArgGlnIleLeu 599
 1968 GTGGAAGTTGAAGCAATGTGCAACACTTCAATTAACAGATTAACAGGAGCTGTGCTG 2027
 600 ValGluValGluArgMetGluCysAlaThrProSerAspIlySGlnIlyMetProValLeu 619
 2028 AGTTGAAATATCACTGTGAGATGAATAAGACATCATTTGTGTGTGCTGTCTCACTGTG 2087

Db	620	SeerLeuAenlleThrCysGlmMetksnlyshTrilleeGlyValSerValLeuSerVal	633
Qy	2088	CTTGTAGTATCTGTTGTAGACAGTCTGTGCTATAAAGTTCTAATTTTACCTGATCCTCTT	2147
Db	640	LeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeuLeu	659
Qy	2148	GCTGGCTGCATAACTATATGTATAGAGTGAACAACTCTATGATGCTTTTGTATCTACTCA	2207
Db	660	AlaGlyCysIleLeuTyrGlyArgGlyGlnSerIleTyrAspAlaPheValIleTyrSer	679
Qy	2208	AGCCAGATGAGAGTGGGTGAAGAAATAGCTAGTAAAGATTTAAAGAAAGAGGGTGCT	2267
Db	680	SerGlnAspGlnAspTyrValArgAsnIleuLeuValLysAsnLeuGlnGlyValPro	699
Qy	2268	CCATTTCAGCTCTGCTCTCACTACAGAGACTTTATTTCCGGGTGTGGCCATTGCTGCCAC	2327
Db	700	ProPheGlnLeuCysLeuHisTyrTyrArgAspPheIleProGlyValAlaIleAlaAsn	719
Qy	2328	ATCATCCCATGAAAGTTTCCATPAAAGCCGAAAGGTGATTTGTGTGGTGCTCCACACATTC	2387
Db	720	IleIleHisGlnGlyPheHisLysSerArgLysValIleValValSerGlnHisPhe	739
Qy	2388	ATCCAGACCCCGTGGTGTATCTTTTAAATATGAGATTGCTCAGACCTGSCAGTTTCTGAGC	2447
Db	740	IleGlnSerArgTyrPyrCysIlePheGlnTyrGlnIleAlaGlnIleTrpGlnPheLeuSer	759
Qy	2448	AGTCGTGTGTGATCATCTTCATTTGCTGCTGAGAAAGTGGAGAAAGCCCTGCTCAGAGAG	2507
Db	760	SerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArgGln	779
Qy	2508	CAGGTGAGAGCTGTACCGCCTTCTCAGCAGAGAACTTACCTGGAGTGGAGAGACAGTGTCT	2567
Db	780	GlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrPyrGlnAspSerVal	799
Qy	2568	CTGGGCGCGGCACATCTTCTGGAGAGAGTCAAGAAAGCCCTGCTGGAGTGAATTCATGG	2627
Db	800	LeuGlyArgHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlyLysSerTrp	819
Qy	2628	AATCCAGAGAGAAACAGTGGGTACAGAGATGCATTTGGCAGAGAGCAACATCTTATC	2681
Db	820	AsnProGlnGlnTyrThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle	837
RESULT 9			
AAE16116			
ID	AAE16116	standard; protein; 837 AA.	
XX	AC	AAE16116;	
DT	26-MAR-2002	(first entry)	
DE	Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.		
KW	Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder; interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.		
OS	Homo sapiens.		
FT	Key	Location/Qualifiers	
FT	Misc-difference 211	/label= Unknown	
FT	FT	/note= "Encoded by AAY"	
PN	WO200190151-A2.		
PD	29-NOV-2001.		
PF	23-MAY-2001; 2001WO-US016766.		
PR	25-MAY-2000; 2000US-0207558P.		
PA	(SCHE) SCHERING CORP.		
PI	Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y,		

XX WP1: 2002-083085/11.
DR N-PSDB; AAD26506.
XX
XX New DNAX Toll like receptor (DTRL) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
PS
XX Claim 3; Page 240-243; 297pp; English.
XX
XX The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTRL) protein and their corresponding
CC nucleic acids. The DTRL is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTRL is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTRL is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTRL or its various fragments. The
CC purified DTRL can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTRL or cells that express it. The present sequence is
CC human DTRL protein, alternative version. The DTRL4 gene is located on
CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
CC be similar to the sequence shown in page 41 (AAB16102). However these
CC sequences differ at several locations
XX
XX Sequence 837 AA;
SQ

Alignment Scores:
Pred. No.: 0 Length: 837
Score: 4308.50 Matches: 836
Percent Similarity: 95.22% Conservative: 0
Best Local Similarity: 95.22% Mismatches: 1
Query Match: 64.08% Indels: 41
DB: 5 Gaps: 1

US-09-396-985B-3 (1-3811) x AAB16116 (1-837)

QY 48 ATGTCGCTCGCGGCTGCGCTGGAGACTGTATCCAGCCATGGCTTCTCTCTGCGTG 107
DB 1 MetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCysVal 20
QY 108 AGACCAAGAAAGCTGGGAGCCCTCGCTGAGACTTTGGCCCTTAAACACACAGAAAGACTGG 167
DB 21 ArgProGlnSerTyrGluProCysValGlu----- 30
QY 168 CATGAAACCCAGAGCTTCAGACTCCGAGCCTCAGCCCTTACCCCGATTCCATTGCTT 227
DB 30 ----- 30
QY 228 CTTCGTAATGCTGCGCGTTTATACGAGAGTGTTCTTAATATTACTTATCAATGATG 287
DB 31 -----ValProAsnIleThrTyrGlnCysMet 39
QY 288 GAGCTGAATTTCTACAAAATCCCGACAACTCCCTTTCAACCAAGAAAGCTGGAGCTG 347
DB 40 GluLeuAsnPheTyrLysIleProAsnLeuProPheSerThrTyrAsnLeuAspLeu 59
QY 348 AGCTTAAATCCCTAGAGCATTTAGAGCACTATAGCTTTCAAGTTTCCAGAACTGACG 407
DB 60 SerPheAsnProLeuAspArgIleLeuAlaLysTyrSerPhePheSerPheProGluLeuGln 79
QY 408 GTGCTGATTTATCCAGGCTGTGAATCCAGACAAATTTGAAGATGGGGCATATCAGACCTA 467
DB 80 ValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSerLeu 99
QY 468 AGCCACCTCTCTACTTAAATATTGACAGAAACCCCATCCAGAGTTTACGCTGGAGCC 527

Db 100 SerHisLeuSerThrIleuLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
QY 528 TTTTCGAGCTATTCAGATTTAAGAGCTGTGGCTGTGGAGCAAAATCAGACTTCGA 587
Db 120 PheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSerLeu 139
QY 588 GAGAACTTCCCAATCTGACATCTCAAAAATTGAAAAGAACTTAATGTGGCTCAAACTTT 647
Db 140 GluAsnPheProIleGlyHisLeuLysThrIleuLysGluLeuAsnValAlaHisAsnLeu 159
QY 648 ATCCAACTCTTCAAAATTACCTGAGATATTTTCTAATCTGACCAATCTTAAGACCTTGAAC 707
Db 160 IleGlnSerPheLysLeuProGlnLysPheSerAsnLeuThrAsnLeuGlnHisLeuAsp 179
QY 708 CTTTCAGAGAAAGAAATGAAATGATATTTATTTGACAGACCTTGGGGGTCTACATCAAAAG 767
Db 180 LeuSerSerAsnLysIleGlnSerIleLysCysThrAspLeuArgValLeuHisGlnMet 199
QY 768 CCCCTACTCAATCTCTTTAGACCTGTCCCTGAAACCTTGAACCTTTATCCAAACGAGT 827
Db 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeu***ProMetAsnPheIleGlnProGly 219
QY 828 GCATTTAAAGAAATTAAGCTTCAATTAAGCTGACTTAAGAAATAATTTGATAGCTTAAT 887
Db 220 AlaPheLysGlnLysIleArgLeuHisLysLeuThrIleuArgAsnAsnPheAspSerLeuAsn 239
QY 888 GTAATGAAAACTGTATTCAGAGCTGTGGCTGTTTGAAGTCCATGGTTGGTCTGGGA 947
Db 240 ValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeuGly 259
QY 948 GAATTTAGAATGAAAGAAACTTGAAAAAGTTGACAAATCTGCTAGAGGCTGTGC 1007
Db 260 GluPheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeuCys 279
QY 1008 AATTGACACTGAGAAATTCGACTTAAGCACTTAAGACTTACTGACTCGATGATATTAT 1067
Db 280 AsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIleIle 299
QY 1068 GACTTTATTAATGTTTGAAGAAATGTTCTCATTTTCCCTGGTGGTGGTCAATTGAA 1127
Db 300 AspLeuPheAsnLysLeuThrAsnValSerSerPheSerLeuValSerValIleGln 319
QY 1128 AGGGTAAAGACTTTTCTTAATAATTCGATGCGAACATTTAGAAATTAAGTTAACTGAAA 1187
Db 320 ArgValLysAspPheSerTyrAsnPheGlyTyrGlnHisLeuGlnLeuValAsnGlyLys 339
QY 1188 TTTGACAGCTTCCACATTAAGAACTCAAACTCTCTCAAAAAGCTTACCTTCCATCCAC 1247
Db 340 PheGlyGlnPheProThrIleuLysLeuLysSerLeuLysArgLeuThrPheThrSerAsn 359
QY 1248 AAAGGTGGGAATGCTTTTTCAGAAATGATCTACCAAGCTTGAGTTTCTAGATCTCAGT 1307
Db 360 LysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGlnPheLeuAspLeuSer 379
QY 1308 AGAAATGGCTTGAATTCAAAGGTGCTGTCTCAAAAGTATTTGGGACAAACAGACTTA 1367
Db 380 ArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyIleThrIleSerLeu 399
QY 1368 AAGTATTTAGATGTGAGCTTCAATGTGTATTATTCATGAGTTCAAACTTCTGGGCTTA 1427
Db 400 LysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419
QY 1428 GAACAACTGAAACATCGATTTCCAGACTTCCAAATTTGAAACAAATGAGTGAATTTCA 1487
Db 420 GlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPheSer 439
QY 1488 GTAATCCATCACTAGAAACCTCATTTACCTTGAACATTTCTCATACTCAACAGAGTT 1547
Db 440 ValPheLeuSerLeuAspGlnLeuIleTyrLeuAspIleSerHisThrHisThrArgVal 459
QY 1548 GCTTTCAATGCAATCTTCAATGGCTGTGCTGAGTCTCGAAGCTTTGAAATGGCTGGCAAT 1607
Db 460 AlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGlyAsn 479

QY 1608 TCTTTCCAGAAAACCTTCCTTCAGATATCTTCAGAGAGCTGAGAAACTTGACTTCCGTG 1667
Db 480 SerPheGlnGluAsnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPheLeu 499
QY 1668 GACCTCTCTCAGTGTCAACTGGAGGAGTTGTCTCCAAAGCACTTTAACTCACTCTCCAGT 1727
Db 500 AspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSerSer 519
QY 1728 CTTTCAGGTAATTAATTAAGCCCAACAACTTCTTTTCAATGGAATAGCTTCCATAAG 1787
Db 520 LeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyrLys 539
QY 1788 TGTGTGAATCCCTCCAGAGTCTTGAATTAACAGTCTCAATCAATCAATGACTTCCAAAAA 1847
Db 540 CysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLysLys 559
QY 1848 CAGGAACTAACAGCAATTTTCCAAAGTACTAGCTTCTTAATCTTACTCAGAAATGACTTT 1907
Db 560 GlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
QY 1908 GCTTGTACTTGTGAACACCAAGCTTCTCGCAATGATCAAGACAGAGGAGCTCTTG 1967
Db 580 AlaCysThrCysGlnHisGlnSerPheLeuGlnTyrIleLysAspGlnArgGlnLeuLeu 599
QY 1968 GTGGAAGTTGAACGAATGGAATGTGCAACACCTTCAGATTAAGCAGGCGATGCTGTGCTG 2027
Db 600 ValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnLysMetProValLeu 619
QY 2028 AGTTGAATATACCTGTCAAGTGAATGAATGAACCAATCATTTGTGTGTGCTCTCAGTGTG 2087
Db 620 SerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSerVal 639
QY 2088 CTTGTGATATCTGTTGTAGCACTTCTGTCTTAATGTTTCACTTCACTGATGCTTCTT 2147
Db 640 LeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeuLeu 659
QY 2148 GCTGCTGCATTAAGATATGTAGAGGTGAAAACATCTATGAGCCTTGTATTACTACTCA 2207
Db 660 AlaGlyCysIleLysTyrGlnArgGlnLeuAsnIleTyrAspAlaPheAlaIleTyrSer 679
QY 2208 ACCCAGAGTGAAGACTGGTGAAGAAATGACTTAAGAAATTTAGAAAGAGGGTGCCT 2267
Db 680 SerGlnAspGluAspTyrValArgAsnGlnLeuValLysAsnLeuGlnGlnValPro 699
QY 2268 CCATTTACGCTCTGCTTTCATCAACAGAGACTTTATTCCTGGGTGGCCATTCCTGCCAAC 2327
Db 700 ProPheGlnLeuCysLeuHisTyrTyrArgAspPheIleProGlyValAlaIleAlaAsn 719
QY 2328 ATCATCATGAAGTTTCCATTAAGAACCCGAAAGGTGATTTGTGTGGTGTCCAGCACTTC 2387
Db 720 IleIleHisGlnGlnPheHisLysSerAspArgLysValIleValValSerGlnHisPhe 739
QY 2388 ATCCAGAGCCGTGTGTATCTTTGAATATGAATTTCTCAGACCTGCGAGTTTCTGAC 2447
Db 740 IleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGlnThrTyrGlnPheLeuSer 759
QY 2448 AGTCGTCTGTGATATCTTCAATGTGCTCGCAAGAGTGGAGAAACCTTGTCCAGGCGAG 2507
Db 760 SerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuAspGln 779
QY 2508 CAGGTGAGCTGTAACCGCTTCTCAGCAGAGAAACATTTACCTGAGTGGAGGACAGTGTCT 2567
Db 780 GlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnLysTyrLysAspSerVal 799
QY 2568 CTGGGGCGGACATCTTTCAGAGCAGACTCAGAAAAGCCCTGTGATGTAATATCATG 2627
Db 800 LeuGlyArgHisIlePheThrPyrArgLeuArgLysAlaLeuLeuAspLysLysSerTyr 819
QY 2628 AATCCAGAAAGAAACAGTGGGTACAGAGATGCATTTGGCAGGAAGCAACATCTATC 2681
Db 820 AsnProGlnGlyThrValGlnThrGlyCysAsnTyrGlnGlnAlaThrSerIle 837


```

Db      421  LeuAspIseSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 440
QY      1578  AGCTCGAAGACTCTTGAAAAATGCGTGGCAATTTCTTCCAGAAAACATCTTCCAGATATC 1637
Db      441  SerLeuGlnValLeuLeuSerMetAlaGlyAsnSerPheGlnIleAsnPheLeuProAspIle 460
QY      1638  TTCACAGAGCTGAGAAAACCTTGACCTTCTGAGACCTCTCTGAGTGCATGAGCAGATTG 1697
Db      461  PheThrGlnLeuLeuArgAsnLeuThrPheLeuAspLeuSerGlnGlySerGlnLeuGlnLeu 480
QY      1698  TTCCTCAACAGCATTTAACTCACTCTCCAGTCTTCCAGTACTAAATATGACCAACAAAC 1757
Db      481  SerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsn 500
QY      1758  TTCTTTTCATGTGATAGTATGCTTCTTAACTGATGTCGTAACCTCCCTCCAGGTTCTTGA 1817
Db      501  PhePheSerLeuAspThrPheProGlyLysCysLeuAsnSerLeuGlnValLeuAspGly 520
QY      1818  AGCTCAATCAATCAATATGACTTCCAAAAACAGAACTACAGCATTTTCCAGATGACTTA 1877
Db      521  SerLeuAsnHisIleLeuThrSerLysLysGlnGlnLeuGlnHisPheProSerSerLeu 540
QY      1878  GCTTTCTTAAATCTTACTCAGAAATGACTTTGCTTGTATCTTGTGAACAACAGATTTCTG 1937
Db      541  AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
QY      1938  CAATGATATCAAGACCAAGAGGAGCTCTTGTTGAGATTGAAGATGAATGATGCAACA 1997
Db      561  GlnThrPheLysAspGlnArgGlnLeuValGlnValGlnArgMetGlnCysAlaThr 580
QY      1998  CCTTCAGATTAAGACGAGCATGCTGCTGCTGAGTTGATATCACTGTCAGATGAATTAAG 2057
Db      581  ProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsnLys 600
QY      2058  ACCATCATTTGCTGTCGCTCTCAAGTGTGCTTGTAGTATCTGTTGAGCATTTCTGTC 2117
Db      601  ThrIleIleGlnLysValSerValLeuSerValLeuValSerValAlaValLeuVal 620
QY      2118  TATTAAGTTCTATTTTCCCTGATGCTCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 2177
Db      621  TyrLysPheThrPheHisLeuMetLeuValGlyCysIleLysTyrGlyArgGlyGln 640
QY      2178  AACATCATATGATGCTTGTATCTACTCAAGCCAGATGAGGATGAGTATGAGTATGAG 2237
Db      641  AsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTrpValArgAsnGln 660
QY      2238  CTAGTAAAGAATTTAGAAAGAGGGTGCCTTCATTTGAGCTCTGCTTCACTACAGAGAC 2297
Db      661  LeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuGlnCysLeuHisTyrArgAsp 680
QY      2298  TTTATTTCCCGGTGTGGCATTTGCTGCGCAACATCATCATGAAGTTTCCATAAAGCCGA 2357
Db      681  PheIleProGlnValAlaIleAlaAlaAsnIleIleHisGlnGlyPheHisLysSerArg 700
QY      2358  AAGGTGATGTGTGGTGTGCTCCAGCACTTCACTCAGAGCCGCTGAGTATCTTGAATAT 2417
Db      701  LysValIleValValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGlnTyr 720
QY      2418  GAGATTGCTCAGACCTTGAGCATTTCTGAGCAGTGTGCTGATCATCTTCAATGTCCTG 2477
Db      721  GlnIleLeuGlnThrTrpGlnPheLeuSerSerArgLysIleIlePheIleValLeu 740
QY      2478  CAAAGAGTGAAGAAAGACCTGCTCAGCAGCAGGTGAGCTGTAACCCCTTCTCAGAGG 2537
Db      741  GlnLysValGlnLysThrLeuLeuArgArgGlnValGlnLeuTyrArgLeuLeuSerArg 760
QY      2538  AACACTTACCTGAGTGAAGAGACAGTGTCTGAGGAGGAGCAATCTTCTGAGACGATC 2597
Db      761  AsnThrTyrLeuGlnTrpGlnLeuSerValLeuGlnArgHisIlePheTrpArgAlaGln 780
QY      2598  AGAAAGCCCTGCTGATGTTAAATCATGGAATCCAGAAAGAAACAGTGGTATCAGATGC 2657

```

```

Db      781  ArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlyThrValGlyThrGlyCys 800
QY      2658  AATTGGCAGAGAACCAACATCTATC 2681
Db      801  AsnTrpGlnGlnAlaThrSerIle 808

RESULT 11
ID      AD057785
AD057785 standard; protein; 808 AA.
AC      AD057785;
DT      12-AUG-2004 (first entry)
XX
DB      Gorilla toll-like receptor 4 SEQ ID NO:6.
XX
KM      toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW      immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KM      sepsis; severe sepsis; septic shock; asthma; gorilla.
XX
OS      Gorilla gorilla.
XX
PN      MO2004042365-A2.
XX
PD      21-MAY-2004.
XX
PF      03-NOV-2003; 2003MO-US036247.
PR      01-NOV-2002; 2002US-0423113P.
XX
PA      (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI      Messier W;
DR      WPI; 2004-400726/37.
DR      N-PSDB; AD057783, AD057784.
XX
PT      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT      sequence of the Old World monkey with that of a human.
XX
PS      Example 1; SEQ ID NO 6; 111pp; English.
XX
CC      The invention relates to a novel method for identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an old world monkey
CC      comprising comparing the TLR4 polynucleotide sequence of the Old World
CC      monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC      method of the invention has antibacterial, immunosuppressive, and
CC      antiasthmatic activity. The method is useful in identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC      change may be associated with reduced sensitivity to Gram-negative
CC      bacterial infection. The methods, agents and composition are useful in
CC      treating sepsis, severe sepsis or septic shock and asthma. The present
CC      sequence represents gorilla TLR4.
XX
SQ      Sequence 808 AA;

Alignment Scores:
Pred. No.: 0
Score: 4167.00
Percent Similarity: 99.75%
Best Local Similarity: 99.38%
Query Match: 61.97%
DB: 8
Length: 808
Matches: 803
Conservative: 3
Mismatch: 2
Indels: 0
Gaps: 0

US-09-396-985B-3 (1-3811) x AD057785 (1-808)

QY      258  GTGGTCTTAATATTACTTATCATGATGAGTGAATTTCTTCAAAAAATCCCGACACAC 317
Db      1  ValValProAsnIleThrTyrGlnCysMetGlnLeuAsnPheTyrLysIleProAspAsn 20
QY      318  CTCCTCTTCAACCAAGAACTGAGCTGAGCTTTAATCCCTGAGGACATTTAGGACAC 377

```

Db 21 LeuProPheSerThriTyrsaenLeuAspLeuSerPheasnProleuAtrghisLeuGlySer 40
 QY 378 TATAGCTCTTCAGTTTCCAGAACTGACAGCTGTGATTTATCCAGCTGTGAAATCCG 437
 Db 41 TySerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluLeuGln 60
 QY 438 ACAATGAAAGATGGGCGATATCAGAGCTTAAGCCACCTCTCTCAATTAATATGACAGCA 497
 Db 61 ThrIleGluAspIleValTyrglnSerLeuSerHisleuSerThriLeuIleLeuThrgly 80
 QY 498 AACCCCATCCAGAGTTTAAAGCCCTGGAGACCTTTTCTGAGCTATCAAGTTTACAGAACTG 557
 Db 81 AsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIlySleu 100
 QY 558 GTGGCTGTGGAGCAATCTGAGATCTGTGAGAACTTCCCACTTGGACATCTCAAAACT 617
 Db 101 ValAlaValAlaGlnThrsanLeuAlaSerLeuGluAsnProIleGlyHisLeuIlySthr 120
 QY 618 TTGAAAGAACTTAATATGCTGCTCAACAATCTTATCCAAATCTTCAAAATTAATGAGTATTT 677
 Db 121 LeuIlyGluLeuAsnValAlaHisAsnLeuIleGlnSerPheIlySleuProGluTyrrhe 140
 QY 678 TCTAATCTGACCAATCTGAGCACTTGGACCTTTCCAGCAACAAGATTCAAAGTATTTAT 737
 Db 141 SerAsnLeuThrsanLeuGlnIlyTyrrLeuAspLeuSerSerAsnIlyIleGlnSerIleTy 160
 QY 738 TGGACAGACTTGGGGTTCACATTCAAATGCCCTCTACTCAATCTCTTTAGACTGTGC 797
 Db 161 CysThrsanLeuArgValLeuHisGlnMetProleuLeuAsnLeuSerLeuAspLeuSer 180
 QY 798 CTGAACCTTAAGCACTTATCCAAACAGAGGCTATTAAGAAATTAAGGCTTCAATAGCTG 857
 Db 181 LeuAsnProMetThrPheIleGlnProGlyAlaPheIlySleuIleArgLeuHisIlySbleu 200
 QY 858 ACTTAAGAATAATTTTGAATGATTAATTAATGATAAGAACTTGTAATTCAGAGCTGTGCT 917
 Db 201 ThrLeuArgAsnAsnPheAspSerLeuAsnValMetIlyThrcysIleGlnIlyLeuAla 220
 QY 918 GGTTTGAAGTCCATGTTGGTTCCTGGAGAAATTAAGAAATGAAGAACTTGGAAAG 977
 Db 221 GlyLeuGlnValArgArgLeuValLeuGlyGluPheArgAsnGluIlyAsnLeuGluIly 240
 QY 978 TTGGAACAATCTGCTAGAGGGCTGTGCAATTTGCAATTTGCAAGAAATTCGATTAAGA 1037
 Db 241 PheAspIlySerAlaLeuGlnIlyLeuCysAsnLeuThriIleGlnIlyPheArgLeuAla 260
 QY 1038 TACTAGACTACTACCTCGATGATATTAATTAATTAATTAATTAATTAATTAATTAAT 1097
 Db 261 TyrrLeuAspIlyTyrrLeuAspAspIleIleAspLeuPheAsnCysLeuThrsanValSer 280
 QY 1098 TCAATTTCCCTGGTGAAGTGTGACTATTAAGAAAGGTAAGAACTTTTCTTAATTTGCGA 1157
 Db 281 SerPheSerLeuValSerValThriIleGlnArgValIlyAspPheSerTyrrAsnProGly 300
 QY 1158 TGGCAACATTTAATAATTAATTAATTAATTAATTTGCAAGTTTCCCACTTGAACCAAC 1217
 Db 301 TrpGlnHisLeuGlnLeuValAsnCysIlySthrPheGlyGlnPheProThrsanLeuIlySbleu 320
 QY 1218 TCTCTCAAAAGGCTTACTTCACTTCCAAACAAAGTGGAGATGCTTTTTCAGAACTTGAT 1277
 Db 321 SerLeuIlyArgLeuThrsanThrsanSerAsnIlyGlyAlaAsnAlaPheSerGluValAsp 340
 QY 1278 CTRCCAAAGCTTGAAGTTTCAAGATCTCAAGTAAGAAATGGCTTGAAGTTTCAAGGTTGCTG 1337
 Db 341 LeuProSerLeuGlnPheLeuAspLeuSerArgAsnGlyLeuSerPheIlySbleuCysCys 360
 QY 1338 TCTCAAGATGATTTGGGACCAACAGAGCTTAAGATTAATTAATTAATTAATTAATTAAT 1397
 Db 361 SerGlnSerAspPheGlyThrsanThrsanSerLeuIlyTyrrLeuAspLeuSerPheAsnGlyVal 380
 QY 1398 ATTACATGAGTTCAAACTTCTGGGCTTAAGAAACAATGACATCTGATTTTCAGACAT 1457
 Db 381 IleThrsanSerSerAsnPheLeuGlyLeuGlnGlnLeuGlnIleAsnIlySbleuAspPheGlnHis 400

QY 1458 TCCAAATTTGAAACAATGAGTGAAGTTTTCAGTATTCATCACTCAGAAACCTCATTTAC 1517
 Db 401 SerAsnLeuIlyGlnMetSerGluPheSerValPheLeuSerLeuArgAsnLeuIlyTy 420
 QY 1518 CTGACATTTCTCATACTCACAACAGAGTGTGCTTCAATGGAATCTTCAATGGCTTGTGC 1577
 Db 421 LeuAspIleSerHisThrsanThrsanArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 440
 QY 1578 AGTCTGAAAGTCTTGAATAATGGCTGGCAATCTTTCCAGAGAAACCTTCTTCCAGATATC 1637
 Db 441 SerLeuGlnValLeuIlySmetAlaGlyAsnSerPheGlnGluAsnPheLeuProAspIle 460
 QY 1638 TTCACAGAGCTGAGAAACTTGAACCTTCCAGACCTTCTCAGAGTCAACTGAGCAGTTG 1697
 Db 461 PheThrsanLeuArgAsnLeuThrsanPheLeuAspLeuSerGlnCysGlnLeuGlnIlyLeu 480
 QY 1698 TCTCCAAACAGACTTAATCACTCTTCCAGTCTTCCAGTACTAATATGAGCCACAAC 1757
 Db 481 SerProThrsanAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsn 500
 QY 1758 TTTCTTTCACTGGATACGTTTCTTAAAGTCTGAACTCCCTCCAGGTTCTTGATTC 1817
 Db 501 PhePheSerLeuAspThrsanPheProTyrrCysLeuAsnSerLeuArgValLeuAspTy 520
 QY 1818 AGTCTCAATCACATPATGACTTCCAAAACAGAGCACTACAGACTTTTCCAGTACTCTA 1877
 Db 521 SerLeuAsnHisIleMetThrsanSerIlySlyGlnIlyLeuGlnHisPheProSerSerLeu 540
 QY 1878 GCTTTCTTAATCTTAATCTGAGATGACTTGTGCTGTGATCTTGTGAACACAGAGTTTCTG 1937
 Db 541 AlaPheLeuAsnLeuThrsanThrsanAspPheAlaCysThrsanGlnHisGlnSerPheLeu 560
 QY 1938 CAATGATCAAGACCAAGGAGGAGCTCTTGTGGAAGTTGAACGAATGAATGTGCAACA 1997
 Db 561 GlnTrpIleIlyAspGlnArgGlnLeuLeuValGlnValArgMetGlnCysAlaThr 580
 QY 1998 CCTTCAGATTAACAGGAGCAATGCTGTGCTGCAATTTGAATATGACCTGTGAGATTAAG 2057
 Db 581 ProSerAspIlyGlnIlyMetProValLeuSerLeuAsnIleThrcysGlnMetCysIly 600
 QY 2058 ACCATCATGTGTGTGCTGCTCTCAGTGTGCTGTGATCTGTGTGACAGTTCTGTGC 2117
 Db 601 ThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaAlaValLeuVal 620
 QY 2118 TATTAAGTTATTTTCACTGATGCTTCTTGTGCTGTGCTGCAATAAGTATGAGGTGA 2177
 Db 621 TyrrLeuPheTyrrPheHisleuMetLeuAlaGlyCysIleIlyTyrrGlyArgGlyIly 640
 QY 2178 AACATCTAAGAGCCTTGTGTTATCTAATCAACAGAGAGAGAGACCTGGTAAAGTGA 2237
 Db 641 AsnValTyrrAspAlaPheValIleTyrrSerSerGlnAspGlnAspTrpValArgAsnGln 660
 QY 2238 CTAGTAAGAATTTGAAGAAGGGGTGCTCAATTTCACTGTGCTGCTTCACTACAGAGAC 2297
 Db 661 LeuValIlyAsnLeuGlnIlyValAlaProPheGlnLeuCysLeuHisIlyTyrrArgAsp 680
 QY 2298 TTTATTTCCGCTGTGGCCATCTCTGCAACATCATCATGAAAGTTTCCATAAAGCCGA 2357
 Db 681 PheIleProGlyValAlaIleAlaIleAsnIleIleHisGlnIlyPheHisIlySerArg 700
 QY 2358 AAGGTGATTTGTGTGTGTCAGAGCACTTCAACAGAGCCGTGGTATCTTTGAATAT 2417
 Db 701 LysValIleValAlaValSerGlnHisPheIleGlnSerArgTrpCysIlePheGlnIly 720
 QY 2418 GAGATTGTCTCAGACCTGAGAGTTTCTGAGCAGTGTGCTGTGATATCTTCAATGTCCTG 2477
 Db 721 GluIleAlaGlnThrsanThrsanPheLeuSerSerArgAlaGlyIleIlePheIleValLeu 740
 QY 2478 CAGAAAGTGAAGAAGACCTGTCTCAGAGCAAGGTGAGCTGTACCGCTTCCAGACAG 2537
 Db 741 GlnIlyValGlnIlyThrsanLeuArgGlnGlnValGlnLeuTyrrArgLeuSerArg 760

QY 2538 AACACTTACCTGAGTGGAGAGACAGTGTCTGGGGCGGACATCTTGTGAGACAGATC 2597
 |||||
 Db 761 AenThTyLeuGlutTrpGluApsSerValLeuGlYArgHisIleHetTrpAglAglLeu 780
 |||||
 QY 2598 AGAAAAGCCCTGCTGATGTAATCATGGAATCCAGAAAGAAACAGTGGGTACAGGATGC 2657
 |||||
 Db 781 ArgYAlaIleuLeuApsGlySerSerTrpAenProGluGlyThrValGlyThrGlyCys 800
 |||||
 QY 2658 AATTGGCAGGAGAACATCTATC 2681
 |||||
 Db 801 AenTrpGlnGlnAlaThrSerIle 808
 |||||
 RESULT 12
 ADO57803
 ID ADO57803 standard; protein; 808 AA.
 AC ADO57803;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Chimpanzee toll-like receptor 4 SEQ ID NO:24.
 XX
 KM toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KM sepsis; severe sepsis; septic shock; asthma; chimpanzee.
 XX
 OS Pan troglodytes.
 XX
 PN WO2004042365-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 03-NOV-2003; 2003MO-US036247.
 XX
 PR 01-NOV-2002; 2002US-0423113P.
 XX
 PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
 XX
 PI Messier W;
 XX
 DR WPI; 2004-400726/37.
 DR N-PSDB; ADO57801, ADO57802.
 XX
 PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX
 PS Disclosure; SEQ ID NO 24; 111pp; English.
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents chimpanzee TLR4.
 XX
 SQ Sequence 808 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 808
 Score: 4164.00 Matches: 803
 Percent Similarity: 99.63% Conservative: 2
 Best Local Similarity: 99.38% Mismatches: 3
 Query Match: 61.93% Indels: 0
 DB: 8 Gaps: 0
 US-09-396-985B-3 (1-3811) X ADO57803 (1-808)

QY 258 GTGTTCCCTAATATTACTTATCATGATGAGAGCTGAATTTCTAACAATATCCCGACAAC 317
 |||||
 Db 1 ValValProAsnIleThrTyrlncYsMetGluLeuAenPheTyIleIleProAsn 20
 |||||
 QY 318 CTCCTCTTCTCAACAAGAACTGGACCTGACCTTTAATCCCTGAGCATTTAGGCACG 377
 |||||
 Db 21 LeuProPheSerThrIleAsnLeuApsLeuSerPheAenProLeuAglHisLeuGlySer 40
 |||||
 QY 378 TTTAGCTTCTTAGTTTCCCGAAGCTGAGGTCGTAATTTATCCAGGGTGAATTCGAG 437
 |||||
 Db 41 TyrSerPhePheSerPheProGluLeuGlnValLeuApsLeuSerArgCysGluIleGln 60
 |||||
 QY 438 ACAATTTGAAGATGGGACATATCAGAGCCCTAGCCACCTCTTACCTTATATTATTCAGAGA 497
 |||||
 Db 61 ThrIleGluApsGlyAlaTyrlncIleSerLeuSerHisLeuSerThrLeuIleLeuThrGly 80
 |||||
 QY 498 AACCCCATCAGAGTTTAGCCCTGGAGCCCTTTTGTGAGCTATCAAGTTTACAGAACTG 557
 |||||
 Db 81 AenProIleGlnSerIleuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIlySer 100
 |||||
 QY 558 GTGGCTGTGGAGACAATCTAGCATCTCTAGGAAGCTCCCATTTGGACATCTCAAAACT 617
 |||||
 Db 101 ValAlaValAlaGluThrAsnLeuAlaSerLeuGluAenPheProIleGlyHisLeuIlyStr 120
 |||||
 QY 618 TTGAAGAAGACTTAATGTGGCTCACAATCTTATCCAACTTTTCAAAATTACCTGATATTT 677
 |||||
 Db 121 LeuIlySGluLeuAenValAlaHisAsnLeuIleGlnSerPheIlyLeuProIlyTrpHe 140
 |||||
 QY 678 TCTAATCTGACCAATCTAGAGCATTTGACCTTTCCAGCAACAAGATTCAAGATTTAT 737
 |||||
 Db 141 SerAenLeuThrAsnLeuGluHisLeuApsLeuSerSerValIleGlnSerIleTy 160
 |||||
 QY 738 TGCACAGACTTGGCGGTCTTACATCAAAATGCCCTACTCAATCTCTTAAACCTGATCC 797
 |||||
 Db 161 CysTrpAspLeuArgValLeuHisGlnMetProLeuLeuAenLeuSerLeuApsLeuSer 180
 |||||
 QY 798 CTGAACCCATGAACTTTATCCAAACAGGTGATTTAAAGAAATTAGGCTTATAGCTG 857
 |||||
 Db 181 LeuAenProMetAsnPheIleGlnProGlyAlaPheIlySGluIleArgLeuHisIlySer 200
 |||||
 QY 858 ACTTTAAGAAATTAATTTTGTATAGTTAAATGTAATGAAAACTTGTATTCAGGCTCGCT 917
 |||||
 Db 201 ThrLeuArgAsnAsnPheApsSerLeuAenValMetIlyThrCysIleGlnIlyLeuAla 220
 |||||
 QY 918 GGTTTAAGAGTCCATCGTTTGTCTCGGAGAAATTGAAGAAAGAACTTGGAAAG 977
 |||||
 Db 221 GlyLeuGluValHisArgLeuValIleuGlyGluPheArgAenGluGluAenLeuGluIly 240
 |||||
 QY 978 TTTGACAAATCTGCTCTAGAGGCGCTGTGCAATTTGACCATTTGAAGAAATTCGATTAGCA 1037
 |||||
 Db 241 PheApsIlySerHisLeuGlnIlyLeuGlyAsnLeuThrIleGlnIlyPheArgLeuAla 260
 |||||
 QY 1038 TACTTAGACTTACTACCTCGATGATATTTATGACTTATTTAATTTGTTTGACAAATGTTCT 1097
 |||||
 Db 261 TyrLeuAspTyrlncLeuApsPheIleIleApsLeuPheAenCysLeuThrAsnValSer 280
 |||||
 QY 1098 TCATTTTCCCTGTGAGTGTGACTTATGAAAAGGTTAAAGACTTTTCTATATATTTCCGA 1157
 |||||
 Db 281 SerPheSerLeuValSerValThrIleIlySerValIlyAAsPheSerIlyTrpPheGly 300
 |||||
 QY 1158 TGGCAACATTTAGAAATTAGTAACTGTAAATTTGGACAGTTTCCCATTTGAAACTCAAA 1217
 |||||
 Db 301 TrpGlnHisLeuGluLeuValIlyCysIlySerPheGlyGlnPheProThrIleuIlySer 320
 |||||
 QY 1218 TCTCTCAAAAGGCTTACTTTCATCTTCCAAACAAGGTGGAAATGCTTTTTCAGAACTTGA 1277
 |||||
 Db 321 SerLeuIlyArgLeuThrPheThrSerAenIlySGlyAlaHisApsSerGluValAps 340
 |||||
 QY 1278 CTACCAAGCTTGAAGTTTATAGATCTCAGATAGAAATGCTTGAAGTTTCAAGGTTCTCT 1337
 |||||
 Db 341 LeuProSerLeuGluPheLeuApsLeuSerArgAenGlyLeuSerPheIlySGlyCysCys 360
 |||||
 QY 1338 TCTCAAGATGATTTTGGACAACAAGCTTAAGATTTATGATCTGAGCTTCAATGGTGT 1397

```

Db      |||
361 SerGlnSerAspPheGlyThrThrSerLeuSerLeuSerPheAsnGlyVal 380
QY      |||
1398 ATACCAAGTGAATCAACCTCTGGGGTTAGAAACAATAGACATCGGATTTCCAGCAT 1457
Db      |||
381 IleThrIleSerSerAsnPheLeuGlyLeuGlnGlnLeuGlnIleuAspPheGlnHis 400
QY      |||
1458 TCCAAATTTGAAACAATAGATGAGTTTTCAGTATTTCTATCAGTACAGAAAACCTCATTTAC 1517
Db      |||
401 SerAsnLeuSerGlnMetSerGlnPheSerValPheLeuSerLeuAsnGlnIleTyr 420
QY      |||
1518 CTTCAGATTTCTCATACTCACCAGAGTTGCTTTCAGTGCATCTTCAATGGCTTGCC 1577
Db      |||
421 LeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 440
QY      |||
1578 AGTCTGGAATCTTGAAGAAATGGCTGGCAATTTCTTCCAGAAAACCTTCCAGATATC 1637
Db      |||
441 SerLeuGlnValLeuSerMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIle 460
QY      |||
1638 TTCACAGAGCTGAGAAACTTGACCTTCTGAGACCTCTCAGTGTCAACTGGAGCAGATTG 1697
Db      |||
461 PheThrGlnLeuSerGlnAsnLeuThrPheLeuAspLeuSerGlnGlnLeuGlnLeu 480
QY      |||
1698 TCTCCACAGACATTTAACTCACTCTCCAGTCTTCAGGTACTAAATATAGCCACAACAC 1757
Db      |||
481 SerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsn 500
QY      |||
1758 TTCTTTTCATTGGATACGTTTCTTATATAGTGTCTGAACTCCCTCCAGGTTCTTGATTAC 1817
Db      |||
501 PhePheSerLeuAspThrPheProTyrGlyCysLeuAsnSerLeuGlnValLeuAspTyr 520
QY      |||
1818 AGTCTCAATCACTAAAGACTTCCAAAAGAGAACTACAGCAATTTCCAGAGACTA 1877
Db      |||
521 SerLeuAsnHisIleMetThrSerLeuSerGlnGlnLeuGlnHisPheProSerSerLeu 540
QY      |||
1878 GCTTTCTTAAATCTTACTCAGAAATGACTTTGCTTGTATCTTGTGAACACAGAGTTTCCTG 1937
Db      |||
541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
QY      |||
1938 CAATGATCAAGACCCAGAGGACGCTTTGGTGGAAAGTTGAACGATGGAATGTGCACA 1997
Db      |||
561 GlnThrPheLeuAspGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAlaThr 580
QY      |||
1998 CCTTCAGATAAGACGGGACGCTGCTGCTGAGTTGAATATCACCTTCAGATGAATTAAG 2057
Db      |||
581 ProSerAspGlnGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsnLys 600
QY      |||
2058 ACCATCATTTGGTGTGCTGCTCTCAGTGTGCTTGTATCTGTTGAGCAGTTCTGTC 2117
Db      |||
601 ThrIleIleGlyValSerValLeuSerValLeuValValSerValValAlaValLeuVal 620
QY      |||
2118 TATATAGTTCTATTTTCACTGATGCTTCTTGTGGCTGCATAAAGTATGGTAGAGTGA 2177
Db      |||
621 TyrIlePheTyrPheHisIleMetLeuLeuAlaGlySerIleLeuTyrGlyValGlyGln 640
QY      |||
2178 AATCATCATATATGCTTTTATATCTACTCAAGCCAGATGAGATCGGTTGAAGAAATGAG 2237
Db      |||
641 AsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspIlePheValAlaGlyAsnGln 660
QY      |||
2238 CTAGTAAAGAAATTTAGAAAGAGGGGCTCTTCATTTAGCTTCCCTTCACTACAGAGAC 2297
Db      |||
661 LeuValValSerAsnLeuGlnGlnGlyValProProPheIleuSerGlnHisIleTyrArgAsp 680
QY      |||
2298 TTATATCCGAGTGGCCATTTGCTGCCAACAATCATCATGAAGTTTCCATTAAGCCGA 2357
Db      |||
681 PheIleProGlyValAlaIleAlaIleAlaAsnIleIleHisGlnGlyPheHisIleSerArg 700
QY      |||
2358 AAGGTATTTGTTGGTGGTCCACGACTTATCCAGAGCCGCTGGTGTATCTTGAATAT 2417
Db      |||
701 LysValIleValValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlnTyr 720
QY      |||
2418 GAGATTCTGAGACCTGGCAGATTCTGAGCAGTGTGCTGGTATCATTTCAATGTCTGTG 2477

```

```

Db      |||
721 GlnIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeu 740
QY      |||
2478 CAGAGAGTGAAGAGAACCTGTCTCAGACAGACAGGTGAGACTGTACCGCTTCTCAGCAGG 2537
Db      |||
741 GlnLysValGlnLysThrLeuSerArgGlnValGlnLeuTyrArgLeuLeuSerArg 760
QY      |||
2538 AACCTTACCTGGAGTGGAGAGACAGTGTCTCGGGCGGACATCTTCTGGAGACGATC 2597
Db      |||
761 AsnThrTyrLeuGlnThrGlnAspSerValLeuGlyArgHisIlePheThrArgArgLeu 780
QY      |||
2598 AGAAAAGCCCTGCTGGATGTGAATATCATGGAATCCGAAGAAACAGTGGGTACAGATGC 2657
Db      |||
781 ArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlyThrValGlyThrGlyCys 800
QY      |||
2658 AATTGGCAGGAGCAACATCTATC 2681
Db      |||
801 AsnTrpGlnGlnAlaThrSerIle 808

RESULT 13
AAM86352
ID AAM86352 standard; protein; 799 AA.
XX
AC AAM86352;
XX
DT 15-MAR-1999 (first entry)
XX
DE Human DNAX toll-like receptor DTLR4.
XX
KW DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW Interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW modulate inflammatory function; morphological effect;
KW immunological disorder.
XX
OS Homo sapiens.
XX
XX
PN WC0850547-A2.
XX
PD 12-NOV-1998.
XX
PF 07-MAY-1998; 98MO-US008979.
XX
PR 07-MAY-1997; 97US-0044293P.
PR 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
XX
WP1: 1999-059670/05.
XX
DR N-PSDB; AAV80666.
XX
PT Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
PT metabolism, modulate inflammatory function or innate immunity responses.
XX
XX
PS Example; Page 115-117; 171pp; English.
XX
XX
CC The present invention specifically describes human DNAX toll-like
CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC in the present invention. Also described are: (1) a fusion protein
CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC an antibody or antibody fragment which specifically binds to a DTLR
CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC host cell comprising the vector of (4). The host cell of (5) can be used
CC to produce the DTLR proteins. The DTLR proteins can be used to alter
CC phosphate metabolism, to modulate inflammatory function, innate immunity
CC responses or morphological effects. The DTLR proteins can be used in the
CC treatment of conditions exhibiting abnormal expression of the receptors
CC of their ligands. These abnormalities are typically manifested by
CC immunological disorders
XX
SQ Sequence 799 AA;

```


Alignment Scores:

Pred. No.: 0 Length: 799
Score: 4141.00 Matches: 799
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.59% Indels: 0
DB: 2 Gaps: 0

US-09-396-985B-3 (1-3811) x AAW6352 (1-799)

QY 285 ATGAGAGTGAATTTCTACAAAATCCCGACAACTCCCTTCTCAACCAAGAACTTGGAC 344
DB 1 MetGluLeuasnPheTyrlYsIleProaspAsnLeuProPheSerThrIYsAsnLeuasp 20
QY 345 CTGAGCTTTAATCCCGGAGGACATTTTACGAGCATATGCTTCCAGTTTCCCGAAGACTG 404
DB 21 LeuSerPheasnProLeuAlghIshLeuGlySerTySerPhePheSerPheProGluLeu 40
QY 405 CAGGTGCTGATTTATTCAGGTGTGAATCCAGACATTTGAGATGGGCGATATCAGAGC 464
DB 41 GluValLeuasnProLeuSerArgCySgluIleGlnThrIleGluaspGlyAlaTyrgInser 60
QY 465 CTAGCCACCTCTCTACCTTAATATTGACGAAACCCCATCCAGATTAGCCCTGGGA 524
DB 61 LeuSerThIshLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaleuGly 80
QY 525 GCGTTTCTGACATCATGATTACAGAACTGTGGCTGGTGGAGACAAATCTAGACATCT 584
DB 81 AlshPheSerGlyLeuSerSerLeuGlnuPheValAlaValGluThrAsnLeuAlaser 100
QY 585 CTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAGAACTTAATGTGGCTCAAAAT 644
DB 101 LeuGluAsnPherProIleGlyhIshLeuYlshThrLeuYsGluLeuAsnValAlahIAsn 120
QY 645 CTTATCCAACTTTTCAAAATTAAGTATTTTCTTAATCTGACCAATCTAGACACTTG 704
DB 121 LeuIleGlnSerPheYsLeuProGluYrPheSerAsnLeuThrAsnLeuGluhIshLeu 140
QY 705 GACCTTTCAGCAACAAGATTCAAAAGATTATTATTTGACAGACTTGGGGGTTCTACATCA 764
DB 141 AsnLeuSerSerAsnYsIleGlnSerIleTyrcYsThrAspLeuArgValshLeuhsIghI 160
QY 765 ATGCCCTTACTCATCTCTCTTTAGACCTGTCCCTGAAACCTTATGAACTTTATCCAA 824
DB 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPhelIleGlnPro 180
QY 825 GGTGCATTTAAAGAAATTAGGCTTCATAGCTGACTTTAAGAAATTAATTTGATGATTA 884
DB 181 GlyAlaPheYsGluIleArgLeuhsIshYsLeuThrLeuArgAsnAsnPheserSerLeu 200
QY 885 AATGATATGAAAACTTGATTTACAAAGTCTGGCTGGTTTGAAGTCCATCGTTGGTTCTG 944
DB 201 AsnValaMetYsThrCySIIleGlnGlyLeuAlaGlyLeuGluValhIshAsnGluValaLeu 220
QY 945 GGAGAAATTTGAATGAAGAAACTTGGAAAGTTTGAACAATCTGCTTACAGAGGCTG 1004
DB 221 GlyGluPheArgAsnGluGlyAsnLeuGlnuYsPheAspYsSerhIshleuGluGlyLeu 240
QY 1005 TGCATTTTGAACCTTGAAGAAATTCGATTGACATTAAGATTAAGATTAATTTGATGAT 1064
DB 241 CyAsnLeuThrIleGluGluPheArgLeuAlaTyrcLeuAspYrTyrcLeuAspAspIle 260
QY 1065 ATGACCTTATTAATTTGACAAATGTTTCTTCAATTTCCCTGGGAGATGAGATATT 1124
DB 261 ILeaspLeuPheAsnCySLeuThrAsnValaSerSerPheSerLeuValSerValThrIle 280
QY 1125 GAAAGGATAAAGACTTTTCTTAATTTGATTTGAGTGGCAACATTTAGATTAAGTAACTGT 1184
DB 281 GluArgValaYsAspPheSerTyrcAsnPhelGlyTTrpGlnhIshleuGluLeuValaAsnCyS 300
QY 1185 AAATTTGGACAGTTTCCCACTGAATGAATCAAAATCTCTCAAAAGCTTACTTCACTTCC 1244

DB 301 YsPheGlyGlnPheProThrLeuYsLeuYsSerLeuYsArgLeuThrPheThrSer 320
QY 1245 AACCAAGGTGGGAATCTTTTTCAGAAAGTTGATCTCAAGCCTTGAGTTTCTAGATCTC 1304
DB 321 AsnYsGlyGlyAsnAlaPheSerGluValaAspLeuProSerLeuGluPheLeuAspLeu 340
QY 1305 AGTAGAAATGGCTTGAGTTTCAAGGTTGCTGTCTCAAAAGTATTTTGGACCAACGAC 1364
DB 341 SerArgAsnGlyLeuSerPheYsGlyCySserGlnSerAspPheGlyThrThrSer 360
QY 1365 CTAAAGTATTTAGATCTGAGCTTCAATGSGTGTATTAACATAGATTCAAACTTCTGGGC 1424
DB 361 LeuYsTyrcLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPhelLeuGly 380
QY 1425 TTAGAACACTGAACATCTGATTTCCAGCAATTCCAATTTGAAACAAATGAGTAGATT 1484
DB 381 LeuGluGlnLeuGluhIshLeuAspPheGlnhIshSerAsnLeuYsGlnMetSerGluPhe 400
QY 1485 TCAGATTTCTTCACTCAAGAAACCTCATTTACCTTGACATTTCTCATACTCAACACAGA 1544
DB 401 SerValPheLeuSerLeuArgAsnLeuIleTyrcLeuAspIleSerThIshThrArg 420
QY 1545 GTTGCTTTCAATGGCATCTTCAATGAGCTGTGTCCAGTCTGGAAGTCTGAAAAATGCTGGC 1604
DB 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValaLeuYsMetAlaGly 440
QY 1605 AATTTCTTCAGAGAAACTTCCCTTCAGATATCTTCAACAGACTGAGAAACTTGACCTTC 1664
DB 441 AsnSerPheGlnGluAsnPherProAspIlePheThrGluLeuArgAsnLeuThrPhe 460
QY 1665 CTGAGACTTCTCAAGTCACTGAGCACTGAGCACTGTGTCTCAACAGCAATTTACTACTCTCC 1724
DB 461 LeuAspLeuSerGlnCySgluGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 480
QY 1725 AGTCTCAGAGTACTAAATTAAGCCCAACAACTTTTCTTCAATGGATACGTTTCTTAT 1784
DB 481 SerLeuGlnValaLeuAsnMetSerhIshAsnAsnPheserSerLeuAspPhrPheProTyrc 500
QY 1785 AAGTGTCAATCTCCCTCCAGGTTCTGATTAAGTCAAGTCAATCACTAATGACTTCCAA 1844
DB 501 YsCySLeuAsnSerLeuGlnuValaLeuAspYrSerLeuAsnhsIleMetThrSerYs 520
QY 1845 AAACAGGAATCAAGCAATTTTCCAAAGTACTAGCTTTCTTAATCTTACTCAGATGAC 1904
DB 521 YsGlnGluLeuGlnhIshPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
QY 1905 TTTGCTTGACTTTGTGAACAACAGAGTTTCTGCAATGATTAAGGACAGAGGCGCTC 1964
DB 541 PheAlaCySThrCySgluhsIshGlnSerPheLeuGlnTrpIleYsAspGlnArgGlnLeu 560
QY 1965 TTGGTGAAGTTGAACGAATGGAATGTGCACACCTTCAGATTAAGCAGGCGATGCTGTG 2024
DB 561 LeuValaGluValaGluArgMetGluCySAlaThrProSerAspYsGlnuIshMetProVal 580
QY 2025 CTGAGTTTGAATATCACTGTGAGATGAATGAATGAACCATCATTTGATGTGCTGCTCAGT 2084
DB 581 LeuSerLeuAsnIleThrCySgluMetAsnYsThrIleIleGlyValaSerValaLeuSer 600
QY 2085 GTTGCTTGATTAATCTGTGTGAGCAGTCTGTGCTATTAAGTTCTATTTTCACTGATGCTT 2144
DB 601 ValaLeuValaValaSerValaValaValaLeuValaTyrcYsPheTyrcPhehIshLeuMetLeu 620
QY 2145 CTTGCTGCTGATTAAGTATGATGTGAGAGTGAACATATATGAGCCCTTGTTATCTAC 2204
DB 621 LeuAlaGlyCySIIleYsTyrcIshYrGlyGluAsnIleTyrcAspAlaPheValIleTyrc 640
QY 2205 TCAAGCAGATGAGAGCTGGGTGAAGATGAAGTGAATTAAGAAATTTGAAGAGGGGTG 2264
DB 641 SerSerGlnAspGluAspTyrcValaArgAsnGluLeuValaYsAsnLeuGluGlyVala 660
QY 2265 CTTCACTTTCAAGCTGTGCTTCACTACAGAGACTTATTTCCGGGTGGCCATTGCTGCC 2324
DB 661 ProProPheGlnLeuCySLeuhsIshTyrcArgAspPheIleProGlyValaAlaIleAlaAla 680

QY 2325 AACATCATCATGAAGGTTTCCATAAAAGCCGAAGGTGATTGTGTGCCAGAC 2384
DB 681 AsnIleIleHsIgluIgluPheHIsIeSerArgIysValIleValIalValSerGlnHis 700
QY 2385 TTGATCCAGAGCCGCTGCTGTATCTTGAATPAGATGCTGACACCTGGAGTTTCTG 2444
DB 701 PheIleIleSerArgIysIlePheIleGluIleValIleGlnIleThrIlePheIleu 720
QY 2445 AGCAGTGTGCTGTATCATCTTCTGATGCTGAGAGGTGAGAGACCCGCTGAGG 2504
DB 721 SerSerArgIalagIyIleIlePheIleValIleGlnIleValIleGlnIleLeuArg 740
QY 2505 CACAGGTGAGGTGTATCCGCTTCTGAGAGAGAACCTTACCTGAGTGGAGAGACAGT 2564
DB 741 GlnGlnValIgluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 760
QY 2565 GTCTGTGGGCGGACATCTTCTGAGAGAGACTGAGAAAGCCCTGCTGATGGTAATCA 2624
DB 761 ValIleuGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 780
QY 2625 TGAATCCAGAGAGACAGTGGGTGACGATGCAATGGAGAGAGAGACATCTATC 2681
DB 781 TrpAsnProGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 799
RESULT 14
AAE16093
ID AAE16093 standard; protein; 799 AA.
AC AAE16093;
DT 26-MAR-2002 (first entry)
XX Human DNAX Toll like receptor (DTLR) 4 #1.
DE Human DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW Human, DNAX Toll like receptor; DTLR; screening; immunomodulator; chromosome 9q32-33.
XX Interleukin 1; IL-1;
OS Homo sapiens.
XX MO200190151-A2.
XX 29-NOV-2001.
XX 23-MAY-2001; 2001MO-US016766.
XX 25-MAY-2000; 2000US-0207558P.
XX (SCHE) SCHERING CORP.
XX Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SMK, Liu Y;
XX WPI, 2002-083085/11.
XX N-PSDB; AAD26283.
XX New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX Claim 1; Page 35; 297pp; English.
XX The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-

CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33
XX
SQ Sequence 799 AA;
Alignment Scores:
Pred. No.: 0 Length: 799
Score: 4141.00 Matches: 799
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.59% Indels: 0
DB: 5 Gaps: 0
US-09-396-985B-3 (1-3811) x AAE16093 (1-799)
QY 285 ATGAGAGCTGAATTTCTACAAATCCCGACAACTCCCTTCTCAACCAAGACTGGAC 344
DB 1 MetGluLeuAsnPheIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 20
QY 345 CTGAGCTTTAATCCCTGAGGCACTTTAGGAGCTATAGCTTCTTCACTTCCAGAACTG 404
DB 21 LeuSerPheAsnProLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 40
QY 405 CAGGTGCTGATTTATCCAGGTGTGAATCCAGCAATGAGAGTGGGCAATTCAGAC 464
DB 41 GlnValLeuAsnProLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 60
QY 465 CTGAGCACTCTCTACCTTAATATTGACAGAAACCCATCCAGAGTTAGGCTTGAG 524
DB 61 LeuSerHisLeuSerHisLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 80
QY 525 GCCTTTCTGAGACTATCAAGTTTACAGAACTGTGTGCTGTGAGACAAATCTGACATCT 584
DB 81 AlaPheSerGlyLeuSerSerLeuGlnIleuValIleuIleuIleuIleuIleuIleuIleu 100
QY 585 CTGAGAACTTCCCATTTGAGACATCTCAAACTTTGAAAGAACTTAATGTGCTCAAT 644
DB 101 LeuGluAsnProIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 120
QY 645 CTATCCAACTCTTCAATTTACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTG 704
DB 121 LeuIleGlnSerPheIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 140
QY 705 GACCTTTCAGACAAAGATTCAGAACTATTTATGACAGACTGGGGTCTTACATCA 764
DB 141 AspLeuSerSerAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 160
QY 765 ATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGACCCCTATGAACTTTATCCAACT 824
DB 161 MetProLeuIleuAsnLeuSerLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 180
QY 825 GGTGATTTAAAGAAATTTAGGCTTCAATAGCTGATCTTAAAGAAATTTGATAGTTTA 884
DB 181 GlyAlaPheIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 200
QY 885 AATGTATGAAAACTTTGATTCAGGCTGCTGCTGTTGAAATCCATCGTTGCTTG 944
DB 201 AsnValMetIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 220
QY 945 GAGAAATTTAGAAATGAGAAAGAACTTTGAAAGTTTGAATCTTCTAGAGGCTTG 1004
DB 221 GlyGluPheArgAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 240
QY 1005 TGAATTTGACATTTGAAAGAAATTTGCAATTTGAGATTTGACTTACCTGATGATTT 1064
DB 241 CysAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 260
QY 1065 ATGACTTATTTAATTTGTTGACAAATGTTTCTTCAATTTCCCTGTGAGTGTGACTATT 1124
DB 261 IleAspLeuPheAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 280

QY 1125 GAAAGGTAAGAACTTTTCTTAATTAATTCGAGCACTTTAGATTAAGTATCTG 1184
 DB 281 GUAAGValValAspSerPheSerThrAsnGlyTyrPheGlnHisLeuGlnLeuValAsnGlyVal 300
 QY 1185 AAATTTGACAGATTTCCCACTTGAATGAAATCTGAAATCTTCAAAAGGCTTACTTTCCTGTC 1244
 DB 301 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 320
 QY 1245 AAGAAAGTGGGAATGCTTTTTCAGAAAGTGAATCTACCAAGCTTTGAGTTTCTAGATCTTC 1304
 DB 321 AsnLysGlyGlyAsnAlaPheSerGlnValAlaPheLeuProSerLeuGlnPheLeuAspLeu 340
 QY 1305 AGTAAAGAAATGCTTGAATTCGAAAGGTTGCTTCTCAAAAGTGAATTTGGACAACAGC 1364
 DB 341 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
 QY 1365 CTAAAGTATTAGATCTGAGCTTCAATGCTGTATTATCAATGAGTTCAAACTTCTTGAGGC 1424
 DB 361 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
 QY 1425 TTGGAACAACATAACATCTGGAATTTCCAGCATTTCCAAATTTGAAACAAAGATGAGTTT 1484
 DB 381 LeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPhe 400
 QY 1485 TCAGTATTCCTATCACTCAGAAACCTCAATTTACTGACATTTCTCACTCAACACAGCA 1544
 DB 401 SerValPheLeuSerLeuAspGlnLeuIleTyrLeuAspIleSerHisThrHisThrHis 420
 QY 1545 GTTGCCTTCAATGAGCATCTTCAATGCTTTCGAGTCTGAGATCTTGAATGCTGAGC 1604
 DB 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly 440
 QY 1605 AATTCCTTCCAGGAAACCTTCCTCCAGATATCTTCAACAGCTGAGAACTTGACCTTC 1664
 DB 441 AsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPhe 460
 QY 1665 CTGACACTCTCTCAGTGTCAACTGAGACAGTGTGCTCAACAGCATTTAACTGACTCTCC 1724
 DB 461 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 480
 QY 1725 AGTCTTCAAGTAAATATATGAGCCACAACTCTTTTCAATGATGATGATTCCTTAT 1784
 DB 481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProLys 500
 QY 1785 AAGTGTCTGAACCTCCCGCAGTCTTGATTAAGCTCTCAATCAACAAAGATTCCTCAAA 1844
 DB 501 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 520
 QY 1845 AAACAGGAACATAAGCACTTTTCCAAAGTCTAGACTTTTAAATCTTACTCAGAAATGAC 1904
 DB 521 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
 QY 1905 TTTGCTTGAATCTTGTGAACCAAGATTTCTGCAATGATCAAGACCAAGGCAAGCTC 1964
 DB 541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeu 560
 QY 1965 TTGCTGAATTTGAACGAATGGAATGGAACACTTCAATTAAGCAAGGCAAGCTCTG 2024
 DB 561 LeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProVal 580
 QY 2025 CTGAGTTTGAATATCACTGTCAGATGAATTAAGCACTCATGCTGCTGCTGCTGCTGCTGCT 2084
 DB 581 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 600
 QY 2085 GTGCTGTAGATCTGTGTGAGCAAGTCTGCTATTAAGTTCTATTTTCACTGATGCTT 2144
 DB 601 ValLeuValValSerValValAlaValLeuValTyrLysPheThrPheHisLeuMetLeu 620
 QY 2145 CTTCCTGCTGCTGATAAAGTATGTAAGGTAAGGTAAGCACTATGATGCTTGTATCTTAC 2204
 DB 621 LeuAlaGlyCysIleLysTyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIleTyr 640

QY 2205 TCAGCCAGATAGAGACTGCTGTAAAGATGAGTAAAGATTAAGAAAGGAGTG 2264
 DB 641 SerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlnGlyVal 660
 QY 2265 CCTCCATTTCACTGCTGCTTCACTACAGAGACTTTATTCCTCCGGTGGCCATTGCTGCC 2324
 DB 661 ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 680
 QY 2325 AACATCATCAAGAAAGTTCATTAAGACGAAAGGTAAGTGTGCTGCTCCAGCAC 2384
 DB 681 AsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValValSerGlnHis 700
 QY 2385 TTCAATCCAGAGCCGCTGTGTATCTTGAATATGAGATTCCTCAAGCTGCGAGTTCTG 2444
 DB 701 PheIleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPheLeu 720
 QY 2445 AGCAGTCTGCTGTATCATCTTCAATTCCTGCGAGAGGTGAGAAAGCCTGCTCAG 2504
 DB 721 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuArg 740
 QY 2505 CAGCAGTGGAGCTGTACCGCTTCTCAGCAGAAACACTTACCTGAGTGGAGCAGT 2564
 DB 741 GlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTrpGlnAspSer 760
 QY 2565 GTCTGTGGCGCGACACTTCTTGAAGACGACTCAGAAAGCCCTGCTGATGTAATCA 2624
 DB 761 ValLeuGlyArgHisIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 780
 QY 2625 TGGAAATCCAGAAAGAACAGTGGGTACAGATGCATTTGGCAGAGAACCAATCTATC 2681
 DB 781 TrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle 799
 RESULT 15
 ABB83162
 ID ABB83162 standard; protein; 799 AA.
 AC ABB83162;
 XX 09-AUG-2002 (first entry)
 DT
 XX
 DE Human Toll-like receptor-4, Tlr4.
 DE
 XX Human; virucide; antibacterial; fungicide; parasiticide; receptor;
 KM cytotoxic; immunostimulatory; scavenger receptor; Toll receptor;
 KM respiratory tract infection; Toll-like receptor; Tlr4.
 OS Homo sapiens.
 OS
 XX
 PN MO200235236-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 26-OCT-2001; 2001WO-FR003352.
 XX
 PR 27-OCT-2000; 2000FR-00013883.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 XX
 PT Jeanmin P, Magistrelli G, Herbault N, Bonnefoy J;
 XX WPI; 2002-383586/41.
 DR N-PSDB; ABB83318.
 XX
 PT Identifying agent that binds to scavenger receptors and signals through a
 PT cytoxic T cell response.
 PS
 PS Disclosure; Page 58-60; 71pp; French.
 CC
 CC The present invention relates to a method for identifying new therapeutic
 CC compounds (1) by selecting molecules that bind to scavenger receptors and
 CC signal through a Toll receptor. The present sequence is the protein
 CC sequence for human Toll-like receptor-4, Tlr4, which was used to

CC illustrate the method of the invention. (1) are useful as carriers and/or
 CC adjuvants in prophylactic or therapeutic vaccines, particularly where the
 CC antigen is derived from a virus, bacterium, yeast, fungus, parasite or
 CC tumour cell, especially a pathogen that causes respiratory tract
 CC infection, also more generally for inducing an immune response. (1) can
 CC also be used for specific targeting of active agents (antigens etc.) to
 CC antigen-presenting cells (especially immature dendritic cells), for
 CC subsequent internalisation by these cells

SO Sequence 799 AA:

Alignment Scores:

Pred. No.:	0	Length:	799
Score:	4141.00	Matches:	799
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	61.59%	Indels:	0
DB:	5	Gaps:	0

US-09-396-985B-3 (1-3811) x ABB83162 (1-799)

QY 285 ATGAGAGCTGAATTTCTACAAATCCCGACAACTCCCTTCTACACCAAGAACTTGAC 344
 DB 1 MetGluLeuasnPheTyrLysIleProAsnLeuProPheSerThrLysAsnLeuAsp 20
 QY 345 CTGAGCTTTATCCCTGAGGCACTTTAGGAGCTTATAGCTTCTCAGTTCCCGAAGCTG 404
 DB 21 LeuSerPheasnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 40
 QY 405 CAGGTGCTGATTTATTCAGGTGTGAATCCAGCAATTTGAAGATGGGGCATATCAGAGC 464
 DB 41 GluValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 60
 QY 465 CTAAGCACTCTCTACCTTATATTTGAACAGAAACCCCATCCAGAGTTTACCCCTGGA 524
 DB 61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
 QY 525 GCGTTTCTGAGATCATCAAGTTTACAGAAAGCTGGGTGCTGAGCAAAATCTAGCATCT 584
 DB 81 AlaPheSerGlyLeuSerSerLeuGlnLeuValAlaValGluThrAsnLeuAlaSer 100
 QY 585 CTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAGAACTTAAATGGTGCACAAAT 644
 DB 101 LeuGluAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 120
 QY 645 CTTATCCAACTTTCAATTAATACCTGAGTATTTTCTATCTGACCAATCTAGACACTTG 704
 DB 121 LeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu 140
 QY 705 GACCTTCCAGCAACAAGATTCAGAGTATTTATTTGACAGACTGGGGGTTTCTACATCAA 764
 DB 141 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuAspValLeuHisGln 160
 QY 765 ATGCCCTACTCATCTCTCTTTAGACCTGCTCCCTGAACCTTGAACCTTATTCACACA 824
 DB 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
 QY 825 GGTGCTATTAAGAAATTAAGGCTTCATTAAGCTGCTTTAAGAAATTAATTTGATAGTTA 884
 DB 181 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu 200
 QY 885 AATGTATGAAGAACTTTATTCAGAGTCTGGCTGGTTTGAAGGCTCATCGTTGGTCTG 944
 DB 201 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisAspGluValLeu 220
 QY 945 GGAAGAAATTTGAAGAACTTTGAAGAAAGTTTGAACAAATCTGCTAGAGGGGCTG 1004
 DB 221 GlyGluPheArgHisGlnGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu 240
 QY 1005 TGCATTTTGAACATTTGAAGAAATTCGATTAAGCATTAATTAAGCTTACCTGATGATATT 1064
 DB 241 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspLysTyrTyrLeuAspAspIle 260

QY 1065 ATGACTTATTTAATTTGACAAATGTTTCTTCAATTTCCCTGAGTGCATATT 1124
 DB 261 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
 QY 1125 GAAAGGTTAAAGACTTTTCTTATTAATTTGAGATGGCAACATTTAGATTAAGTACTGT 1184
 DB 281 GluArgValLysAspPheSerTyrAsnPheGlyTyrProIleHisLeuGluLeuValAsnCys 300
 QY 1185 AATTTGAGACATTTCCCATTTGAACCTCAAAATCTCAAAAGGCTTACTTCACTTCC 1244
 DB 301 LysPheGlyGlnPheProIleLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 320
 QY 1245 AACAAAGTGGGAATGCTTTTTCAGAAATGATCTACCAAGCTTGAAGTTTCAAGATCTC 1304
 DB 321 AsnLysGlyLysAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340
 QY 1305 AGTGAAGATGGCTTGAATTTCAAGGTTGCTGTTCTCAAAAGTATTTGGGACACAGC 1364
 DB 341 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
 QY 1365 CTAAGATTTATGATCTGAGCTTCAATGCTGTTATTAACATGATGTTAACTTTGGGC 1424
 DB 361 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
 QY 1425 TTGAACAACTAGAACATCTGGAATTCACACTTCCAAATTTGAAACAAATGAGTGAATT 1484
 DB 381 LeuGluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 400
 QY 1485 TCAGTATTCCTATCACTCAGAAACCTCATTTTACCTTGACATTTCTCATCTACACACGA 1544
 DB 401 SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThrArg 420
 QY 1545 GTTGCTTTCAATGACATCTTCAATGCTGTTTCCAGTCTGCAAGTCTTGAAGAAATGGCTGC 1604
 DB 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValIleLysMetAlaGly 440
 QY 1605 AATTCCTTCCAGGAAACCTTCCCTCCAGATATCTTCAAGAGCTGGAAGAACTTGACCTTC 1664
 DB 441 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 460
 QY 1665 CTGAGACTCTCTCAGTGTCACTGAGAGCACTTGTCTCAACAGCATTTTAACTGACTTCC 1724
 DB 461 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 480
 QY 1725 AGTCTTCAAGTACTTAATATGAGCCACACAACTCTTTTCAATGATAGCTTCTTAT 1784
 DB 481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 500
 QY 1785 AAGTGTCTGAACCTCCCTCCAGGTTCTTGATTAAGTCAATCACTAATGACTCCAAA 1844
 DB 501 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 520
 QY 1845 AAAACAGAACTACAGCAATTTTCCAAAGTACTGATCTTTCTTAATCTTACTCAGAAATGAC 1904
 DB 521 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
 QY 1905 TTTGCTTGTATCTTGAACACAGAGTTCCTGCAATGATCAAGACACAGGACAGCTC 1964
 DB 541 PheAlaCysThrCysGluHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeu 560
 QY 1965 TTGGTGAAGTGAAGAAATGGAATGTGCAACCTTCAAGATTAAGACAGGCAAGCTGTG 2024
 DB 561 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 580
 QY 2025 CTGAGTTTGAATATCACTGCTCAGATGAATTAAGACCATCATTTGGTGTGCTGCTCAGT 2084
 DB 581 LeuSerLeuAsnHisLeuThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 600
 QY 2085 GTGCTTGATGATCTGTTGTTAGACGATTCGTGCTATTAAGTCTTATTTTCACTGATGCTT 2144
 DB 601 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeu 620
 QY 2145 CTTCGCTGGCTGATTAAGTATGTTAGAGGTGAAGAAATCTATGATGCCCTTTGTTATCTAC 2204

```
Db      621  LeuAlaGlyCysIleuSTyrGlyArgGlyGluAsnIleTyrAspAlaPheValIleTyr 640
QY      2205  TCAAGCCAGATGAGACTGGGTAAAGAAATGACCTAGTAAAGATTAGAAAGAGGGGTG 2264
Db      641  SerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlyVal 660
QY      2265  CCTCCATTTCAGCTGCTGCTTCACTACAGAGACTTATTCCTCCGGTGTGGCATTGCTGCC 2324
Db      661  ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 680
QY      2325  AACATCATCCATGAGGTTTCCATAAAAGCCGAAAGGTGATTGTGTGTGTCACAGCAC 2384
Db      681  AsnIleIleHisGlnGlyPheHisIleYserArgLysValIleValValSerGlnHis 700
QY      2385  TTCATCCAGAGCCGCTGGTGTATCTTGAATATGAGATTGCTCAGACCTGGCAGTTTCTG 2444
Db      701  PheIleGlnSerArgTrpCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPheLeu 720
QY      2445  AGCAGTGTGCTGTATCATCTTATGTCCTGCAGAGGTGGAGAAAGCCGTGTCAGG 2504
Db      721  SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg 740
QY      2505  CAGCAGGTGAGCTGTATCCGCTTCTCAGCAGGAAACATTACCTGAGTGGAGAGACAGT 2564
Db      741  GlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnAspSer 760
QY      2565  GTGCTGGGGGGGACATCTTCTGAGAGCAGCTCAGAAAAGCCCTGCTGAGTGGTAAATCA 2624
Db      761  ValLeuGlnYargHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 780
QY      2625  TGAATCCAGAGAGACAGTGGGTACAGATGCATTCAGCAGAGCAACATCTATC 2681
Db      781  TrpAsnProGlnGlnThrValGlnThrGlyCysAsnTrpGlnGlnAlaThrSerIle 799
```

Search completed: March 29, 2005, 17:01:15
Job time : 237.22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 14:31:58 ; Search time 33.481 Seconds
(without alignments)
16993.973 Million cell updates/sec

Title: US-09-396-985B-3

Perfect score: 6724
Sequence: 1 acggggccactgtctgtcac.....tctcactgacagagacta 3811

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+np,model -DEV=Xlh
-Q=/cgn2_1/USPRO.spool/US09396985/raimac 28032005 155744 21170/app_query.fasta_1.85098
-DB=Issued_Patents_AA -OPMT=fastaan -SUFFIX=rai -MINMATCH=0.1 -LOOFCB=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NOEM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USBR=US09396985.@CGN_1_1_732.@rnat 28032005 155744 21170 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOBERRY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA.*

1:	/cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2:	/cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3:	/cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4:	/cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5:	/cgn2_6/ptodata/1/iaa/PTCTUS.COMB.pep.*
6:	/cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4394	65.3	844	4	US-09-949-016-9438
2	619.5	9.2	661	1	US-08-514-014-4
3	619.5	9.2	661	2	US-08-833-823-4
4	599.5	8.9	784	4	US-09-982-308B-23
5	539	8.0	775	4	US-09-949-016-8799
6	325	4.8	605	3	US-09-063-950-5
7	306.5	4.6	623	4	US-09-949-016-10995
8	306	4.6	605	1	US-08-190-802A-49
9	306	4.6	605	3	US-08-477-346-49
10	306	4.6	605	3	US-08-473-089-49
11	306	4.6	605	4	US-08-487-072A-49
12	306	4.6	605	4	US-09-538-092-1087

13	298	4.4	603	1	US-08-190-802A-50	Sequence 50, Appl
14	298	4.4	603	3	US-08-477-346-50	Sequence 50, Appl
15	298	4.4	603	3	US-08-473-089-50	Sequence 50, Appl
16	298	4.4	603	4	US-08-487-072A-50	Sequence 50, Appl
17	298	4.4	662	4	US-09-538-092-1325	Sequence 1325, Ap
18	298	4.4	662	4	US-09-949-016-6619	Sequence 6619, Ap
19	298	4.4	665	4	US-09-949-016-10710	Sequence 10710, A
20	295.5	4.4	1525	3	US-09-191-647-2	Sequence 2, Appl
21	295.5	4.4	1525	3	US-09-540-245A-2	Sequence 2, Appl
22	295.5	4.4	1525	3	US-09-540-153-2	Sequence 2, Appl
23	293.5	4.4	1525	3	US-09-170-496D-264	Sequence 264, App
24	293.5	4.4	907	4	US-09-170-496D-278	Sequence 278, App
25	293.5	4.4	1529	4	US-09-312-283C-396	Sequence 396, App
26	290	4.3	1112	3	US-09-353-585-3	Sequence 3, Appl
27	286	4.3	1112	3	US-09-353-585-2	Sequence 2, Appl
28	283.5	4.2	1166	4	US-10-101-664A-900	Sequence 900, App
29	281.5	4.2	1523	3	US-09-182-024A-2	Sequence 2, Appl
30	275	4.1	620	4	US-09-307-794A-73	Sequence 73, Appl
31	275	4.1	620	4	US-09-305-125A-73	Sequence 73, Appl
32	275	4.1	620	4	US-09-302-775A-73	Sequence 73, Appl
33	275	4.1	620	4	US-09-306-700-73	Sequence 73, Appl
34	275	4.1	620	4	US-09-303-603A-73	Sequence 73, Appl
35	275	4.1	620	4	US-09-304-920A-73	Sequence 73, Appl
36	275	4.1	620	4	US-09-309-064-73	Sequence 73, Appl
37	275	4.1	620	4	US-09-305-381A-73	Sequence 73, Appl
38	275	4.1	620	4	US-09-306-618-73	Sequence 73, Appl
39	274.5	4.1	863	2	US-08-666-271-2	Sequence 2, Appl
40	274.5	4.1	1091	3	US-08-986-485-5	Sequence 5, Appl
41	274.5	4.1	1480	3	US-09-191-647-7	Sequence 7, Appl
42	274.5	4.1	1480	3	US-09-540-245A-7	Sequence 7, Appl
43	274.5	4.1	1480	3	US-09-540-153-7	Sequence 7, Appl
44	274.5	4.1	1480	5	PCT-US91-09055-2	Sequence 2, Appl
45	272.5	4.1	1480	3	US-09-182-024A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-9438
; Sequence 9438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9438
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9438

Alignment Scores:

Pred. No.: 0
Score: 4394.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 65.35%
DB: 4
Length: 844
Matches: 844
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-09-396-985B-3 (1-3811) x US-09-949-016-9438 (1-844)

QY 150 ACACACAGAAAGCTGGAGTAAACCCAGAGCTTCAGACTCCGAGAGCTCAGCCCTTC 209

Db 1 ThrThGlnbSerTrpHisglnThrGlnSerPheGlnThrProGlnProGlnProPhe 20
QY 210 ACCCGCATTCATGCTCTTCTGCTAAATGCTCCGCTTTTATCAGGAGGTGGTTCCTAAT 269
Db 21 ThrProIleProleuLeuLeuAlaLysCysCysArgPheIleThrGlnValValProAsn 40
QY 270 ATTACTTATCAATGAGCATGAGCTGAATTTCTACAAATCCCGAGCAACCTCCCTCTCA 329
Db 41 IleThrTyGlnCysMetGlnLeuAsnPheTyLysIleProAsnAsnLeuProPheSer 60
QY 330 ACCAAGAACCTGGACCTGACCTTTAAATCCCTGAGCATTTAGCAGCTATAGCTTCTTC 389
Db 61 ThrLysAsnLeuAsnLeuSerPheAsnProLeuAlaArgHisLeuGlySerTySerPhePhe 80
QY 390 AGTTTCCGACAACTGCAGGTGCTGGAATTATCCAGGTGTGAATCCAGACATTTGAAGAT 449
Db 81 SerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAsp 100
QY 450 GGGGCAATATCAGAGCTTAAGCCATCCCTCTACCTTAATATGACAGGAAACCCATCCAG 509
Db 101 GlyAlaTyGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGlnAsnProIleGln 120
QY 510 AGTTTACCCCTGGAGGCTTTTCTGACATATCAAGTTTACAGAACTGTGCTGTGAG 569
Db 121 SerLeuAlaLeuGlnAlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGln 140
QY 570 ACAAACTAGCATCTCTAGAAACTTCCCATTTGACATCTCAAACTTTGAAAGACTT 629
Db 141 ThrAsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGlnLeu 160
QY 630 AATGTGCTACAACTCTTATCCAACTCTTGAATTCCTGAGATTTTCTATCTGACCC 689
Db 161 AsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGlnTyPheSerAsnLeuThr 180
QY 690 AATCTAGACACTTGGACCTTTCAGACCAACAAGATTCAAAGATTTTATTCACAGACTTG 749
Db 181 AsnLeuGlnHisLeuAsnLeuSerSerAsnLysIleGlnSerIleTyCysThrAspLeu 200
QY 750 CGGGTCTACATCAATGCCCCCTACTCATCTCTTTAGACCTGTGCCGAAACCTATG 809
Db 201 ArgValLeuHisglnMetProLeuLeuAsnLeuSerLeuAsnProMet 220
QY 810 AACTTATCCAAACAGGTGATTTAAAGAAATTAAGCTTCATAGCTGACTTTAAGAAAT 869
Db 221 AsnPheIleGlnProGlnAlaPheLysGlnIleArgLeuHisLysLeuThrLeuAlaGAsn 240
QY 870 AATTTTGATAGTTTAAATGTATGAAAACTTGATTCAGAGTCTGCTGCTTTAGAGATC 929
Db 241 AsnPheAspSerLeuAsnValMetLysThrCysIleGlnLysLeuAlaGlyLeuGlnVal 260
QY 930 CATCGTTTGGTCTGGGAGAAATTTAGAAATGAAGAAACTTGGAAAAGTTTGACAAATCT 989
Db 261 HisArgLeuValIleuGlnGlnPheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSer 280
QY 990 GCCTCTGAGGGGCTGTGCAATTTGACATTTGAAGAATTCGATTAGCATCTTAAGACTAC 1049
Db 281 AlaLeuGlnIleGlyLeuCysAsnLeuThrIleGlnIlePheArgLeuAlaTyLysLeuAspLys 300
QY 1050 TACCTCGATGATATTAATGACTTAATTAATTTGTTTGAACAATGTTTCTTATTTCCCTG 1109
Db 301 TyLeuAsnAspArgIleIleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeu 320
QY 1110 GTAGGTGACTATTTGAAGAGGTAAGAACTTTTCTTAATAATTTCCGATGGCAACTTTA 1169
Db 321 ValSerValIleThrIleGlnArgValLysAspPheSerTyAsnPheGlyLysProGlnHisLeu 340
QY 1170 GAATTAAGTAACTGAATTTTGGACAGTTTCCCATTTGAAATCTCAAACTCTCAAAAG 1229
Db 341 GlnLeuValAsnCysLysPheGlyGlnPheThrLeuLysSerLeuLysSerLeuLysArg 360
QY 1230 CTACTCTCACTTCCAAAGGAGGTGAGTCTTTTCAGAAAGTTGATTCACCAAGCTT 1289

Db 361 LeuThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGlnValValAspLeuProSerLeu 380
QY 1290 GAGTTTCTAGACTCAGTAGAAATGGCTTTAGCTTCAAGGTTTGCGTTCTCAAGATGAT 1349
Db 381 GlnPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCysCysSerIleSerAsp 400
QY 1350 TTTGGGACAAACAGCCTAAAGTATTTAGATCTGACCTTCATAGTGTTATTAACATGACT 1409
Db 401 PheGlyThrThrSerLeuLysTyLeuAsnLeuSerPheAsnGlyValIleThrMetSer 420
QY 1410 TCAAACTTTGGGCTTGAACAACAATACTGAAACATCTGGAATTTCCAGACTTCCATTTGAAA 1469
Db 421 SerAsnPheLeuGlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLys 440
QY 1470 CAAATGAGAGATTTTTCAGTATTCCTATCAGCTCAGAAACCTGATTTACCTTACATTTCT 1529
Db 441 GlnMetSerGlnPheSerValPheLeuSerLeuAspGAsnLeuIleTyLeuAspLysSer 460
QY 1530 CATACTCACACAGAGTTGCTTTCAATGGACATCTTCATAGGCTTGTCCAGTCTCGAAGTC 1589
Db 461 HisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnVal 480
QY 1590 TTGAATAATGGCTGGCAATCTTTCCAGAAACTTCTCCAGATATCTTCAACAGACTG 1649
Db 481 LeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGlnLeu 500
QY 1650 AGAAATTTGACCTTCCCTGGACCTCTCAGTGTCAACTGGACAGTGTCTCCACAGCA 1709
Db 501 ArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnLysLeuSerProThrAla 520
QY 1710 TTTAATCACTCTCCAGCTTTCAGGTAAGTAATATGAGCCACAACTTCTTTTCATTTG 1769
Db 521 PheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeu 540
QY 1770 GATACGTTTCTTAATAGTGTCTGAATCTCCCTCCAGTCTTGTATTAACAGTCTCAATC 1829
Db 541 AspThrPheProTyLysCysLeuAsnSerLeuGlnValLeuAspLysSerLeuAsnHis 560
QY 1830 ATTAATGACTCCAAATAAGAGAACTACAGCACTTTTCCAAAGTACTTACTTCTTAAT 1889
Db 561 IleMetThrSerLysLysGlnGlyLeuGlnHisPheProSerSerLeuAlaPheLeuAsn 580
QY 1890 CTTACTCAGAAATGACTTTGCTTGTATCTTGTGAACACAGAGTTTCTGCAATGATCAAG 1949
Db 581 LeuThrGlnAsnAspPheHisLysThrCysGlnHisglnSerPheLeuGlnTrpLys 600
QY 1950 GACAGAGGCAAGCTTGTGTGAGTGAAGTGAACGAATGGAATGTGCACACCTTCAAGTAAG 2009
Db 601 AspGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAlaIleThrProSerAspLys 620
QY 2010 CAGGGGAGTCTGTGTGACTTTGAATATCACCTGTCAAGTAAATGAAGCAATCATTTGGT 2069
Db 621 GlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGly 640
QY 2070 GTGTGCGTCTCAGTGTGCTTGTAGTATCTGTTGTGACAGTTCTGCTCTTAAGTTCTAT 2129
Db 641 ValSerValLeuSerValLeuValValSerValValAlaValLeuValLysTyLysPheTy 660
QY 2130 TTTCACTGATGTCTTGTGCTGCTGCTCAATAAAGTATGTGAGAGSTGAATAATCTATGAT 2189
Db 661 PheHisLeuMetLeuLeuAlaGlyCysIleLysTyGlyArgGlyGlnLeuHisIleTyLysAsp 680
QY 2190 GCCTTTGTTATCTACACAGGATGAGATGAGAGTGGGTAAAGAAATGAGTAAAGAAAT 2249
Db 681 AlaPheValIleTyLysSerSerGlnAspArgLysPheValArgAsnGlnLeuValLysAsn 700
QY 2250 TTAGAGAAAGGGGTGCTCATTTTCACTTCACTGCTGCTTCACTACAGAGACTTTATTTCCCGT 2309
Db 701 LeuGlnGlnGlyAlaProPhePheGlnLeuCysLeuHisIleTyLysArgAspPheIleProGly 720
QY 2310 GTGGCCATTTGCTCCAAACATCATCATGAGGTTTTCATAAAGCCGAAAGGTGATGTT 2369
Db 721 ValAlaIleAlaIleAsnIleIleHisglnGlyPheHisLysSerArgLysValIleVal 740

QY 2370 GTGGTGTCCAGCACTTTCATCCAGACCGGTGTATCTTGAATATGAGATTGCTCAG 2429
 DB 741 ValValSerGlnHisPheIleGlnSerArgTyrPheCysIlePheGlnTyrGlnIleAlaGln 760
 QY 2430 ACCGTGCACTTCTGAGCAGTGTGTGTATCATCTTATGCTTCCAGAGAAAGGTGAG 2489
 DB 761 ThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIleValGln 780
 QY 2490 AAGACCTCTCTCAGCAGCAGGTGTGAGTGTACCGCTTCTCAGCAGAACTTACCTG 2549
 DB 781 LysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeu 800
 QY 2550 GAGTGGAGAGACAGTGTCTGTGGGGCGGACATCTTCTGAGAGCACTCAGAAAAGCCTG 2609
 DB 801 GluTrpGluAspSerValLeuGlyArgHisIlePheThrArgArgLeuArgValAlaLeu 820
 QY 2610 CTGGATGTAAATCATGAAATCCAGAAAGAAAGTGGTACAGATGCAATTGGCAGAA 2669
 DB 821 LeuAspGlyLysSerTyrPheAsnProGluGlyThrValGlyThrGlyCysAsnTrpGlnIle 840
 QY 2670 GCAACATCTATC 2681
 DB 841 AlaThrSerIle 844
 RESULT 2
 US-08-514-014-4
 ; Sequence 4, Application US/08514014
 ; Patent No. 5707829
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John
 ; APPLICANT: Kelleher, Kerry
 ; APPLICANT: Catlin, McKeough
 ; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 ; TITLE OF INVENTION: ENCODED THEREBY
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Genetics Institute, Inc. -- Legal Affairs
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/514,014
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; REFERENCE/DOCKET NUMBER: G16000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 661 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-514-014-4
 Alignment Scores:
 Pred. No.: 8.56e-58
 Score: 619.50
 Percent Similarity: 45.45%
 Best Local Similarity: 29.33%
 Length: 661
 Matches: 200
 Conservative: 110
 Mismatches: 277

Query Match: 9.21% Indels: 95
 DB: 1 Gaps: 24
 US-09-396-985B-3 (1-3811) x US-08-514-014-4 (1-661)
 QY 222 TTGCTTCTTGCTAAATGCTGCCGTTTATACG-----GAGGTG 260
 DB 12 ValLeuPheSerAlaGlyCysIleValIleThrSerTrpAspGlnMetCysIleGlyLys 31
 QY 261 GTTCTTAATATTAATTATCAATGCAATGAGATGGAATTTCTACAAATCCCGCAACCTC 320
 DB 32 GluAlaAsnLysThrTyrAsnGlySerGluAsnLeuGlyLeuSerGlnIleProAspThrLeu 51
 QY 321 CCTTCTCAACCAAGAACTGTGAGCTTTAATCCCTTGAGGACATTTAGGACCTAT 380
 DB 52 ProAsnThrThrGluPheLeuGlnIlePheSerPheAsnPheLeuProThrIleHisAsnArg 71
 QY 381 ACCTTCTTCAGTTTCCAGAACTGCAAGGTCTGATTTATCCAGGTGTGAATCCAGACA 440
 DB 72 ThrPheSerArgLeuMetAsnLeuThrPheLeuAspLeuThrArgCysGlnIleAsnTrp 91
 QY 441 ATTGAAGATGGGCAATATCAAGCCTTAAGCCACTCTCTACTTAATATGACAGAAAC 500
 DB 92 IleHisGluAspThrPheGlnSerHisIleGlnLeuSerThrLeuValLeuThrGlyAsn 111
 QY 501 CCCATCCAGATTGACCCCTGGAGCCTTTCTGAGCTATCAAGTTTACAGAACTGGTG 560
 DB 112 ProLeuIlePheMetAlaGlnThrSerLeuAsnGlyProLysSerLeuLysHisLeuPhe 131
 QY 561 GCTGTGAGACAAATCTAGCATCTGTAGAACTTCCCATTTGACATCTCAAACTTTG 620
 DB 132 LeuIleGlnThrGlyIleSerAsnLeuGlnPheIleProValHisAsnLeuGlnLeu 151
 QY 621 AAAGACTTAATGTGGCTTCACATCTTATCCATCTTCAATTAACCTGAGATTTTCT 680
 DB 152 GluSerLeuTyrLeuGlySerAsnHisIleSerSerIleLysPheProLysAspPhePro 171
 QY 681 AATCGAACCAATCTGAGCACTTGAGCCTTCCACACCAAGTCAAAAGTATTATTTC 740
 DB 172 ---AlaArgAsnLeuValLeuAspPheGlnAsnAlaIleHisTyrIleSerArg 190
 QY 741 ACAGACTTGGGGTTCATCATCAAAATGCCCTACTCAATCTCTTTAGACCTGTCCCTG 800
 DB 191 GluAspMetArgSerLeuGlnIle-----AlaIleAsnLeuSerLeuAsnGly 208
 QY 801 AACCTTAAGACTTATTCACACAGCTGCTATTAAGAATTAAGCTTATAGCTGACT 860
 DB 209 AsnAsnValLysGlyIleGlnLeuGlyAlaPheAspSerThrValPheGlnSerLeu--- 227
 QY 861 TTAAGAAATTAATTTGATAGTTTAATGAATGAAGAACTGTATCAAGTGTGCTGCT 920
 DB 228 -----AsnPheGlyGlyThrProAsnLeuSerValIlePheAsnGlyLeuGlnAsn 244
 QY 921 TTAGAAGTCCATCGTTTGTCTGTGAGAAATTTAGAAATGAAGAACTTGAAGAAATTT 980
 DB 245 SerThrThrGlnSerLeuThrPheGlnIleAspAsp---GluAspIle 263
 QY 981 GACAAATCTCTTGAAGGGCTGTGCAATTGATGCAATGAAGAAATTCGATAGCATAC 1040
 DB 264 SerSerAlaMetLeuLysGlyLeuGlyMetSerValGluSerLeuAsnLeuGln--- 282
 QY 1041 TTAGACTACTACCTGATGATTTATTAAG---TATTATTAATGTTTGAAGAAATGCTTCT 1097
 DB 283 ---GluHisArgPheSerAspIleSerSerThrThrPheGlnCysPheThrGlnLeuGln 301
 QY 1098 TCATTTTCCCTGTGAGTGTGACTATGAAGAGTGAAGAACTTTCTTATTAATTTCCGA 1157
 DB 302 GluLeuAspLeuThrAlaThrHisIleuLysGlyLeuProSer-----Gly 316
 QY 1158 TGGCAACATTTTGAATTAAGTTAAC----- 1181
 DB 317 MetLysGlyLeuAsnLeuLeuLysIleuValLeuSerValAsnHisPheAspGlnLeu 336

```

QY 1182 TGTAAATT-----GAGAGTTTCCCATG-----AAATC 1214
    |||:::|||||:::|||||:::
Db 337 CysGlnIleSerAlaIAsnPhetProSerLeuThrIleuArgIleuVal 356
QY 1215 AAATCTGCAAAAGGCTTACTTCCATCCAAAGGGGAACTTTTTCAGAAATT 1274
    |||:::|||||:::|||||:::
Db 357 LysLysLeuHisLeuGlyValGlyCysLeuGlnLysLeuGlyValAsn----- 371
QY 1275 GATCTCAAGGCTGAGTTTCTAGATCTCAGTAAATGGCTGAGTTTCAAGGTTGC 1334
    |||:::|||||:::|||||:::
Db 372 -----LeuGlnThrLeuAspLeuSerHisAsnSprIleGluAlaSerAspCys 387
QY 1335 TGTCTCAAGTATTTGGGACAAACAGCTAAAGTATTTAGTCTGAGTTCAATGAT 1394
    |||:::|||||:::|||||:::
Db 388 CysSerLeuGlnLeuLysAsnLeuSerHisLeuGlnThrLeuAsnLeuSerHisAsnGln 407
QY 1395 GTTATTACCATGATGTTCAAC--TTCTGGGCTTGAACAACTAGACATCTGGATTTC 1451
    |||:::|||||:::|||||:::
Db 408 ProLeuGlyLeuGlnSerGlnAlaPhelyGluCysProGlnLeuGlnLeuAspLeu 427
QY 1452 CAG-----CATTCATTTGAAACAAATAGAGATTTC-----GPAATTC 1493
    |||:::|||||:::|||||:::
Db 428 AlaPhetArgLeuHisIleAsnAlaProGln--SerProPhetGlnAsnLeuHisPhe 446
QY 1494 CTATCACTCAAGAACTCATTTAC-----CTTGACATTTCTCATCTGACACAGAGTT 1547
    |||:::|||||:::|||||:::
Db 447 LeuGlnValLeuAsnLeuThrGlyCysPheLeuAspThrSerAsnGlnHis----- 463
QY 1548 GCTTCAAGGACCTTCAATGGCTGTGCTGCAAGTCTGAAATGGCTGGCATT 1607
    |||:::|||||:::|||||:::
Db 464 -----LeuLeuAlaGlyLeuProValLeuArgHisLeuAsnLeuLysGlyValAsn 479
QY 1608 TCTTTCAGGAAAACTTCCTT-----CCAGATATCTTCAACAGAGCTGAAACTTGACC 1661
    |||:::|||||:::|||||:::
Db 480 HisPheGlnAspGlyThrIleThrLysThrAsnLeuGlnThrValGlySerLeuGln 499
QY 1662 TTCCTGACCTCTCTGACGTGTCAGTGAAGCACTGTCTTCCACAGCATTTAACTCATC 1721
    |||:::|||||:::|||||:::
Db 500 ValLeuIleLeuSerSerCysGlyLeuLeuSerIleAspGlnGlnAlaPheHisSerLeu 519
QY 1722 TCCAGTCTTCAAGTAAATATAGACACACAACTTCTT-----TCATTGATAG 1775
    |||:::|||||:::|||||:::
Db 520 GlyLysMetSerHisValAspLeuSerHisAsnSerLeuThrCysAspSerIleAspSer 539
QY 1776 TTTCCTTAT-----AAGTGTGAACTCCCTCCAGGTTCTTGAT 1814
    |||:::|||||:::|||||:::
Db 540 LeuSerHisLeuLysGlyIleTyLeuAsnLeuAlaIAsnSerIleAsnIleIleSer 559
QY 1815 TACAGTCTCAATCAATAATGACTTCCAAAAACAGAACTACAGCATTTTCCAGTAGT 1874
    |||:::|||||:::|||||:::
Db 560 ProArgLeuLeuProIleLeu-----SerGln 568
QY 1875 CTAGCTTTCTTAATCTTACTAGATGACTTGTGTTGTTACTTGTGAACACAGAGTTTC 1934
    |||:::|||||:::|||||:::
Db 569 GlnSerThrIleAsnLeuSerHisAsnProLeuAspCysThrCysSerAsnIleHisPhe 588
QY 1935 CTGCAATGATCAAGAGCAGAGGACAGCTCTGTGTGGAAGTTGAAGAAATGAAATGCA 1994
    |||:::|||||:::|||||:::
Db 589 LeuThrTrpTyrIleGlySerLeuAsnLeuHisLysLeuGlnIleSerGlnGlnThrCysAla 608
QY 1995 ACACCTTCAGATAGACAGGAGCATGCTGTGCTGATTTGAATATCACTGTGATGATGAT 2054
    |||:::|||||:::|||||:::
Db 609 AsnProProSerLeuArgIleValLysLeuSerAspValLysLeuSerCysGlyIle--- 627
QY 2055 AAGACATCATTTGGTGTGGCTGCTCAGTGTGCTGTGATATCTGTTGAGAGATTTCG 2114
    |||:::|||||:::|||||:::
Db 628 ---ThAlaIleGlyIlePhePheLeuIleValPheLeuLeu---LeuLeuAlaIleLeu 645
QY 2115 GTCTAT 2120
    |||:::|||||:::|||||:::
Db 646 LeuPhe 647

```

RESULT 3

```

US-08-833-823-4
; Sequence 4, Application US/08833823
; Patent No. 5969093
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OR INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,823
; FILING DATE: 10-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/514,014
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI6000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-823-4

Alignment Scores:
Pred. No.: 8.56e-58 Length: 661
Score: 619.50 Matches: 200
Percent Similarity: 45.45% Conservative: 110
Best Local Similarity: 29.33% Mismatches: 277
Query Match: 9.21% Indels: 95
DB: 2 Gaps: 24

US-09-396-985b-3 (1-3811) x US-08-833-823-4 (1-661)
222 TTGCTTCTGTAATAGCTGCGCTTTTATACG-----GAGGTG 260
    |||:::|||||:::|||||:::
Db 12 ValLeuPheSerAlaGlyCysLysValIleThrIleThrAspGlnMetCysIleGlnLys 31
QY 261 GTTCTTATATTACTTATATCATGATGAGCTGAATTCTTCAAAATCCCGACAACTTC 320
    |||:::|||||:::|||||:::
Db 32 GluAlaAsnLysThrTyrAsnGlySerGlnAsnLeuGlyLeuSerGlnIleProAspThrLeu 51
QY 321 CCCTTCTCAACGAACAACTGACCTGAGCTTTATCCCTGAGGACATTAGCAGCTAT 380
    |||:::|||||:::|||||:::
Db 52 ProAsnThrThrGlnPheLeuGlnPheSerPheAsnPheLeuProThrIleHisAsnArg 71
QY 381 ACCTTCTTCAAGTTTCCAGAACTGCAAGGTGCTGATTTATCCAGGTGTGAATCCAGACA 440
    |||:::|||||:::|||||:::
Db 72 ThrPheSerArgLeuMetAsnLeuThrPheLeuAspLeuThrArgCysGlnIleAsnTrp 91
QY 441 ATTGAAGATGGGACATATCAGAGCTTAAGCCACTCTTACCTTAATATGACAGGAAC 500
    |||:::|||||:::|||||:::

```


Db 92 IleHisGluAspThrPheGlnSerHisIleGlnLeuSerThrLeuValLeuThrGlyAsn 111
 QY 501 CCATCCAGAGTTTAGCCCTGGAGCCCTTTCTGAGCTATCATGATTACAGAACTGGTG 560
 Db 112 ProLeuIlePheMetAlaGluThrSerLeuAsnGlyProIysSerLeuIleuHisPhePro 131
 QY 561 GCTGTGAGACAAATATGACATCTAGAGAACTTCCCATCTGAGATCTCAAACTTTG 620
 Db 132 LeuIleGlnThrGlyIleSerAsnLeuGlnPheIleProValHisAsnLeuGluAsnLeu 151
 QY 621 AAGAAGCTTAATGTGGCTCAATCTTAATCAATCTTTCAAAATTAACCTGAGATTTTCT 660
 Db 152 GluSerLeuIleuSerLeuSerHisIleSerSerIleIysPheProIysAspPhePro 171
 QY 681 AATGTACCAATGTAGACACTTGGACCTTTCAGACAAACAAAGTTCAAGTATTATTCG 740
 Db 172 ---AlaArgAsnLeuIleuValLeuAspPheGlnAspAsnAlaIleHisIleSerArg 190
 QY 741 ACAGACTGGGGGTCTACATCAATGCCCCCTACTCATCTCTTTAGACTGCTCCCTG 800
 Db 191 GluAspMetArgSerLeuGlnGln-----AlaIleAsnLeuSerLeuAsnPheAsnGly 208
 QY 801 AACCTATGACTTTATCCACACAGGCTTTAAAGAAATTAGCTTCAATAGCTGACT 860
 Db 209 AspAsnValIleGlyIleGlnLeuGlyAlaPheAspSerThrValPheGlnSerLeu--- 227
 QY 861 TTAGAATAATTTGATGTTAAATGTATGAAACTGTATTCAAGCTCGGCTGGCT 920
 Db 228 -----AsnIleGlyIleThrProAsnLeuSerValIlePheAsnGlyLeuGlnAsn 244
 QY 921 TTAGAAGTCATGTTGGTTCTGGAGAAATTTAGAAATGAAGAACTTGAAGAAATT 980
 Db 245 SerThrThrGlnSerLeuThrPheGlnAspIleAspAsp---GluAspIle 263
 QY 981 GACAAATCTGCTTAAAGGCGCTGTGCATTTGACATGAGAAATTCGGATTAAGCATAC 1040
 Db 264 SerSerAlaMetLeuIleuSerGlyLeuGlyLeuSerValGluSerLeuAsnLeuGln--- 282
 QY 1041 TTAGACTACCTGATGATGATATTATTTGAC---TTATTTAATGTTTGAACAATGTTCT 1097
 Db 283 ---GlnHisArgPheSerAspIleSerSerThrThrPheGlnCysPheThrGlnLeuGln 301
 QY 1098 TCATTTTCCCTGGTGTGATGATGATGATGAAAGGCTTCTTATTAATTTCCGA 1157
 Db 302 GluLeuAspLeuThrAlaThrHisLeuIleGlyLeuProSer-----Gly 316
 QY 1158 TGGCAACATTAGATTAAGTAAAC----- 1181
 Db 317 MetIleGlyLeuAsnLeuLeuIleuValLeuSerValAsnHisPheAspGlnLeu 336
 QY 1182 TGTAAATT-----GACACGTTCCCACTTG-----AAATC 1214
 Db 337 CysGlnIleSerAlaAlaAsnPheProSerLeuThrHisLeuIleArgIleAsnVal 356
 QY 1215 AATCTCTCAAAAAGGCTTCACTTCAACAAAGGCTGGAAATGCTTTTTCAGAAATT 1274
 Db 357 IysIleLeuHisIleuGlyValGlyCysLeuGlnIleuLeuGlyAsn----- 371
 QY 1275 GATCTACCAAGCCTTGATTTTGTAGATCTTCAAGAAATGCTTGAAGTTCAAGGTTGC 1334
 Db 372 -----LeuGlnThrLeuAspLeuSerHisAsnAspIleGlnAlaSerAspCys 387
 QY 1335 TGTTCCTCAAGTATTTGGACAAACCCCTTAAATATTATTTAGATCTGAGCTTCAATGT 1394
 Db 388 CysSerLeuGlnIleuIysAsnLeuSerHisIleGlnIleuAsnLeuSerHisAsnGln 407
 QY 1395 GTTATTCATGAGTTCAAAAC---TTCTTGGCTTGAACAATGAGATCATGATGATTC 1451
 Db 408 ProLeuGlyLeuGlnSerGlnAlaPheIysGluCysProGlnLeuGlnLeuLeuAspLeu 427
 QY 1452 CAG-----CATTCGAATTTGAAAACAATAGTACGATTTTCA-----GTATTC 1493
 Db 428 AlaPheThrArgLeuHisIleAsnAlaProGln---SerProPheGlnAsnLeuHisPhe 446

QY 1494 CTATCACTCAGAAACCTCATTTAC-----CTTGACATTTCTCATACTCAGACAGATT 1547
 Db 447 LeuGlnValLeuAsnLeuThrIleThrCysPheLeuAspThrSerAsnGlnHis----- 463
 QY 1548 GCTTTCAATGAGCATCTTCAATGAGCTTGTTCAGCTTTCGAAAGCTTTGAAATGCGTGCAN 1607
 Db 464 -----LeuLeuIleGlyLeuProValLeuArgHisIleuAsnLeuIleuGlyAsn 479
 QY 1608 TCTTTCCAGAAAACCTCTT-----CCAGATATCTTCAACAGAGCTGAGAAACTTGACC 1661
 Db 480 HisPheGlnAspGlyThrIleThrIysThrAsnLeuGlnThrValIleSerLeuGln 499
 QY 1662 TTCCTGAGACTCTTCAGAGTCACTGAGACAGAGCTGTCCAAACAGATTTTAATCACTC 1721
 Db 500 ValLeuIleLeuSerSerCysGlyLeuLeuSerIleAspGlnAlaPheHisSerLeu 519
 QY 1722 TCCAGCTTCAAGTACTAATATATGAGCCAAACAACTTTT-----TCATTTGATAG 1775
 Db 520 GlyIysMetSerHisValAspLeuSerHisAsnSerLeuThrCysAspSerIleAspSer 539
 QY 1776 TTTCTTAT-----AAGTGTGAATCTCCCTCAGGTTCTTGAT 1814
 Db 540 LeuSerHisLeuIleGlyIleThrIleuAsnLeuAlaIleAsnSerIleAsnIleSer 559
 QY 1815 TACAGTCTCAATCACAATATGACTTCCAAAAACAGAACTACAGCATTTTCCAGTACT 1874
 Db 560 ProArgLeuLeuProIleu-----SerGln 568
 QY 1875 CTAGCTTTCTTAATCTTACTCAGATGACTTGTGCTTGTATCTTGACACAGAGTTTC 1934
 Db 569 GlnSerThrIleAsnLeuSerHisAsnProLeuAspCysThrCysSerAsnIleHisPhe 588
 QY 1935 CTGCATGATCAAGACCAAGGAGGAGCTTGTGTGAGAAATTGAACGAATGATGCA 1994
 Db 589 LeuThrTrpIleGlyGlnAsnLeuHisIleuIleuGlnGlySerGlnGlnIleThrCysAla 608
 QY 1995 ACACCTTGAGTAAGAGGAGCATGCGCTGCTGATGATTAATATACCTGATCAGATGAT 2054
 Db 609 AsnProProSerLeuArgIleValIleuSerAspValIleuSerCysGlyIle--- 627
 QY 2055 AAGACCATCATTTGTTGTGTGCTGCTCAGTGTGCTTGTATCTTGTAGACAGTTCTG 2114
 Db 628 ---ThrAlaIleGlyIlePhePheLeuIleValPheLeuLeu---LeuLeuAlaIleLeu 645
 QY 2115 GTCTAT 2120
 Db 646 LeuPhe 647
 RESULT 4
 US-09-982-308B-23
 / Sequence 23, Application US/09982308B
 / Patent No. 6531290
 / GENERAL INFORMATION:
 / APPLICANT: Dalie, Barbara
 / APPLICANT: Fan, Xuedong
 / APPLICANT: Lundell, Daniel
 / APPLICANT: Lunn, Charles A.
 / APPLICANT: Tan, Jimmy C.
 / APPLICANT: Zavadny, Paul J.
 / TITLE OF INVENTION: Mammalian TNF-alpha Convertases
 / FILE REFERENCE: JB06010C
 / CURRENT APPLICATION NUMBER: US/09/982,308B
 / CURRENT FILING DATE: 2001-10-17
 / PRIOR APPLICATION NUMBER: 09/156,163
 / PRIOR FILING DATE: 1998-09-17
 / PRIOR APPLICATION NUMBER: 08/889,909
 / PRIOR FILING DATE: 1997-07-10
 / PRIOR APPLICATION NUMBER: 60/021,710
 / PRIOR FILING DATE: 1996-07-12
 / NUMBER OF SEQ ID NOS: 23
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 23

```

; LENGTH: 784
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-982-308b-23

Alignment Scores:
Pred. No.: 1,46e-55 Length: 784
Score: 599.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 8.92% Indels: 219
DB: 4 Gaps: 38

US-09-396-985b-3 (1-3811) x US-09-982-308b-23 (1-784)

QY 306 ATCCCGGACAACTCCCTTCACACCAAGACCTGACCTTAATCCCTGAG 365
   |||||
Db 46 IleProSerGlyLeuThrGluAlaValLysSerLeuAspLeuSerAsnAsnArgIleThr 65
   |||||
QY 366 CATTAGGACGATATGCTTCTTCAGTTCCCGAAGCTGACGCTGATTTATCCAG 425
   |||||
Db 66 TyrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValLeuThrSer 85
   |||||
QY 426 TGTGAATCCAGACAAATTGAAGATGGGACATATCAGAGCTTAAGCCACTCTTACCTTA 485
   |||||
Db 86 AangLyIleAsnThrIleGluGluAspSerPheSerSerLeuGlySerLeuGluHisIleu 105
   |||||
QY 486 AATTGACAGAAACCCCATCCAGAGTTTACCCCTGGAGCCTTTTCTGACATCAAGT 545
   |||||
Db 106 AspLeuSerLysAsnThrLeuSerAsnLeuSerSerLysPheLysProLeuSerSer 125
   |||||
QY 546 TTACAGAGCTG-----GTGGCTGTGAG 569
   |||||
Db 126 LeuThrPheLeuAsnLeuLeuGlnLysAsnProTyrLysThrLeuGlyLutThrSerLeuPhe 145
   |||||
QY 570 ACAAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAAACT----- 617
   |||||
Db 146 SerHisLeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIle 165
   |||||
QY 618 -----TTGAAAGAACTTAATGTGGCTCACAACTTT 647
   |||||
Db 166 GlnArgLysAspPheAlaGlyLeuThrPheLeuGlnGluLeuGlnIleAspAlaSerAsp 185
   |||||
QY 648 ATCCAACTCTTCAATTAACCTGAGTATTTTCTAATCTGACCAATCTGAGACCTTGAGAC 707
   |||||
Db 186 LeuGlnSerLysGln---ProLysSerLeuLysSerIleGlnAsnValSerHisLeuIle 204
   |||||
QY 708 CTTTCAGAACAAAG-----ATTCAAAGTATT 734
   |||||
Db 208 LeuHisMetLysGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerVal 224
   |||||
QY 735 TATTCAGACAGCTTGGGGGTTCATCAATCAATGCCCTACTCAATCTCTTTAGACCTG 794
   |||||
Db 225 GlnCysLeuGlnLeuLys-----AspThr 232
   |||||
QY 795 TCCCTTAACCCCTTGAAGCTT-----ATCCAAACAGAGCTGATTAAAGAAATTAGGCTT 848
   |||||
Db 233 AspLeuAspThrPheHisIlePheSerGluLeuSerThrGlyLutThrAsnSerLeu---Ile 251
   |||||
QY 849 CATTAAGCTGATTAAGAAAT-----AATTTGATAGTTTA---AATGTAAATGAA 896
   |||||
Db 252 LysLysPheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMetLys 271
   |||||
QY 897 ACTGTG-----ATTCAAGGTCTGGCTGTTTGAAGTCCATGTTGGTCTG----- 944
   |||||
Db 272 LeuLeuAsnGlnIleSerGlyLeuLeuGlnLutLeuGlnPheAspAspCysThrLeuAsnGly 291
   |||||
QY 945 ----GGAGAAATTGAATGAATGAAGAACTTGGAAAAGTTTGACAAATCTGCTAGAGGGC 1001
   |||||
Db 292 ValGlyAsnPheArgLysSerAspAsnAspArgValIleAspProGlyLysValGln--- 310
   |||||
QY 1002 CTGTGCAATTTGACCAATTGAAGAAATTCGATTAGCA-----TACTTAGACTACTGCTC 1055
   |||||

```

```

Db 311 -----ThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyr----- 326
QY 1056 GATGATATATTAATGATTTATTAATGTTTGACAAATGTTTCTTATTTCCCTGGTAGT 1115
   |||||
Db 327 ---AspLeuSerThrLeuTyrSerLeuThrGluArgValLys-----Arg 340
   |||||
QY 1116 GTGACTAATGAAAGGGTAAAGACTTTTCTTAATATTCGATGCAACATTATGAAATTA 1175
   |||||
Db 341 IleThrValGluAsnSerLysValPhe-----Leu 350
   |||||
QY 1176 GTTAACTGTAAATTTGGACAGATTTCACATTTGAAATCTCAATCTCTCAAAAGGCTTACT 1235
   |||||
Db 351 ValProCysLeuLeuSerGln----- 357
   |||||
QY 1236 TTCACCTTCCAAAGGTGGGAATGCTTTTCAGAAATGATCTTACCAAGCTTGAGTTT 1295
   |||||
Db 358 -----HisLeuLysSerLeuLutYr 364
   |||||
QY 1296 CTGATCTCAGTGAAT-----GGCTTGAAGTTTCAAGGTGCTGTCT 1340
   |||||
Db 365 LeuAspLeuSerGluAsnLeuMetValGluGluTyrLeuLysAsnSerAlaCys----- 382
   |||||
QY 1341 CAAAGTATTTGGACAAACAGCCTTAAAGTATTTAGATCTGAGCTTCAATGCTTATT 1400
   |||||
Db 383 -----GluAspAlaTrpProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 397
   |||||
QY 1401 ACCATGAGTCAAACTTCTGGGCTTAGAACAACATCGATGATTTCCAGCATTC 1460
   |||||
Db 398 -----HisLeu-----Ala 400
   |||||
QY 1461 AATTGAAACAATAGTGAATTTTCAGTATTCCTATCACTCAGAACTCATTTACCTT 1520
   |||||
Db 401 SerLeuGluLysThrGlyGlu-----ThrLeuLeuThrLeuLysLeuThrAsnIle 418
   |||||
QY 1521 GACATTTCTCATATCTCACACCAAGTGTCTTCAATGGCATTTCAATGGCTTGCCACT 1580
   |||||
Db 419 AspIleSerLys----- 422
   |||||
QY 1581 CTGGAAGCTTGAAGAAATGGCTGGCAATTTCTTTCAGAGAAACTTCCTCAGATATCTTC 1640
   |||||
Db 423 -----AsnSerPheHisSer-----MetProLutThrCys 432
   |||||
QY 1641 ACAGAGCTGAGAACTTGACCTTCTCTGACCTCTCTCAGTGTCAACCTGAGACAGTGTCT 1700
   |||||
Db 433 GlnTrpProGluLysMetLysThrLeuAsnLeuSerSerThrArgIleHisSerValThr 452
   |||||
QY 1701 -----CAAACGACATTTAATCACTCTCCAGTCTTCAGGTACTAATATGAGCCAC 1751
   |||||
Db 453 GlyCysIlePro-----LysThrLeuGlnIleLeuAspValSerAsn 466
   |||||
QY 1752 AAC-----AATCTTTTCAATTGAT----- 1772
   |||||
Db 467 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLysLysGluLeuTyrIleSerArg 486
   |||||
QY 1773 -----ACGTTTCT---TATAAGTCTCGAACTCCCTCAGGTCTTGATTAC 1817
   |||||
Db 487 AsnLysLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValLeuLysIle 506
   |||||
QY 1818 AGCTTCATCACATATATGATCTTCAAAAAACGAACTTACAGCATTTTCCAAAGTACTTA 1877
   |||||
Db 507 SerArgAsnAlaIleThrThrPheSerLysGlnLeuAspSerPhe---HisThrLeu 525
   |||||
QY 1878 GCTTTCTTAAATCTTACAGATACATCTTGTTGTTTACTTGTGGAACACAGAGTTTCCG 1937
   |||||
Db 526 LysThrLeuGluAlaGlyGlyAsnAsnPheIleCysSerCysGluPheLeuSerPheThr 545
   |||||
QY 1938 CAATGATCAAGACAGACGCTCTTGCTGAGATT-----GAACGA 1982
   |||||
Db 546 Gln-----GluGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsn 561
   |||||
QY 1983 ATGGAATGTGAACACTTTCAGATGAACAGGAGCATGCTGCTGCTGATTTGAATATCAC 2042
   |||||
Db 562 TyrLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581
   |||||

```

Qy	2043	-----TGCAGATGAATAAGAACCATTTGGGTGGCGGCTCCGACGTGGCTTGA	2093
Db	582	ValSerGluCysHisArgIleAlaLeuValSerGlyMetCysValAlaLeuPheLeuLeu	601
Qy	2094	GTATCTGTGTGACAGTTCTGGCTGTATGAATTTCTAT-----TTTCACTGTATGCTTTCT	2147
		::: :::	::: :::
Db	602	IleLeuLeuThrGlyValLeuCysHisArgPheHisGlyLeuThrGlyMetLeuMet	621
Qy	2148	GCTGGCTGCATTAAGATGATGTAGA-----GTTGAAAATCATC---TAT	2186
		::: :::	
Db	622	TPAlaIrrPLeuGlnAlaLysArgGlyProArgGlyAlaProSerArgAsnIleCysTyr	641
Qy	2187	GATGCGCTTTGTATCTACTCAAGCCGAGATGAGAGATGGGGTGAAGATGAGTAAAG	2246
Db	642	AspAlaPheValSerTyrSerGluArgAspAlaTyrTrpValGluHisMetValGln	661
Qy	2247	AATTAGAAAGAGGGGTGCTCCATTTTCAGTCTTGCTTCATACAGACATTATTTCC	2306
Db	662	GluLeuGluAsnPheAsnProProPheTyrLeuCysLeuHisValArgAspPheIlePro	681
Qy	2307	GGTGTGGCCATTGCTGCGCCAACTATCCATGAAAGTTTCATTAAGCCGAAAGTGAT	2366
Db	682	GlyIrrPLeuIleIleAspAsnIleIle---AspSerIleGluHisSerHisIrrPVal	700
Qy	2367	GTGTGGTGTCCGACACTTCATCCAGAGCCGCTGGTGTATCTTTGAATATGATTTGCT	2426
Db	701	PheValIleLeuSerGluAsnPheValIrrPSerGluTrpCysLysTyrLeuAspPheSer	720
Qy	2427	CAGACCTGGCAGTTTCTGAGCAGATCGTGTGTGATCATTTCTATTCCTGCGAAGAGTG	2486
Db	721	HisPheArgLeuPheAspGluHisAsnAspAlaAlaIleLeuIleLeuLeuGluIrrProIle	740
Qy	2487	GAGAAGACCTCTCTCAGGACGACAG---GTGAGCTGTACCGCTTTCAGACGAAACACT	2543
Db	741	GluIrrPValAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrIrrPThr	760
Qy	2544	TACTGAGATGGGAGAGACAGTGTCTCGGGCGGCGACATCTTTCGAGAGACGACTGAAAA	2603
Db	761	TyrLeuGluIrrProMetAspGluAlaGlnArgGluGlyPheIrrPValAsnLeuArgAla	780
Qy	2604	GCCCTG 2609	
Db	781	AlaIle 782	

RESULT 5
 US-09-949-016-8799
 ; Sequence 8799, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8799
 ; LENGTH: 775
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-8799

Alignment Scores:	5.63e-49	Length:	775
Pred. No.:	539.00	Matches:	218

Percent Similarity:	41.22%	Conservative:	120
Best Local Similarity:	26.59%	Mismatches:	264
Query Match:	8.02%	Indels:	218
DB:	4	Gaps:	37

US-09-396-985B-3 (1-3811) x US-09-949-016-8799 (1-775)

QY	306	ATCCCGGCAACCTCCCTTCTCAACCAAGACCTGGACCTTAATACCCCTGAG	365
DB	81	IIleProsergIyLeuthrThgluaIlaValIysSerLeuAspLeuSerAsnAsnArgIleThr	100
QY	366	CATTAGGACGACTTAGCTTCTCAGTTTCCCAAGACTGACGGCTCGATATTATCCAG	425
DB	101	TYrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaValLeuThrSer	120
QY	426	TGTGAATTCAGACATTTGAAGATGGGAGCATATCAGACGCTTAACCACTCTTACCTTA	485
DB	121	AsnGylIleAsnThrIIleGluGlnAspSerPheSerSerLeuGlySerLeuGlnHleu	140
QY	486	ATATTGACAGAAACCCCATCCAGAGTTTACCTGGAGCCCTTTTCTGACATCAAGT	545
DB	141	AspLeuSerTYrAsnTYrLeuSerAsnLeuSerSerSerTrpPheIysProLeuSerSer	160
QY	546	TTACAGAAAGCTG-----GTGCGGTGGAG	569
DB	161	LeuthrPheLeuAsnLeuLeuGlyAsnProTYrIysThrLeuGlyGlnThrSerLeuPhe	180
QY	570	ACAATCTAGCATCTTACAGAACTTCCCATTCGACATCTCAAACT-----	617
DB	181	SerIleSerIleThrIysLeuGlnIIleLeuArgValIleAsnMetAspThrPheThrIle	200
QY	618	-----TTGAAGAACTTAAATGTGGCTCACAACTCTT	647
DB	201	GlnArgIysAspPheAlaGlyLeuThrPheLeuGlnGluIleAspAlaSerAsp	220
QY	648	ATCCAACTTTCGAATTAACCTGAGATATTTCATATGACCAATCTAGACACTGGAC	707
DB	221	LeuGlnSerTYrGlu--ProIysSerLeuIysSerIIleGlnAsnValSerIleLeuLe	239
QY	708	CTTCCGACCAAG-----ATTCAAATGATT	734
DB	240	LeuIleMetIysGlnHIsIIleLeuLeuLeuGlnIlePheValaSerValThrSerSerVal	259
QY	735	TATTGACAGACTTGGGGTTTACATCAATGCCCCCTACTCAATCTCTTAGACCTG	794
DB	260	GluCysLeuGlnLeuArg-----AspThr	267
QY	795	TCCCTGAACCTTAAGAACTT-----ATCCACACAGTGCATTTAAAGAAATAGCTT	848
DB	268	AspLeuAspThrPheHIsPheSerGluLeuSerThrGylGlnThrAsnSerLeu--Ile	286
QY	849	CATPAGCGACTTAAGAAT-----AATTTGATAGTTA--AATGTATGAAA	896
DB	287	LysIysPheThrPheAsnValIleThrAspGlnSerLeuPheGlnValMetIys	306
QY	897	ACTTGT-----ATTCAAGTCTGCTGCTGTTTAGAAGTCCATCGTTGGTCTG-----	944
DB	307	LeuLeuAsnGlnIleSerGylLeuLeuGlnLeuGlnIlePheAspArgCysThrLeuAsnGly	326
QY	945	---GGAGATTTAGAAATGAAAGAACTTGAAAGTTTGACAAATCTGCTTGAAGGC	1001
DB	327	ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyIysValGln--	345
QY	1002	CTGGCAATTGGACATTTGAAGATTCGATAC-----TACTTAGACTATACCTC	1055
DB	346	-----ThrLeuThrIIleArgGluLeuHIsIIleProArgPheTYrLeuPheTYr-----	361
QY	1056	GATGATATTATGACTATTATTAATGTGTTGCAAAATGTTTCTTCAATTTCCCTGGTAGT	1115
DB	362	---AspLeuSerThrLeuTYrLeuSerLeuThrGluArgValIys-----Arg	375
QY	1116	GTGACTATTGAAGGGTAAAGACTTTTCTTATTAATTTCCGATGGCAACATTTAGAAATTA	1175

```

Db      376  ILeThrValGluAsnSerLysValPhe-----Leu 385
Qy      1176 GTTAACTGTAATTTGGACAGTTTCCACATTGAAATCTCTCAAAAGGCTTACT 1235
Db      386  ValProCysLeuLeuSerGln----- 392
Qy      1236 TTCACCTTCCAGAAAGGTGGGAATGCTTTTTCAGAGTTGATCTACCAAGCCTTGAGTTT 1295
Db      393  -----HisLeuLysSerLeuGluTyr 399
Qy      1296 CTAGATCTCAGTGAAT-----GGCTTGAAGTTTCAAGGTTGCTGTTCT 1340
Db      400  LeuAspLeuSerGluAsnLeuMetValGluGluTyrLeuLysAsnSerAlaCys----- 417
Qy      1341 CAAAGTGATTTTGGGACCAACGCCCTAAAGTATTGATGATCGTCAAGCTTCAAGTGTATT 1400
Db      418  -----GluAspAlaTyrProSerLeuGlnThrLeuIleLeuLysArgGlnAsn----- 432
Qy      1401 ACCAATGAGTTCAAACTTCTGGGCTTAGAAACAATGACATCTGGATTCTCAGCATTC 1460
Db      433  -----HisLeu-----Ala 435
Qy      1461 AATTGAAACAATGAGTGAATTTTCAGATTCTTATCACTGACAAACCTCATTTACCTT 1520
Db      436  SerLeuGluLysThrGlyGlu-----ThrLeuLeuThrLeuLysAsnLeuThrAsnIle 453
Qy      1521 GACATTCTCATACTGACACACAGATTGGTTCAATGGCATTTCAATGGCTTGTCCACT 1580
Db      454  AspIleSerLys----- 457
Qy      1581 CTGGAAGTCTTGAAATGGCTGGCAATCTTTCAGAAACCTTCCAGATATCTTC 1640
Db      458  -----AsnSerPheHisSer-----MetProGluThrCys 467
Qy      1641 ACAAGACCTGAGAACTTGACCTTCTGACACCTCTCTCAGTGTCACTGACAGAGTTGTCT 1700
Db      468  GlnTyrProGluLysMetLysTyrLeuAsnLeuSerThrArgIleHisSerValThr 487
Qy      1701 -----CSAACAGCATTTAACTCAGCTCTCGAGCTTCAGGTACTTAATTAAGCCAC 1751
Db      488  GlyCysIlePro-----LysThrLeuGlnIleLeuAspValSerAsn 501
Qy      1752 AAC-----AACTCTTTTCATTGAT----- 1772
Db      502  AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGluLeuTyrIleSerArg 521
Qy      1773 -----ACGTTTCTCT--TATTAAGTCTGAACTCCCTCAGGTTCTTGATTAC 1817
Db      522  AsnLysLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValLeuLysIle 541
Qy      1818 AGTCTCAATCAGATATGACTTCCAAAAACAGAACTACAGCATTTTCCAGTACTCTTA 1877
Db      542  SerArgAsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe--HisThrLeu 560
Qy      1878 GCTTTCTAAATCTTACAGATGAGTCTTGTGATCTGTGTAACACAGAGTTTCTGT 1937
Db      561  LysThrLeuGlnAlaLeuLysIleAsnAsnPheIleCysSerCysGluThrLeuSerPheThr 580
Qy      1938 CAATGATTAAGGACCAAGAGCAGCTTGTGGTGAAGTT-----GAACA 1982
Db      581  Gln-----GluGlnGlnAlaLeuAlaLysValLeuIleAspTyrProAlaAsn 596
Qy      1983 AAGGAATGTAACAACCTTCAGATTAAGCAGGCGATCGCTGTGATGTAATATCAC 2042
Db      597  TyrLeuCysAspSerProSerThrIleValArgGlyGlnGlnAlaGlnAspValArgLysSer 616
Qy      2043 -----TGTCAAGTGAATAAGACATCATGATGATGATGCTGCTGCTCAAGTGTCTGA 2093
Db      617  ValSerGluCysHisIleArgThrIleAlaLeuValSerGlyMetCysCysValAlaLeuPheLeuLeu 636
Qy      2094 GTATCTGTTGTAAGACGTTCTGTGATTAAGTTCTAT-----TTTCAACCTGATGCTTCTT 2147
Db      637  IleLeuLeuThrGlyAlaLeuCysHisIleArgPheHisGlyLeuThrTyrMetLysMetMet 656

```

```

Qy      2148 GCTGGCTGATTAAGTATATGTAGA-----GGTGAACAATC---TAT 2186
Db      657  TrpAlaTyrPheGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTyr 676
Qy      2187 GATGCTTTGTTATCTACTCAAGCCAGATGAGACGTGGTGAAGATGAGCTAGTAAAG 2246
Db      677  AspAlaPheValSerTyrSerGluTyrGlnAlaTyrTrpValGluAsnLeuMetValGln 696
Qy      2247 AATTGAAAGAAAGGGTCCCTTCATTTGACGTCTGCGCTTCTCAAGAGACTTATGCC 2306
Db      697  GluLeuGluAsnPheAsnProPheLysLeuCysLeuHisLysArgAspPheIlePro 716
Qy      2307 GGTGTGGCATTGTCTGCCAACATCATTCAGTAAGGTTTCCATTAAGCCGAAAGGTGATT 2366
Db      717  GlyLysTrpIleIleAspPheIleIle---AspSerIleGluLysSerHisLysThrVal 735
Qy      2367 GTTGTGTGTCCAGACACTTCAATCCAGACCGCTGTGTATCTTTGAATPAGATTTGCT 2426
Db      736  PheValLeuSerGluAsnPheValLysSerGluTyrCysLysTyrGluLeuAspPheSer 755
Qy      2427 CAGACCTGGCAGTTTCTGACAGAGTGTGCTGTATCATTTGATGTTCTCGAGAAAGTG 2486
Db      756  HisPheArgLeuPheAspGluAsnAsnAspAlaAlaIleLeuIleLeuLeuGluProIle 775

RESULT 6
US-09-063-950-5
/ Sequence 5, Application US/09063950C
/ Patent No. 623085
/ GENERAL INFORMATION:
/ APPLICANT: HOLZMAN, Douglas A.
/ TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES
/ TITLE OF INVENTION: THEREFOR
/ FILE REFERENCE: MEI-019
/ CURRENT APPLICATION NUMBER: US/09/063,950C
/ CURRENT FILING DATE: 1998-04-21
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 605
/ TYPE: PRT
/ ORGANISM: Papio hamadryas
US-09-063-950-5

Alignment Scores:
Pred. No.: 9 716-26
Score: 325.00 Length: 605
Percent Similarity: 38.83% Matches: 163
Best Local Similarity: 24.44% Conservative: 96
Query Match: 4.83% Mismatches: 254
DB: 3 Gaps: 154 Indels: 24

US-09-396-985B-3 (1-3811) x US-09-063-950-5 (1-605)
Qy      201 CAGCCCTTCAACCCCG-----ATTCCATTGCTTCTGTCAATAGCTGCCGTTT 248
Db      29  GluProGluThrProGluGlnAlaGluGlyProAlaCysProAlaThrCysAlaCysSer 48
Qy      249 ATCAGAGAGGTGTTCTTAATATTAATTAATCAATGAGAGCTGAATTTTCAAAATC 308
Db      49  TyrAspAspGluValAsnGluLysLeuSerValPheCysSerSerArgAsnLeuThrArgLeu 68
Qy      309 CGCGAACCTCCGCTTCTCAACCAAGAAACCTGACCTGAGCTTTAATCCCTGAGGAT 368
Db      69  ProAspGlyLeuProGlyGlyThrGlnAlaLeuThrPheLysSerAsnAsnLeuSerSer 88
Qy      369 TTAGCAGCTAATAGCTTTCAGTTTCCAGATCTGACAGTGCAGTGTGATTTATCCAGTGT 428
Db      89  IleProProAlaAlaPheArgAsnLeuSerSerLeuAlaPheLeuAsnLeuGlnGly 108
Qy      429 GAAATCCAGCAATTTGAAGATGGGCGATATTCAGACCTTAAGCCCACTCTTAATATA 488
Db      109  GlnLeuGlySerLeuGluProGlnAlaLeuLeuGluGlyLeuGluAsnLeuCysHisIle 128

```

QY 489 TTGACGAGAAACCCCTCAGAGTTTACGCTTGAGACCTTTCT----- 533
 DB 129 LeuGluArgAsnGlnLeuArgSerIleuAlaValGlyThrPheAlaIyrThrProAlaLeu 148
 QY 534 -----GGA 536
 DB 149 AlaLeuGluGlyLeuSerAsnAsnArgLeuSerArgLeuGluAspGlyLeuPheGluGly 168
 QY 537 CTATCAAGTTTACAGAGCTGGTGGCTGGAGACAAATCTAGCATCTCTAGAGAACTTC 596
 DB 169 LeuGlyAsnLeuTrpAspLeuAsnLeuGlyTrpAsnSerIleuAlaValLeuProAspAla 188
 QY 597 CCCATTGACATCTCAAACTTTGAAAGAACTTAATGGCTCAGACATCTTAACTCATCT 656
 DB 189 AlaPheArgGlyLeuGlyLeuArgGlyLeuValLeuAlaGlyAsnArgLeu--Ala 207
 QY 657 TTCAAATTACCTGAGATTCTTCTAATCTGACCAATCTAGACACTTGACCTTCCAGC 716
 DB 208 TyrLeuGlnProAlaLeuPheSerGlyLeuAlaGlnLeuArgGlnLeuAspLeuSerArg 227
 QY 717 AACGAATTCAAAGTATTATTATGACAGACTTGGGCTTCTACATCAATGCCCTACTC 776
 DB 228 AsnAlaLeuArgAlaIle-----LysAlaAsnValPheAlaGlnLeuProArgLeu 244
 QY 777 AATCTCTCTTACGCTGCTCCGACCCCTATGACCTTATCCAAAGCTGATTTAA 836
 DB 245 Gln--LysLeuTrpLeuAspArgAsnLeuIleAlaValAlaProGlyAlaPheLeu 263
 QY 837 GAAATTAGG---CTTCATAGCTGACTTATAGCAATATATTTGATGTTAATGTAAAG 893
 DB 264 GlyLeuLysAlaLeuArgTrpLeuAspLeuSerHisAsn--ArgAlaAlaGlyLeuLeu 282
 QY 894 AAACTTGATTCAGAGCTGCTGGCTGTTTAAAGATCCATGCTTGTGTTGGAGAAATT 953
 DB 283 GluAspThrPheProGlyLeuLeuGlyLeuArgValLeuArgLeu----- 297
 QY 954 AGAATGAGAGAACTTGAAAAAGTTGCAAAATCTGCTAGAGGCGCTGTCATTTG 1013
 DB 298 -----SerHisAsnAlaIleAlaSerLeuArgProArg 308
 QY 1014 ACCATTGAAGAAATCCGATTAGCATCTAGACTTACCTGATGATTTATGACTTA 1073
 DB 309 ThrPheGluAspLeu-----HisPheLeuGlnLeu----- 319
 QY 1074 TTTAATTGTTGACAAATGTTCTTCAATTTCCCTGCTGAGTGTGACTATGAAGGGA 1133
 DB 320 -----GlnLeuGlyHisAsnArgIleArgGlnLeu 329
 QY 1134 AAAAGCTTTCTTAATTTGCGATGCGCAACATTTGAAATTGATTAACGTAAATTGGA 1193
 DB 330 AlaGluArgSerPheGln--GlyLeuGlyGlnLeuGlnValLeuThrLeuAspHisAsn 348
 QY 1194 CAGTTTCCACATTTGAACATCTCTCAAAAAGCTTACTTCACTTCC-----AAC 1247
 DB 349 GlnLeuGlnGlnValLysValGlyAlaPheLeuGlyLeuThrAsnValAlaValMetAsn 368
 QY 1248 AAAGTGGGAATGCTTTTCAAGAGTTGATCTACCAAGCCTTGAGTTTCAATCTCAGT 1307
 DB 369 LeuSerGlyAsnGlyLeuArg-----AsnLeuProGlnGlnValPheArgGlyLeuGly 386
 QY 1308 AAG---AATGGCTTGAGTTTCAAAAGTTGCTGT-----TCTCAAAATGAT 1349
 DB 387 LysLeuHisSerIleuHisLeuGlnGlySerCysLeuGlyAlaArgIleArgProHisTrpPhe 406
 QY 1350 TTTGGACACCAAGCTTAAGTATTATGATCTGAGCTTCAATGTTGTTATACCATGAGT 1409
 DB 407 AlaGlyLeuSerGlyLeuArgLeuPheLeuLysAspAsnGlyLeuValGlyIleGln 426
 QY 1410 TCAAACTTCTTG--GGCTTAGAACACTTGAACATCTGAGATTTCCAGCATTCCAATTG 1466
 DB 427 GluGlnSerLeuTrpGlyLeuAlaGlnLeuGlnLeuAspLeuThrSerAsnGlnLeu 446

QY 1467 AAACAATGAGTAGTTTTCAGTATTCCTATCTACAGAAACCTCATTTACCTTGACATT 1526
 DB 446 ----- 446
 QY 1527 TCTCATCTACACCAAGCTTCTTCAATGCAATCTTCAATGCTTGTCCAGTCTGCA 1586
 DB 447 -----ThrHisLeuPro-----HisGlnLeuPheGlnGlyLeuGlyLysLeuGln 461
 QY 1587 GTCCTGAAATGGCTGGCAATCTTTCCAGAGAAACCTTCCTTCCA---GATATCTTCACA 1643
 DB 462 TyrLeuLeuLeuSerHisAsnArgLeuAlaGln-----LeuProAlaAspAlaLeuGly 479
 QY 1644 GAGCTGAGAACTTACCTTCCCTGAGACCTCTCTCAGTGTCAACTGAGAGCTTGTCTCCA 1703
 DB 480 ProLeuGlnArgAlaPheTrpLeuAspValSerHisAsnArgLeuGlnAlaLeuProGly 499
 QY 1704 ACAGCATTTACTCACTCTCCAGTCTTCAAGGTACTTAATATGACCAACAACTTCTTT 1763
 DB 500 SerLeuLeuAlaSerLeuGlyArgLeuArgTrpLeuAsnLeuArgAsnAsn----- 516
 QY 1764 TCATGATAGCTTCTTATTAAGTGTCTGAACCTCCCTCAGGTTCTTATACAGTTC 1823
 DB 517 SerLeuArgThrPheThrProGln----- 524
 QY 1824 AATCATATATGACTTCCAAAAACAGAACTACAGACTTTTCCAAAGTACTGACTTTC 1883
 DB 525 -----ProProGlyLeuGluArg 530
 QY 1884 TTTAAATCTTACTCAGAAATGACTTGTCTGTACTTGTGAACACCAGAT----- 1931
 DB 531 LeuTrpLeuGlnGlyAsnProTrpAspCysSerCysProLeuLysAlaLeuArgAspPhe 550
 QY 1932 -----TTCCTCGCAATGATC-----AAGGAC 1952
 DB 551 AlaLeuGlnAsnProSerAlaValProArgPheValGlnAlaIleCysGlnGlyAspAsp 570
 QY 1953 CAGAGCAGACTTGTGTGAGAGTTGAACGATGATGATGCAACCTTCCAGATTAAGCAG 2012
 DB 571 CysGlnProProValTyrThrTrpAsnAsnIleThrCysAlaSerProProGlnValAla 590
 QY 2013 GGCATGCTGTGCTGAGTTTG 2033
 DB 591 GlyLeuAspLeuArgAspLeu 597

RESULT 7
 US-09-949-016-10995
 ; Sequence 10995, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH TYPE 2 DIABETES MELLITUS
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 10995
 ; LENGTH: 623
 ; TYPE: PRY
 ; ORGANISM: Human
 ; US-09-949-016-10995

Alignment Scores:
 Pred. No.: 1,03e-23 Length: 623
 Score: 306.50 Matches: 175
 Percent Similarity: 38.17% Conservative: 96

Best Local Similarity: 24.65% Mismatches: 279
 Query Match: 4.56% Indels: 160
 DB: 4 Gaps: 27

US-09-396-985B-3 (1-3811) x US-09-949-016-10995 (1-623)

```

QY 95 CCTCTCCGCTGAGAGCAGAAAGCTGGAGCCCTGCGAGACTTTGGCCCTAAACAC 154
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 15 ProAlaCyArgMetValLeuArgLysGlyGlyLeuAla-----LeuAlaLeuLeu 32
QY 155 ACAGAAAGCTGGCATGAACCCAGAGCTTTACAGACTCCGAGCCCTTACAGCCC 214
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 33 LeuSerTrpValAlaLeuGlyProArg---SerLeuGlyGlyAla-AspProGlyThrPr 51
QY 215 G-----ATTCCATTGCTTGTCTAAATGCTGCCCTTTATGACGGAGGCTGT 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 51 oGlyGlyAlaGlyGlyProAlaCyArgProAlaAlaCySerValCySerTrpAspSerAl 71
QY 263 TCCATATATTACTTATCATGAGCTGAGCTGAATTTCTACAAATCCCGACAACTCCC 322
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 71 AspGlyLeuSerValPheCySerSerTrpArgAsnLeuThrArgLeuProAspGlyValPr 91
QY 323 CTTCACCAAGAACCTGAGCTGAGCTTTAAATCCCTGAGGCAATTGAGCAGCTAAG 382
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 91 oGlyGlyThrGlnAlaLeuThrLeuAspGlyAsnAsnLeuSerSerValProProAlaAl 111
QY 383 CTTCCTCACTTCCCGAAGCTGAGCTGAGCTTTAAATCCAGGTGGAATCCAGACAT 442
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 111 aPheGlnAsnLeuSerSerLeuGlyPheLeuAsnLeuGlnGlyGlnLeuGlySerLe 131
QY 443 TGAAGATGGGGCATATCAGAGCTTACAGCACTCTTACCTTAAATTTGACAGAAACCC 502
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 131 uGlyuProGlnAlaLeuLeuGlyLeuGlyuAsnLeuCyHisLeuHisLeuGlyuArgAsnG 151
QY 503 CATCCAGATTAGCCCTGGAGCCCTTTCT----- 533
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 151 nLeuArgSerLeuAlaLeuGlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLe 171
QY 534 -----GAGCTATCAAGTTTACA 550
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 171 uSerAsnAsnArgLeuSerArgLeuGlyuAspGlyLeuPheGlyuGlyLeuGlySerLeuTr 191
QY 551 GAAGCTGTGCTGTGAGAGCAATCTAGACATCTCTAGAGAACTTCCCATTTGACATCT 610
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 191 pAspLeuAsnLeuGlyTrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLe 211
QY 611 CAAACTTTGAAAGAACTTAATGCTGCTCACAATCTTATCCAACTTTTCAAAATTACCTGA 670
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 211 uGlySerLeuArgGlyLeuValLeuAlaGlyAsnArgLeu--AlaTrpLeuGlnProAl 230
QY 671 GTATTTTCTAATCTGACCAATCTAGAGCACTTGGACCTTCCAGAGCAACAAGATTCAAG 730
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 230 aLeuPheSerGlyLeuAlaGlyLeuArgGlyLeuAspLeuSerArgAsnAlaLeuArgAl 250
QY 731 TATTTATTCACAGACTTGGGGGTCTTACATCAAAAGCCCTTACATCTCTTTAA 790
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 250 aIle-----LysAlaAsnValPheValGlnLeuProArgLeuGln---LysLeuTr 266
QY 791 CCTGTCCCTGAACTTATGAACTTTATCCAAAGGCTGATTTAAAGAAATTAGG---CT 847
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 266 rLeuAspArgAsnLeuIleAlaAlaValAlaPheGlyAlaPheLeuGlyLeuLysAlaLe 286
QY 848 TCATAAGCTGACTTTAAGAAATTAATTTGATAGTTAAATGTAATGAAATCTGTATTC 907
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 286 uArgTrpLeuAspLeuSerHisAsn--ArgValAlaGlyLeuLeuGlyuAspThrPhePr 305
QY 908 AGGTCTGGCTGGTTGGAAGTCAATGCTTTGTTCTGGAGAAATTAGAAATGAGAGAA 967
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 305 oGlyLeuLeuGlyLeuArgValLeuArgLeu----- 315
QY 968 CTTGAAAAAGTTGACAAATCTGCTCTAGAGGGCTGTGCAATTGTGACATTGAGAAATT 1027
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 316 -----SerHisAsnAlaIleAlaSerLeuArgProArgThrPheLysAspLe 331

```

```

QY 1028 CCGATTAGCAATCTTAGACTACTACCTGATGATATATTTAGCTATTTAATTTGTTGAC 1087
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 331 u-----HisPheLeuGlyLeu----- 337
QY 1088 AAATGTTTCTTCAATTTCCCTGGTAGGTGTGATATTGAAAGGTAAGAACTTTCTTA 1147
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 338 -----GlnLeuGlyHisAsnArgLleArgGlnLeuAlaGlyuArgSerPr 352
QY 1148 TAAATTCGAGTGGCAACTTTAATTAATTTAGTTAACTGTAAATTTGACAGTTTCCACAT 1207
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 352 eGlu---GlyLeuGlyGlnLeuGlnValLeuThrLeuAspHisAsnGlnLeuGlnVal 371
QY 1208 GAAACTCAAACTCTCAAAAGGCTTACTTCACTCC-----AACAAAGGTGGAATGC 1261
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 371 llyAslAlaGlyAlaPheLeuGlyLeuThrAsnValAlaValMetAsnLeuSerGlyAsnCy 391
QY 1262 TTTTTCAGAAAGTTGATCTTACCAAGCTTGAAGTTTCTAGATCTCAGTAGA--AATGCTT 1318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 391 vLeuArg-----AsnLeuProGlyGlnValPheArgGlyLeuGlyLysLeuHisSerLe 409
QY 1319 GAGTTTCAAAAGTTCTGT-----TCTCAAAAGTATTTTGGACAAACAG 1363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 409 uHisLeuGlyGlySerCyvLeuGlyArgLleArgProHisThrPheThrGlyLeuSerG 429
QY 1364 CCTAAAGTATTTAGATCTGAGCTTCAATGGTGTATTATTCATGAGTTCAAACTTCTG-- 1421
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 429 yLeuArgArgLeuPheLeuLysAspAsnGlyLeuValGlylGlyGlyGlnGlnSerLeuTr 449
QY 1422 -GGCTTAGAAACAATAGAACATCTGATTTTCCAGATTTCCAAATTTGAAACAAATAGTGA 1480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 449 pGlyLeuAlaGlyLeuLeuGlyLeuAspLeuThrSerAsnGlnLeu----- 464
QY 1481 GTTTTCAGTATCTTATCACTCAAGAAACCTATTACTTGCATTTCTCATCTCACAC 1540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 465 -----ThnHisLe 467
QY 1541 CAGAGTGTCTTCAATGAGCATCTTCAATGCTTGTGCTGCAAGTCTTGAATGAGC 1600
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 467 uPro-----HisArgLeuPheGlnGlyLeuGlyLysLeuGlyTrpLeuLeuSe 484
QY 1601 TGGCAATCTTTTCCAGAAAACTTCTTCCA--GATATCTTCCAGAGCTGAGAACTT 1657
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 484 rArgAsnArgLeuAlaGlyu-----LeuProAlaAspAlaLeuGlyProLeuGlnArgAl 502
QY 1658 GACCTTCCCTGAGCCTCTCTCACTGTCACATGAGAGAGTTGTCCAAAGCATTTAACTC 1717
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 502 aPheTrpLeuAspValSerHisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaPr 522
QY 1718 ACTTCAGTCTTTCAGGTCTAATATATGAGCCACAAACAATCTTTCAATTTGATGATGCT 1777
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 522 oLeuGlyArgLeuArgTrpLeuSerLeuArgAsnAsn-----SerLeuArgThrPh 539
QY 1778 TCCCTTAAGTGTCTGAACCTCCCTCAGGTCTTGTATTAACGTCTCAATCATATATGAC 1837
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 539 eThrProGln----- 542
QY 1838 TTCCAAAAAACAGAACTACAGACATTTTCCAAAGTGTCTAGCTTTCTTAAATCTTACTCA 1897
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 543 -----ProProGlyLeuGlyuArgLeuTrpLeuGlyGly 553
QY 1898 GAATGACTTGTGTTGATCTTGTGAACACACAGAGTTTCCGCAATGAGTCAAGAC----- 1952
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 553 yAsnProTrpAspCyvGlyCyvPro-----LeuLysValaLeuArgAspPheAl 569
QY 1953 -----CAGAGGAGCTTGTGTGGAAGTTGAACGATGAGATG 1990
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 569 aLeuGlnAsnProSerAlaValProArgPheValGlnAlaLleCyvGlyGlyLysAspArg 589
QY 1991 TGCACACCTTTCAGATTAAGCAGAGGAGCTGTGCTGAGTTGAAATATATCTGTCAAGT 2050
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 589 eGlnProProAlaTrpTrpThrTyAsn-----AsnIleThrCyAlaLe 603

```

QY 2051 GAATAGACCATCATGTTGTGTGCTC 2078
Db 603 rProgluValValGlyLeuAepLeu 612

RESULT 8
US-08-190-802A-49
Sequence 49, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Delinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190, 802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-190-802A-49

Alignment Scores:
Pred. No.: 1.14e-23 Length: 605
Score: 306.00 Matches: 160
Percent Similarity: 38.25% Conservative: 94
Best Local Similarity: 24.10% Mismatches: 258
Query Match: 4.55% Indels: 152
DB: 1 Gaps: 24

US-09-396-985b-3 (1-3811) x US-08-190-802A-49 (1-605)

QY 219 CCATTCCTCTTCTTAATGCTGCGTTTATCAGGAGGTGGTCTTATATTAATTAAT 278
Db 39 ProAlaCySerProAlaAlaCySerValCySerThrAspAspAlaAspGluLeuSerVal 58

QY 279 CAATGATGAGGTGAATTTCTCAAAATCCCGACAACCTCCCTTTCACCAAGAAC 338
Db 59 PheCysSerSerArgLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAla 78

QY 339 CTGACCTGAGCTTATATCCCTGAGGACATTAGGACGATAGCTTCTTCAATTCCTCA 398
Db 79 LeuTrpLeuAspGlyAsnAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSer 98

QY 399 GAATGAGGTGCTGATTTATCCAGGTGTGAATCAGACAATTGAGATGGGGCATAT 458

Db 99 SerLeuGlyPheLeuAsnLeuGlnGlyGlyGlnLeuGlySerLeuGluProGlnAlaLeu 118
QY 459 CAGAGCCTAAGCCACCTCTCTACCTTAATATTCACAGAAACCCCATCCAGATTTAGCC 518
Db 119 LeuGlyLeuGluAsnLeuCyShiSleuH1SLeuGluArgAsnG1nLeuArgSerLeuAla 138

QY 519 CTGGAGACCTTTCT----- 533
Db 139 LeuGlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeu 158

QY 534 -----GACATATCAAGTTTACAGAGCTGGCTGTG 566
Db 159 SerArgLeuGluAspGlyLeuPheGlnGlyLeuGlySerLeuTrpAspLeuLeuGly 178

QY 567 GAGACAAATCTAGACCTCTAGAGAACTTCCCATGAGCATCTCAAACTTGAAGAA 626
Db 179 TrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuArgGlu 198

QY 627 CTTAATGTGGCTCAGATCTTATCCATCTTTCAATTTACCTGAGATTTTCTTAATCTG 686
Db 199 LeuValLeuAlaGlyAsnArgLeu---AlaTrpLeuGlnProAlaLeuPheSerGlyLeu 217

QY 687 ACCAATCTAGAGCACTTGACCTTTCCAGCAACAGATTCAAGATTTATTTGACAGAC 746
Db 218 AlaGluLeuArgGlyLeuAspLeuSerSerArgAsnAlaLeuArgAlaLe-----Lys 234

QY 747 TTGGGGGTTCTACATCAATATGCCCTTACTCAATCTCTTTAGACCTGTGCCGAACCT 806
Db 235 AlaAsnValPheValGlnLeuProArgLeuGln---LysLeuTrpLeuAspArgAsnLeu 253

QY 807 ATGAATCTTATCCACAGGTGATTTAAGAAATTAGG---CTTCATAGCTGACTTTA 863
Db 254 IleAlaValAlaProGlyAlaPheLeuGlyLeuValAlaLeuArgTrpLeuAspLeu 273

QY 864 AGAATATATTTGATGATTTAATGTAATGAAACTTGTATTCAGAGCTGTGGCTGTTA 923
Db 274 SerHisAsn---ArgValAlaGlyLeuLeuGluAspThrPheProGlyLeuLeuGlyLeu 292

QY 924 GAATGTCATCGTTTGTGTTCTGGAGAAATTAGAAATGAAGAAACTTGGAAAAATTGAC 963
Db 293 ArgValLeuArgLeu-----Ser 298

QY 984 AATGTGCTGTAGAGGCGCTGTGCAATTTGACCATTTGAAGAAATTCGATTAGCATCTTA 1043
Db 299 HisAsnAlaIleAlaSerLeuArgProArgGlnPheLeuAspLeu----- 313

QY 1044 GACTTACCTCGATGATATTTATTTGACTTATTTAATTTGTTGCAAAATGTTCTTCATT 1103
Db 314 ---HisPheLeuGluGluLeu----- 319

QY 1104 TCCCTGTGATGTGACTATTTGAAAGGTTAAAGACTTTTCTATATTTGCGATGGCAA 1163
Db 320 GlnLeuGlyHisAsnArgIleArgGlnLeuAlaGluArgSerPheGlu---GlyLeuGly 338

QY 1164 CATTTAGATTTAGTTAATCTGAATTTGACAGTTTCCCAATTTGAATCAAAATCTGTC 1223
Db 339 GlnLeuGluValLeuThrLeuAspHisAsnGlnLeuGlnValAlaGlyAlaPhe 358

QY 1224 AAAAGCTTACTTTCACTTCC-----AACAAAGGTGGAAATGCTTTTCAGAAATTGAT 1277
Db 359 LeuGlyLeuThrAsnValAlaValMetAsnLeuSerGlyAsnCySerArg-----Asn 376

QY 1278 CTACCAAGCTTGAGTTTCTAGATCTGAGTACG---AATGCTTGAGTTTCAAGGTTCG 1334
Db 377 LeuProGluGlnValPheArgGlyLeuGlyLysLeuHisSerLeuHisLeuGlnGlySer 396

QY 1335 TGT-----TCTGAAGTGATTTTGGAGCAACCAAGCTTAAGATTAGAT 1379
Db 397 CysLeuGlyArgTrpLeuProHisThrPheThrGlyLeuSerGlyLeuArgArgLeuPhe 416

QY 1380 CTGAGCTTCAATGTGTATTTATCCATGAGTTCAAACTTCTTG---GGCTTGAACAACATA 1436
Db 1380 |||||-----||| |||||-----||| |||||-----||| |||||-----|||

Db 417 LeuLYaSPaSnGLyLeuValGLyILeGLuGLInSerLeuTrpGLyLeuAlaGLuLeu 436
QY 1437 GAACATCTGATTTCCAGATTCCTCAATTGAAACAAATGAGTGGATTTCATTCCTTA 1496
Db 437 LeuGLIleuAspLeuThrSerAsnGLIneu----- 446
QY 1497 TCACTGAGAACTCATTTACCTTGACATTTCTCATCTACACACAGAGTGGCTTCAAT 1556
Db 447 -----ThrIleuPro-----His 451
QY 1557 GGCATCTTCATAGCTTGTCTTCAGCTTCGAAGCTTGAAATGGCTGGCAATTTCTTCAG 1616
Db 452 ArgLeuPheGLInGLyLeuGLyLLeuGLyLeuLeuSerArgAsnAGLeuAla 471
QY 1617 GAAACCTTCCTTCA---GATATCTTCACAGAGTGAGAACTTGACCTTCCTGACCTG 1673
Db 472 GIU-----LeuProAlaSerAlaLeuGLyProLeuGLInArgAlaPheTrpLeuAspVal 489
QY 1674 TCTCAAGTGTCACTGAGAGAGTGTCTCAACAGACATTTAACTCACTCTTCAGCTTCAG 1733
Db 490 SerHisAsnArgLeuGLInAlaLeuProAsnSerLeuLeuAlaProLeuGLyArgLeuArg 509
QY 1734 GTACTTAATATGAGCCACAACTCTTTCTCATTTGATACGTTTCTTAAAGTGTCTG 1793
Db 510 TyLeuSerLeuArgAsnAsn-----SerLeuArgThrPheThrProGLIn----- 524
QY 1794 AACTCCCTCCAGGTTCTTGATTAACGTCTCATCATATGACTTCACAAAACAGAA 1853
Db 524 ----- 524
QY 1854 CTACAGCATTTTCCAGTACTAGCTTTCTTAATCTTACTGAGAAAGTACTTGTCTGT 1913
Db 525 -----ProProGLyLeuGLyLeuArgLeuTrpLeuGLyAsnProTrpAspCys 540
QY 1914 ACTTGTGAACACAGAGTTCTTCGCAATGATGATCAAGAC----- 1952
Db 541 GLYCySerPro-----LeuLYaLalaLeuArgAspPheAlaLeuGLInAsnProSer 556
QY 1953 -----CAGAGCAGCTCTGTGTGAAGTTGAACGAATGGAATGTGCAACCTTCAGAT 2006
Db 557 AlavaLProArgPheValGLInAlaLLeuCyGLInGLyAspAspCysGLInProProAlaTyR 576
QY 2007 AACGAGGAGCATGCTGTGTGATGATTGAATATCACTCTGATGATGAATAAGACCATAT 2066
Db 577 ThrTyAsn-----AsnIleThrCysAlaSerProProGLyValVal 590
QY 2067 GGTGTGTGGTTC 2078
Db 591 GLYLeuAspLeu 594
RESULT 9
US-08-477-346-49
Sequence 49, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025, 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor binding
INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49
Alignment Scores:
Pred. No.: 1,14e-23 Length: 605
Score: 306.00 Matches: 160
Percent Similarity: 38.258 Conservative: 94
Best Local Similarity: 24.104 Mismatches: 258
Query Match: 4.55% Indels: 152
DB: 3 Gaps: 24
US-09-396-985b-3 (1-3811) x US-08-477-346-49 (1-605)
QY 219 CCATTGCTTCTTGAATGCTGCCGTTTATCAAGAGTGAGTTCCTAATATTACTTAT 278
Db 39 ProAlaCyProAlaAlaCyValCySerTyYAspAspAlaAspGLuLeuSerVal 58
QY 279 CAATGATGAGAGTGAATTTCTAACAATCCCGACACCTCCCTTCACCAAGAAC 338
Db 59 PheCySerSerArgAsnLeuThrArgLeuProAspGLyValProGLyLysArgInAla 78
QY 339 CTGACCTGAGCTTTATCCCTGAGGACATTAGGAGCTATAGCTTCTTCAGTTCCCA 398
Db 79 LeuTrpLeuAspGLyAsnAsnLeuSerValProProAlaAlaPheGLInAsnLeuSer 98
QY 399 GAATGACAGGTGTGATTTATCCAGGTGTGAATCCAGACATTTGAAGATGGGCATAT 458
Db 99 SerLeuGLyPheLeuAsnLeuGLInGLyGLInLeuGLySerLeuGLyProGLInAlaLeu 118
QY 459 CAGAGCTTAAGCCACTCTCTACCTTAATATGACAGAAACCCATCCAGATTATGCC 518
Db 119 LeuGLyLeuGLyAsnLeuCyHisLeuHisLeuGLyValArgAsnGLInLeuArgSerLeuAla 138
QY 519 CTGGAGCCTTTCT----- 533
Db 139 LeuGLyThrPheAlaHisThrProAlaLeuAlaSerLeuGLyLeuSerAsnAsnArgLeu 158
QY 534 -----GACTATCAAGTTTACAGAACTGTGTGCTGTG 566
Db 159 SerArgLeuGLyAspGLyLeuPheGLInGLyLeuGLySerLeuTrpAspLeuAsnLeuGLy 178
QY 567 GAGACAAATCTAGCATCTTAGAGAACTCCCATTTGACATCTCAAACTTTGAAAGAA 626
Db 179 TrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGLyLeuGLySerLeuArgGLIn 198
QY 627 CTTAATGAGCTGACATCTTACCAATCTTCAATATCCAGATTTTCTATATCG 686
Db 199 LeuValLeuAlaGLyAsnArgLeu---AlaTyTrLeuGLInProAlaLeuPheSerGLyLeu 217
QY 687 ACCAATCTAGAGCACTTGACCTTTCAGCAACAAGATTCAAGATTATTTATGACAGAC 746

Pred. No.: 1,14e-23 Length: 605
 Score: 306.00 Matches: 160
 Percent Similarity: 38.25% Conservative: 94
 Best Local Similarity: 24.10% Mismatches: 258
 Query Match: 4.55% Indels: 152
 DB: 3 Gaps: 24

US-09-396-985B-3 (1-3811) x US-08-473-089-49 (1-605)

QY 219 CCATTGCTTCTGTAATGCGCGTTTATACAGAGGTGTTCTTAATATTACTTAT 278
 DB 39 ProAlaCysProAlaAlaCysValCysSerTyrAspAspAlaAspGluLeuSerVal 58
 QY 279 CAATGATGAGAGTATTTCTACAAATCCCGACAACTCCCTTCATCAACCAAGAC 338
 DB 59 PheCysSerSerArgAsnLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAla 78
 QY 339 CTGACCTGAGCTTTAATCCCTGAGGACATTAGGACCTATAGCTTTCCAGTTTCCCA 398
 DB 79 LeuThrLeuAspGlyAsnAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSer 98
 QY 399 GAATGCAAGTGTGATTTATCCAGGTGGAATCCAGACATTTGAAATGGGGCATAT 458
 DB 99 SerLeuGlyPheLeuAsnLeuGlnGlyGlyGlnLeuGlySerLeuGlnProGlnAlaLeu 118
 QY 459 CAGAGCTTAAGCACTCTACCTTAAATTGACAGAAACCCCATCCAGATTAGCC 518
 DB 119 LeuGlyLeuGlnAsnLeuCysHisLeuHisLeuGlnArgAsnGlnLeuArgSerLeuAla 138
 QY 519 CTGGGAGCTTTTCT-----GACTATCAAGTTTACAGAACTGCGTGTG 533
 DB 139 LeuGlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeu 158
 QY 534 -----GACTATCAAGTTTACAGAACTGCGTGTG 566
 DB 159 SerArgLeuGlnAspGlyLeuPheGlnGlyLeuGlySerLeuThrAspLeuAsnLeuGly 178
 QY 567 GAGACAATCTAGCATCTTGAAGAACTTCCCATTTGACATCTCAAACTTTGAAAGAA 626
 DB 179 TrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuAspGln 198
 QY 627 CTTAATGTGGCTGACAACTTATCCAACTTTGCAAACTTGAATTTTCTAATCTG 666
 DB 199 LeuValLeuAlaGlyLeuAsnArgLeu--AlaTyrLeuGlnProAlaLeuPheSerGlyLeu 217
 QY 687 ACCAATCTAAGACCTTGGACCTTTCCAGCAACAAGTTCAAGTATTATTGACACAGAC 746
 DB 218 AlaGlnLeuArgGlnLeuAspLeuSerArgAsnAlaLeuArgAlaLe-----Lys 234
 QY 747 TTGCGGGTTCTACATCAATGACCCCTACATCTCTTACGCTGTCCTGAAACCT 806
 DB 235 AlaAsnValPheValGlnLeuProArgLeuGln--LysLeuTyrLeuAspArgAsnLeu 253
 QY 807 ATGAATCTTATCCAAACGAGTGCATTTAAAGAAATTAG--CTTCAATGAGCTGACTTTA 863
 DB 254 IleAlaAlaValAlaIleProGlyAlaPheLeuGlyLeuLysAlaLeuArgTrpLeuAspLeu 273
 QY 864 AGAATAATATTGATGATTAAATGTAATGAAACTTGTAATTCAGAGTCTGGCTGTTTA 923
 DB 274 SerHisAsn--ArgValAlaGlyLeuLeuGlnAspThrPheProGlyLeuLeuGlyLeu 292
 QY 924 GAGTCCATGCTTTGCTTGGGAGATTTAGAAATGAAAGAACTTGAAAGATTGAC 983
 DB 293 ArgValLeuArgLeu-----Ser 298
 QY 984 AAATCTGCTCTAGAGGCTGTGCAATTTGACATTTGAAATTCGATTAGCATACTTA 1043
 DB 299 HisAsnAlaIleAlaSerLeuArgProArgThrPheLysAspLeu----- 313
 QY 1044 GACTACTACCTGATGATATATTGACTTATTATGTTGACAAATGTTTCTTCATTT 1103
 DB 314 ---HisPheLeuGlnGluLeu----- 319

QY 1104 TCCCTGTGAGTGTGACTATTGAAAGGTAAAGACTTTTCTTAATATTGCGATGGCAA 1163
 DB 320 GlnLeuGlnLysAsnArgIleArgGlnLeuAlaGlnArgSerPheGln---GlyLeuGly 338
 QY 1164 CATTTGAAATTAAGTAACTGTAATTTGACAGCTTTCCCACTTGAATCTGAATCTGTC 1223
 DB 339 GlnLeuGlnValLeuThrLeuAspHisAsnGlnLeuGlnGlnValLysAlaGlyAlaPhe 358
 QY 1224 AAAAGCTTACTTCACTTCC-----AAACAAGGTGGGAATGCTTTTTCAGAACTTGAT 1277
 DB 359 LeuGlyLeuThrAsnValAlaValaMetAsnLeuSerGlyAsnCysLeuArg-----Asn 376
 QY 1278 CTACCAAGCTTGAAGTTTCTAGATCTCAGTACA--AATGCTTGAATTTCAAGGTGTC 1334
 DB 377 LeuProGlnGlnValPheArgGlyLeuGlnGlyLysLeuHisSerLeuHisLeuGlnGlySer 396
 QY 1335 TGT-----TCTAAAGTGAATTTGGGACACACAGCTTAAGTATTAGAT 1379
 DB 397 CysLeuGlyArgIleArgProHisThrPheThrGlyLeuSerGlyLeuArgArgLeuPhe 416
 QY 1380 CTGAGCTTCAATGAGTGTATTATCCATGAGTTCAAACTTCTG--GGCTTGAACAACATA 1436
 DB 417 LeuLysAspAsnGlyLeuValGlyIleGlnGlnGlnSerLeuTrpGlyLeuAlaGlnLeu 436
 QY 1437 GAACATCTGATTTTCCAGCATTTCCAAATTTGAAACAAATGAGTGTTCAGTATTCTTA 1496
 DB 437 LeuGlnLeuAspLeuThrSerAsnGlnLeu----- 446
 QY 1497 TCATCAGAAACCTCATTTACCTTGACATTTCTCATATCTCACACAGATTCCTTCAT 1556
 DB 447 -----ThrHisLeuPro-----His 451
 QY 1557 GGCATCTCAATGGCTGTGTCAGTCTCGAAGCTTGAAGAACTGGGACATTTCTTCCAG 1616
 DB 452 ArgLeuPheGlnGlyLeuGlyLysLeuGlnLysLeuLeuLeuSerArgAsnArgLeuAla 471
 QY 1617 GAAAACCTTCTTCCA--GATATCTTACAGAGCTGAGAAACTTGAACCTTCTGAGCTTC 1673
 DB 472 Glu-----LeuProAlaAspAlaLeuGlyProLeuGlnArgAlaPheTrpLeuAspVal 489
 QY 1674 TCTCACTGTCAACTGAGAGATTTGCTCCAAACAGACTTTAATCACTCTCCAGTCTTGC 1733
 DB 490 SerHisAsnArgLeuGlnLysLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuArg 509
 QY 1734 GTACTTAATATGAGCCAAACAACACTTTTTCATTTGATAGACGTTTCTTATAGTGTCTG 1793
 DB 510 TyrLeuSerLeuArgAsnAsn-----SerLeuArgThrPheThrProGln----- 524
 QY 1794 AACTCCCTCCAGGTTCTTGATTACAGTCTCAATCACTAATGACTTCCAAAAACAGAA 1853
 DB 524 ----- 524
 QY 1854 CTACAGCAATTTTCCAAAGTACTGAGCTTTCTTAATCTTACTCAGATGACTTGTCTGT 1913
 DB 525 -----ProProGlyLeuGlnArgLeuArgLeuTrpLeuGlnGlyAsnProTrpAspCys 540
 QY 1914 ACTTGTGAACAACAGAGTTTCTCGAAGTGAACAAGAC----- 1952
 DB 541 GlyCysPro-----LeuLysAlaLeuArgAspPheAlaLeuGlnAsnProSer 556
 QY 1953 -----CAGAGGAGCTCTTGTGTAAGTGAACGATGGAATGGAATGTCACACCTTGACAT 2006
 DB 557 AlaValProArgPheValGlnAlaIleCysGlnGlyLysAspAspCysGlnProProAlaTyr 576
 QY 2007 AACGAGGAGCATGCTGTGCTGAGTTGAATATCATCTGTTCAGATGAATTAAGACATCAT 2066
 DB 577 ThrTyrAsn-----AsnIleThrCysAlaSerProProGlnValVal 590
 QY 2067 GGTGTGTGCGTC 2078
 DB 591 GlyLeuAspLeu 594

RESULT 11

QY 1497 TCACAGAAACCTCATTTACCTTGACATTTCTCATCTCAGACAGAGTTGCTTCAAT 1556
Db 447 -----ThrlsleuPro-----His 451
QY 1557 GGCATCTTCAATGGCTTGTCCAGCTCGAAGCTTGAAAAATGGCTGGCAATCTTTCAG 1616
Db 452 ArgLeuPheGlnGlyLeuGlyLysLeuGlyLysLeuLeuSerArgLeuAla 471
QY 1617 GAAAACTTCTTCA--GATATCTTCAAGAGCTGAGAACTTGACCTTCTGACCTC 1673
Db 472 Gln-----LeuProAlaSprAlaLeuGlyProLeuGlnArgAlaPheTrpLeuAspVal 489
QY 1674 TCTCAGTGTCAACTGGAGAGGTGTCTCCAAAGCAATTAATCACTCTCCAGTCTTCA 1733
Db 490 SerHisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuArg 509
QY 1734 GACTAATATATGAGCCAAACAATCTTCTTCAATGGAATACGTTTCTTATATAGTGTG 1793
Db 510 TyrLeuSerLeuArgAsnSer-----SerLeuArgThrPheThrProGln----- 524
QY 1794 AACTCCTCCAGGTCTTGAATTAAGTCTCATCATATATGACTTCCAAAAACAGAA 1853
Db 524 ----- 524
QY 1854 CTACAGCATTTTCCAGTAGTCTAGCTTCTTAATCTTACTCAGATGACTTGTGT 1913
Db 525 -----ProProGlyLeuGlnArgLeuTrpLeuGlnLysAsnProTrpAspCys 540
QY 1914 ACTGTGAACACCAAGATTTCTGCAATGATGATCAAGAC----- 1952
Db 541 GlyCysPro-----LeuLysAlaLeuArgAspPheAlaLeuGlnAsnProSer 556
QY 1953 -----CAGAGGAGCTCTTGTGTGAGTGAATGGAATGTGCAACCTTCAAT 2006
Db 557 AlaValProArgPheValGlnAlaLeuCysGlnGlyAspAspCysGlnProAlaTyr 576
QY 2007 AAGCAGGAGCATGCTGTGCTGATTTGAATATATCACTGATGATGATTAAGACATCAT 2066
Db 577 ThrTyrAsn-----AsnIleThrCysAlaSerProGluVal 590
QY 2067 GGTGTGTCGCTC 2078
Db 591 GlyLeuAspLeu 594
RESULT 12
US-09-538-092-1087
Sequence 1087, Application US/09538092
GENERAL INFORMATION:
PATENT: Patent No. 6753314
APPLICANT: Glot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuratSeqFormat Version 0.9
SEQ ID NO 1087
LENGTH: 605
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (0)..(0)
OTHER INFORMATION: Polypeptide Accession Number P35858
US-09-538-092-1087

Alignment Scores:

Pred. No.: 1,14e-23 Length: 605
Score: 306.00 Matches: 160
Percent Similarity: 38.25% Conservative: 94
Best Local Similarity: 24.10% Mismatches: 258
Query Match: 4.55% Indels: 152
DB: 4 Gaps: 24
US-09-396-985B-3 (1-3811) x US-09-538-092-1087 (1-605)
QY 219 CCATTGCTTCTTCAATATGCTGCCGTTTATCAGAGAGTGTCTTATATTAATTA 278
Db 39 ProAlaCysProAlaAlaCysValCysSerTyrAspAspAlaAspGluLeuSerVal 58
QY 279 CAATGATGAGCTGATTTTACAAATCCCAACACCTCCCTTCCAAACAAGAC 338
Db 59 PheCysSerSerArgAsnLeuThrArgLeuProAspGlyValProGlyLysThrGlnAla 78
QY 339 CTGACCTGAGCTTAAATCCCTGAGGCAATTTAGCAAGCTTATAGCTTCTTCAAGTTCCCA 398
Db 79 LeuTrpLeuAspGlyAsnAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSer 98
QY 399 GAATGACAGTGTGATTTATCCAGGTGTGAATTCAGAAATTCAGAAATGAGTGGCATAT 458
Db 99 SerLeuGlyPheLeuAsnLeuGlnGlyGlnLeuGlySerLeuGlnProGlnAlaLeu 118
QY 459 CAGAGCTGAAGCACTCTCTACCTTAAATTTAGAGAAACCCCAAGATTAGGCC 518
Db 119 LeuGlyLeuGlnAsnLeuCysHisLeuHisLeuGlnArgAsnGlnLeuArgSerLeuAla 138
QY 519 CTGGAGACCTTTCT----- 533
Db 139 LeuGlyThrPheAlaHisIleThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeu 158
QY 534 -----GACATTCATAGTTTACAGAAAGCTGTGCTGTG 566
Db 159 SerArgLeuGlnAspGlyLeuPheGlnGlyLeuGlySerLeuTrpAspLeuAsnLeuGly 178
QY 567 GAGCAAAATCTACATCTCTAGAGAACTTCCCATTTGAGCATCTCAAACTTGAAGA 626
Db 179 TrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuAlaGln 198
QY 627 CTTAATGTGCTCACATCTTATCCATCTTCAATTAATTCAGTATTTTCTAATCTG 686
Db 199 LeuValLeuAlaGlyAsnArgLeu--AlaTyrLeuGlnProAlaLeuPheSerGlyLeu 217
QY 687 ACCAATCTAGACACTTGACCTTTCCAGCAACAAGATTCAAAGTTTATTCACAGAC 746
Db 218 AlaGluLeuArgGluLeuAspLeuSerArgAsnAlaLeuArgAlaLe-----Lys 234
QY 747 TTGGGGTCTCATCAATGCCCCCTACTCAATCTCTCTTGTAGACCTGTCCCTGAACCT 806
Db 235 AlaAsnValPheValGlnLeuProArgLeuGln--LysLeuTyrLeuAspArgAsnLeu 253
QY 807 ATGAATTTATCCAAACAGATGCTTAAAGAAATTAGG--CTTCATAGCTGACTTTA 863
Db 254 IleAlaAlaValAlaProGlyAlaPheLeuGlyLysLeuAlaLeuArgTrpLeuAspLeu 273
QY 864 AGAAATATTTGATATGTTAAATGTAAGAAACCTTGATTCAGAGTCTGTGCTGTTTA 923
Db 274 SerHisAsn--ArgValAlaGlyLeuLeuGlnAspThrPheProGlyLeuLeuGlyLeu 292
QY 924 GAAGTCATGTTTGGTTCTGGGAGAAATTAGAAATGAAGAAACTTGGAAAAATTGAC 983
Db 293 ArgValLeuArgLeu-----Ser 298
QY 984 AATCTGCTTAGAGGCTGTGCAATTTGACCATTTGAAGAAATTCGATTAAGCATCTTA 1043
Db 299 HisAsnAlaIleAlaSerLeuArgProArgThrPheLysAspLeu----- 313
QY 1044 GACTACTACCTGATGATATATTTAGCTTATTTATTTGACAAATGTTCTTCAATT 1103
Db 314 ---HisPheLeuGlnGluLeu----- 319

Oy	1104	TCCCTGGAGAGTGATCATTTGAATGGGAAAGAAAGCTTTTCTTAATTTGGAGTGGCA	1163
Db	320	GlnLeuGlyHisAsnArg1LeuArg1GlnLeuAlaGluArgSerPheGlu--GlyLeuGly	338
Oy	1164	CATTAGAATAGTTAACTGTAAATTTGGACAGTTTCCACATTTGAATGAATCAATCTCTC	1223
Db	339	GlnLeuGlnValLeuThrLeuAsnSerHisAsnGlnLeuGlnGlnValGlyAlaGlyAlaPhe	358
Oy	1224	AAAAGGCTTACTTTCACTTCC-----AACAAAGGTGGGAATGCTTTTCAGAGAGTTGAT	1277
Db	359	LeuGlyLeuThrHisAsnValAlaValMetAsnLeuSerGlyAsnGlyLeuArg-----Asn	376
Oy	1278	CTACCAACGCTTGAGTTGATCTGATGTCAGTGA---AATGGCTTGAGTTCAAGGTTGC	1334
Db	377	LeuProGlnGlnValPheArgGlyLeuGlyLeuHisSerLeuHisLeuGlnGlySer	396
Oy	1335	TGT-----TCTCAAGTGAATTTTGGACACACAGCCTTAAGATTTAGAT	1379
Db	397	CysLeuGlyArgGlyLeuArgProHisSerThrPheThrGlyLeuSerGlyLeuAlaArgLeuPhe	416
Oy	1380	CTGAGCTTCAATGCTGTTATTAACATGAGTTCAAACTTCTTG--GGCTTAGAACACTA	1438
Db	417	LeuHisAspAsnGlyLeuValGly1LeuGlnGlnSerLeuThrGlyLeuAlaGlyLeu	436
Oy	1437	GAACATCTGGAGTTTCCAGACATTTCCAAATTTGAAACAAAGAAGTTCAGTATTCCTA	1486
Db	437	LeuGlnLeuAspLeuThrSerAsnGlnLeu-----	446
Oy	1497	TCACTCAGAAACCTCATTTACCTTGACATTTCTCATCTCACACAGAGTTGCTTTCAT	1556
Db	447	-----ThrHisLeuPro-----His	451
Oy	1557	GGCATCTTCAATGCTGTCTGCAGTCTCGAAGCTTGAATGGCTGCAATTTCTTCCAG	1616
Db	452	ArgLeuPheGlnGlyLeuGlyLeuGlnGlyLeuLeuLeuSerArgAsnArgLeuAla	471
Oy	1617	GAAAACCTTCTTCCA--GATATCTTCCACAGAGCTGAGAAACTTGACCTTCTGGAAGCTC	1673
Db	472	Glu-----LeuProAlaAspAlaLeuGlyProLeuGlnArgAlaPheThrLeuAspVal	489
Oy	1674	TCTCAGTGTCAACTGAGACAGTGTTCCTCCACACAGACTTAACTCACTCTCCAGTCTTCAG	1733
Db	490	SerHisAsnArgLeuGlnAlaLeuProAsnSerLeuAlaProLeuGlyArgLeuArg	509
Oy	1734	GTACTAAATATGAGCCACACAACTTCTTTTATTGATGATGTTTCTTATTAAGTGTCTG	1793
Db	510	TyrlleuSerLeuArgAsnAsn-----SerLeuAlaGlnPheThrProGln-----	524
Oy	1794	AACCTCCCTCCAGGTTCTTGATTTACAGTCTCAATCATATATGACTTCCAAAAACAGGAA	1853
Db	524	-----	524
Oy	1854	CTACAGCATTTTCCAGAGTGTCTAGCTTCTTAAATCTTACTCAGAAATGACTTGTCTGT	1913
Db	525	-----ProProGlyLeuGlnArgLeuGlnGlyLeuGlnGlyAsnProTyrPaspCys	540
Oy	1914	ACTTGTGAACACAGAGTTTCTCTGCAATGATCAAGAC-----	1952
Db	541	GlyCysPro-----LeuValAlaLeuArgAspPheAlaLeuGlnAsnProSer	556
Oy	1953	-----CAGAGCAGCTCTTGGTGAATGTTAAACGAATGATGTGCAACCTTCAGAT	2006
Db	557	AlaValProArgPheValGlnAlaIleCysGlnGlyAspArgCysGlnProProAlaTyr	576
Oy	2007	AAGCAGGGCAGTCCGCTGCTAGTTGAATATTCACCTCTCAGATGAATAAACAATCATTT	2066
Db	577	ThrTyraen-----AsnIleThrCysAlaSerProProGlnValVal	590
Oy	2067	GGTGTGTGCTGCT 2078	
Db	591	GlyLeuAspLeu 594	

```

US-08-190-802A-50
/ Sequence 50. Application US/08190802A
/ Patent No. 5519003
/ GENERAL INFORMATION:
/ APPLICANT: Mochly-Rosen, Daria
/ APPLICANT: Ron, Dorit
/ TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
/ TITLE OF INVENTION: Thereof
/ NUMBER OF SEQUENCES: 265
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Dehlinger & Associates
/ STREET: P.O. Box 60850
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94306-0850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/190,802A
/ FILING DATE: 01-FEB-1994
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fabian, Gary R.
/ REGISTRATION NUMBER: 33, 875
/ REFERENCE/DOCKET NUMBER: 8600-0139
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 324-0880
/ TELEFAX: (415) 324-0960
/ INFORMATION FOR SEQ ID NO: 50:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 603 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ HYPOTHEITICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
/ INDIVIDUAL ISOLATE: pro. complex- $\alpha$ c, Fig. 33
US-08-190-802A-50

Alignment Scores:
Pred. No.: 8,46e-23 length: 603
Score: 298.00 Matches: 163
Percent Similarity: 37.11% Conservative: 89
Best Local Similarity: 24.01% Mismatches: 260
Query Match: 4.43% Indels: 167
DB: 1 Gaps: 26

US-09-396-985B-3 (1-3811) x US-08-190-802A-50 (1-603)
QY 185 TCAGAGCTCCGAGCCTCA-----GCCCTTCAACCCGATTCATGCTTCTTGTAATG 238
Db :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 28 ThrAspProG|YAlAserIAlAspAlaG|uG|ProG|ncYsP|roValAlaCyS-ThrCy 47
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 239 CTGCGCGTTTATCAGCAGAGGTGGTTCCTAATATTACTTATCAATGACATGAGCGTAATT 298
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 47 sSerHis-----AspAspTyrThrAspG|uLeuSerValPheCySserSerIySAsnLe 65
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 299 CTGCAAAATCCCGAGCAACATCCCTTCCTCAACCAAGAACTGAGCTGAGCTTATCC 358
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 65 uThiHisLeuProAspAspIleP|roValSerThrArgAlaLeuT|P|euAspG|yAsnAs 85
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 359 CCTGAGGCAATTTAGGAGCAGCTATAGCTTCTTGAGTTTCCAGAACTGAGGAGTGAGATT 418
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 85 nLeuSerSerIleProSerAlaAlaPheG|lnAsnLeuSerSerIeuAspPheLeuAsnLe 105
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 419 ATCCAGGTGTGAATTCACAGCAATTGAAGATGGGCAATATCAGAGCTTAAGCACTCTC 478
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

105 uGlnGlySerTrpLeuArgSerLeuGluProGlnAlaLeuLeuGlyLeuGlnIleuLeuLys 125
QY 479 TACCTTAATATGACAGAAACCCCATCCAGAGTTAGCCCTGGAGCCCTTTCGTGACT 538
DB 125 rTyTrLeuH1sLeuGlnArgAsnArgLeuAlaValGlyLeuPheThrH1s 145
QY 539 ATCAAGTTTACAGAACTGGTGGCTGGAGCAAACTAGCATCTCTAGAGAACTTCC 598
DB 145 rProSerLeuAlaSerLeuSerLeuSerLeuLeuGlyArgLeuGlnGluLysLe 165
QY 599 CATTGACATCTCAAAACTTTGAAGAACTTAATGGCT- 638
DB 165 uPheGlnGlyLeuSerH1sLeuTrpAspLeuAlaLeuGlyTrpAsnSerLeuValValLe 185
QY 639 -----CACATCTTATC----- 650
DB 185 uProAspTrpValPheGlnGlyLeuGlyAsnLeuH1sGluLeuValLeuAlaGlyAsnLys 205
QY 651 -CAATCTTTCAAATTCAGTATTTTCTAATCTTACCAATCTAGACACTTGGAGACT 709
DB 205 sLeuThrTrpTrpLeuGlnProAlaLeuPheCysGlyLeuGlyGluLeuArgGlyLeuAspLys 225
QY 710 TTCAGCAACAGAACTTCAAGTATTTATGACAGACTTGGGGTTCTATCACTCAAAATGCC 769
DB 225 uSerArgAsnAlaLeuArgSerVal-----LysAlaAsnValPheValH1sLeuPro 242
QY 770 CCTACTCAATCTCTTTAGACTGTGCTCCAGAACCTATGAACTTTATCCAACTGATGC 829
DB 242 oArgLeuGln--LysLeuTrpLeuAspArgAsnLeuL1eThrAlaValAlaProGlyAla 261
QY 830 ATTTAAGAAATTTAGG---CTTCATAGACTTATAGAAATATTTGATAGTTTAA 886
DB 261 aPheLeuGlyMetLysAlaLeuArgTrpLeuAspLeuSerH1sAsn--ArgAlaAlaG 280
QY 887 TGTATGAAGAACTTGATTCAGAGTGTGGCTGTTTGAAGTCCATCGTTGGTT- 941
DB 280 LysMetGluAspTrpPheProGlyLeuLeuGlyLeuH1sValLeuArgLeuAlaH1sAs 300
QY 942 -----CTGGAGAAATTTAG 955
DB 300 nAlaIleAlaSerLeuArgProArgTrpPheLysAspLeuH1sPheLeuGlnGluLeuG 320
QY 956 A--AATGAAGAACTTGGAAAGTTTGAACAATCTGCTAGAGGCTGTGCAATTT 1012
DB 320 nLeuGlnH1sAsnArgL1eArgGlnLeuGlyLysArgTrpPheGlnGlyLeuGlnLys 340
QY 1013 GACCATTTGAAGAACTTCGATTCAGATCACTAGCACTCTGATGATATTT--ATTGA 1069
DB 340 uGluVal-----LeuThrLeuAsnAspAsnGlnL1eThrGluValArgValG 356
QY 1070 CTTATTTAATTTTGAACAATTTTCTTCAATTTCCCTGGTGAAGTGTGACTATTT- 1124
DB 356 yAlaPheSerGlyLeuPheAsnValAlaValMetAsnLeuSerGlyAsnCysLeuArgSe 376
QY 1125 -----GAAAGGGTA-----AAAACATTTTCTTAAATTTCCGATGGCAACATTT 1168
DB 376 rLeuProGluArgValPheGlnGlyLeuAspLysLeuH1sSerLeuH1sLeuGlnH1sSe 396
QY 1169 AGAATTAGTTAAGTATTTGACAGAGTTTCCACATTTGAATCAAACTCTCAAAAG 1228
DB 396 rCysLeuGlnH1sValArgLeuH1sThrPhe-----AlaGlyLeuSerGlyLeuArg 414
QY 1229 GCTTACTTTCACTTCCAAAGAGTGGAGATGCTTTTTCGAAGTTGAT----- 1277
DB 414 gLeuPheLeuArgAsp-----AsnSerL1eSerSerL1eGlnGlnGlnSerLe 430
QY 1278 -----TACCAAGCTTGAGTTTCTAGATCTCAGTAAAGAAAGCTTGAGTTTCAAAAG 1330
DB 430 uAlaGlyLeuSerGlyLeuLeuGlnLysAspLeuThrThrAspArgLeuThrH1s----- 448
QY 1331 TTGCTGTTTCAAGAGTATTTTGGACAAACAGCTTAAAGTATTTAGATCTGAGCTTCAA 1390
DB 449 -LeuProArgGlnLeuPheGlnGlyLeuGlnH1sLeuGlnGlyLeuLeuLeuSerTrpAs 468

QY 1391 TGTGTATTACCATGATGTTCAAACTTCTTGGGCTTAGAACAATAGAACTGTGATTT 1450
DB 468 nGlnLeuThrTrpLeuSerAlaGluValLeuGly----- 479
QY 1451 CCAGATTTCCAAATTTGAAACAAATGAGTATTTTCAATATTCATATCACTCAGAAACCT 1510
DB 480 -----ProLeuGlnArgAl 484
QY 1511 CATTTACCTTGCATTTTCTCATCTCACACAGAGTTGCTTTCATATGGATTTCAATGG 1570
DB 484 aPheTrpLeuAspL1eSerH1sAsnH1sLeuGluThrLeuAlaGluGlyLeuPheSerXe 504
QY 1571 CTTGTCCAGTCTCGAAGTCTGAAATAGGCTGGCAATTTCTTTCAGAAAACTTCCCTCC 1630
DB 504 rLeuGlyArgValArgTrpLeuSerLeuArgAsnH1sSerLeuGln--ThrPheSerTr 523
QY 1631 AGATATCTTTCACAGAGCTGAGAAACTTGCCTTCTGACCTCTCTCAGTGTCACTGGA 1690
DB 523 o-----GlnProGlyLeuG 528
QY 1691 GCAATTTGTCCAAACAGACTTTAACTCACTCTCCAGTCTTCAAGTACTAAATATGAGCCA 1750
DB 528 uArgLeu----- 530
QY 1751 CAACAACCTTCTTTCATTTGATACGTTTCTTATAGTGTCTGAACCTCCCTCAGAGTTCT 1810
DB 531 -----TrpLeuAspAlaAsnProTrpAspCysSerCysProLeuValAlaLe 546
QY 1811 T--GATTACAGTCTTCATCACAATAATGACTTCCAAAAACAGAACTACAGCATTTTCC 1867
DB 546 uArgAspPheAlaLeuGlnAsn-----ValCysGln----- 554
QY 1868 AAGTACTAGCTTTCTTAAATCTTACTCAGAAATGACTTGTGTTACTTGTGAACACA 1927
DB 554 oGlyValValProArgPheValGlnThr-----ValCysGln----- 566
QY 1928 GAGTTTCTGCAATGATCAGACAGACAGAGAGCTTGTGTGAAGTTGAACGAATGGA 1987
DB 567 -----GlyAspAspCysGlnProValTrpThrTrpAsnAsnLeuH 580
QY 1988 ATGTGCACACCTTTCAGATTAAGCAGGAGCATGCTGTGCTGAGTTTGAATATACCC 2042
DB 580 rCysAlaGlyProAlaAsnValSerGlyLeuAspLeuArgAspValSerGlyThr 598

RESULT 14
US-08-477-346-50
Sequence 50, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072

Db 356 yAlaPheSerGlyLeuPheAsnValAlaValMetAsnLeuSerGlyAsnGlyLeuArgSe 376
QY 1125 -----GAAAGGGTA-----AAAGCTTTCTTATTAATTCGGATGGCAACATTT 1168
Db 376 rLeuProGlnArgValPheGlnGlyLeuAspLysLeuHisSerLeuHisLeuGlnHisSe 396
QY 1169 AGAATTAGTTAACTGTAATTTGGACAGATTTCCACATTCGAACTCAATCTCAAAAG 1228
Db 396 rGlyLeuGlyHisValArgLeuHisThrPhe-----AlaGlyLeuSerGlyLeuArgAr 414
QY 1229 GCTTACTTTCACTTCCAAACAAAGGTGGAAATGCTTTTTCAGAGTTGAT----- 1277
Db 414 gLeuPheLeuArgAsp-----AsnSerHisSerSerHisLeuGlnGlnSerLe 430
QY 1278 -----CTAACCAAGCTTTGAGTTCTAGATCTTCAGTAAATGGCTTGAGTTCAAGG 1330
Db 430 uAlaGlyLeuSerGlyLeuLeuGlnLeuAspLeuThrThrAsnArgLeuThrHis----- 448
QY 1331 TTGCTGTTCTCAAAAGTATTTTGGACCAACAGGCTTAAGATTTAGATCTGAGCTTCAA 1390
Db 449 -LeuProArgGlnLeuPheGlnGlyLeuGlnHisLeuGlnHisLeuLeuLeuSerGlyAs 468
QY 1391 TGGTGTATTAATCCATGAGTTCAAACTTCTGGGCTTAGAACAACTAGAACATCTGATTT 1450
Db 468 ngInLeuThrThrLeuSerAlaGlnValLeuGly----- 479
QY 1451 CCAGCATTCCAATTTGAAACAAATGAGTGAATTTCAATTCCTATCACTCAGAAACCT 1510
Db 480 ----- 1510
QY 1511 CATTACCTTGACATTTCTCATACTCAACACAGATTTGCTTCAATGGCATCTTCAATGG 1570
Db 484 apHeTrPLeuAspHisSerHisAsnHisLeuGlnThrLeuAlaGlnGlyLeuPheSerSe 504
QY 1571 CTGTCAGCTCTCGAAGCTTGAATAAGGCTGGCAATTTCTTCAGAGAAAATCTCTTCC 1630
Db 504 rLeuGlyArgValArgTyrLeuSerLeuArgAsnAsnSerLeuGln---ThrPheSerPr 523
QY 1631 AGATATCTTCACAGAGCTGAGAAAATGACCTTCTGAGACCTCTCTCAGTGTCAACTGGA 1690
Db 523 o-----GlnProGlyLeuGln 528
QY 1691 GCAGTTGTCCTCAACAGACATTTAATCACTCTCCAGTCTTCAGGTACTAAATATAGCCA 1750
Db 528 uArgLeu----- 530
QY 1751 CAACAACTCTTTTCAATGGATACGTTTCCTTATAGTGTCTGAATCCCTCCAGTTCT 1810
Db 531 -----TyrLeuAspAlaAsnProTyrAspCysSerCysProLeuHisAlaLe 546
QY 1811 T--GATTACAGTCTCAATCAATATGACTTCCAAAAACAGAACTACAGCATTTTCC 1867
Db 546 uArgAspPheAlaLeuGlnAsn-----Pr 554
QY 1868 AAGTAGCTAGCTTTCTTAATCTTACTCAGAAATGACTTGTGTACTGTGAACACA 1927
Db 554 oGlyValValProArgPheValGlnThr-----ValCysGln----- 566
QY 1928 GAGTTTCCTCAATGATCAAGACAGAGCAGGAGCTCTGGTGGAGATTGAACGATGA 1987
Db 567 -----GlyAspAspCysGlnProValTyrThrTyrAsnAsnHisLeu 580
QY 1988 ATGTGCAACACTTCAGATTAAGACAGGAGATGCTGTGCTGATTTGAATATACAC 2042
Db 580 rCysAlaGlyProAlaAsnValSerGlyLeuAspLeuArgAspValSerGlnThr 598

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_blue_nzp model

Run on: March 29, 2005, 11:51:33 ; Search time 39.6953 Seconds

(without alignments)
18474.848 Million cell updates/sec

Title: US-09-396-985B-3

Perfect score: 6724
Sequence: 1 acagggccactgcctgcac.....ctccactgacagagaacta 3811

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+npz.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09396985/runat_28032005_155743_21159/app_query.fasta_1.85098
-DB=PIR_79 -QWMT=fastan -SUFFIX=xpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09396985.OCGN 1.1_1164.0runat_28032005_155743_21159 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WMT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	656.5	9.8	661	2	156258
2	474	7.0	786	2	108664
3	454	6.8	1097	2	A29943
4	433	6.4	1389	2	T13852
5	421	6.3	1385	2	T13887
6	404	6.0	1066	2	T13864
7	333.5	5.0	1134	1	A29944
8	325	4.8	605	2	JC5239
9	317.5	4.7	853	2	T17461
10	306	4.6	605	2	A41915
11	299.5	4.5	855	2	T17460
12	299	4.4	603	2	T24315
13	298	4.4	603	2	JC1282
14	298	4.4	662	2	S42799

15	298	4.4	1531	2	T42218	slit-1 protein hom
16	296.5	4.4	994	2	H96510	probable disease r
17	295	4.4	845	2	T07039	Hcr9-0 protein - c
18	293.5	4.4	907	2	JB0176	orphan G protein-c
19	293	4.4	603	2	JC6128	insulin-like growt
20	292	4.3	907	2	JG0193	G protein-coupled
21	291	4.3	855	2	T07015	Cf-4A protein - to
22	290	4.3	1112	2	T10504	disease resistance
23	285	4.2	622	2	JC7973	synleutin - human
24	285	4.2	1134	2	T04587	hypothetical prote
25	282.5	4.2	1019	2	T06519	probable disease r
26	282	4.2	1027	2	B85089	receptor protein k
27	280	4.2	890	2	T00800	disease resistance
28	276.5	4.1	768	2	T17462	disease resistance
29	276.5	4.1	1523	2	T13953	MEG8 protein - ra
30	276	4.1	983	2	G84524	probable disease r
31	274.5	4.1	863	2	A55173	Cf-9 protein precu
32	274.5	4.1	1091	2	A58532	glial cell membran
33	274.5	4.1	1469	2	B36665	slit protein 2 pre
34	274.5	4.1	1480	2	A36665	slit protein 1 pre
35	272.5	4.1	766	2	T01817	hypothetical prote
36	272.5	4.1	1109	2	T18536	receptor-like prot
37	271	4.0	1143	2	T10636	hypothetical prote
38	268	4.0	910	2	G84648	probable disease r
39	266.5	4.0	1784	2	C96615	hypothetical prote
40	263.5	3.9	1064	2	B86465	probable protein k
41	262.5	3.9	967	2	T48210	hypothetical prote
42	262.5	3.9	1051	2	T13174	gpi50 protein - fr
43	259	3.9	1029	2	T00712	protein kinase hom
44	259	3.9	1232	2	T05322	hypothetical prote
45	257	3.8	738	2	T19938	hypothetical prote

ALIGNMENTS

RESULT 1
156258
RP105 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 26-Jul-1996 #sequence_rev150n 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: 156258
R/Miyake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A>Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a m
A/Reference number: 156258; PMID:95204928; PMID:7897216
A/Accession: 156258
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-661 <RES>
A/Cross-references: UNIPROT:Q62192; GB:D37797; NID:g761711; PIDN:BA07043.1; PID:g76171

Alignment Scores:

Pred. No.: 2,63e-41
Score: 656.50
Percent Similarity: 45.31%
Best Local Similarity: 28.72%
Query Match: 9.76%
DB: 2
Length: 661
Matches: 199
Conservative: 115
Mismatch: 290
Indels: 89
Gaps: 17

US-09-396-985B-3 (1-3811) x 156258 (1-661)
QY 192 CCGGAGCCCTCAGCCCTTCAACCCGATTCATTGCTTCAATAGCGCCGTTTATC 251
DB 3 ProAspIleSerCysPheLeuValAlaLeuPheLeuLaser--CysArgAlaThr 21
QY 252 ACG-----GAGGTGGTCTCAATATTAATTAATCATGATCATGAG 290
DB 22 ThSesSerAspGlnIleCysGllleGluYsgIValAsnLysThrIleCysGluAen 41
QY 291 CTGAATTTCTCAAAATATCCCGACCAACTTCCTTCAACCAACCAACTGACGACG 350
DB 42 LeuGlyLeuAsnIleProGlyThrLeuProAsnSerThrGlnCysLeuGluPheSer 61

```

QY 351 TTTAATCCCTGAGCATTTAGGACGATTAAGCTTTCTTCAGTTTCCAGAACTGACAGT 410
    ||||| ||| : : : : : |||
Db PheAsnValLeuProThrIleGlnAsnThr-ThrPheSerArgLeuIleAsnLeuThrPhe 81
QY 411 CTGGATTTATCCAGGCTGTAATTCAGACAAATTGAAGAGGGCATTCAGACCTTAAGC 470
    ||||| ||||| : : : : : |||||
Db LeuAspLeuThrArgCysGlnIleTyrTrpIleHisIleGluAspThrPheGlnSerGlnHis 101
QY 471 CACCTCTCTCAATTAATTTAGACAAACCCATCCAGAGTTTAAAGCCCTGGAGACTTT 530
    ||||| ||||| : : : : : |||||
Db ArgLeuAspThrLeuValLeuThrAlaAsnProLeuIlePheMetAlaGluThrAlaLeu 121
QY 531 TCTGCACTATCAAGTTTACAGAGCTGTGCTGAGAGACAATCTAGCATCTAGAG 590
    ||||| : : : : : ||||| : : : : : |||||
Db SerGlyProValAlaLeuValHisIlePhePheIleGlnThrGlyIleSerSerIleLeuP 141
QY 591 AACTCCCAATTTGACATCTCAAAACTTTGAAGAACTTAATGTGCTCAAACTTTATC 650
    ||||| : : : : : ||||| : : : : : |||||
Db PheIleProLeuHisValGlnGlnIleThrLeuGlnSerLeuTyrLeuGlySerAsnHisIle 161
QY 651 CAATCTTTCAAAATTTACCTGATTTTCTTAATCTGACCAATCTAGAGCATCTGGACCTT 710
    ||||| ||||| : : : : : |||||
Db SerSerIleLeuValLeuProGlyValPheProThr--GluValLeuValLeuAspPhe 180
QY 711 TCCAGCAACAAGATTCAAAGTATTTATTTGACAGACTTGGCGGTTTCATCACTAAATGCC 770
    ||||| : : : : : ||||| : : : : : |||||
Db GlnAsnAsnAlaIleHisTyrIleLeuSerIleGluAspMetSerSerLeuGlnGln-- 198
QY 771 CTACTCAATCTCTTTTAAAGCTGTGCTCCCTGACCCCTTAACCTTTATCCAAACAGCTGCA 830
    ||||| ||||| : : : : : ||||| : : : : : |||||
Db AlaThrValLeuSerLeuLeuAsnGlyAsnAspIleAlaGlyIleGluProGlyAla 218
QY 831 TTTAAAGAATTTAGGCTTCAATAGCTGACCTTAAAGAAATAATTTGATTTAAATGTA 890
    ||||| ||||| : : : : : |||||
Db PheAspSerAlaValPheGlnSerLeu-----AsnPheGlyIleThrGlnAsn 234
QY 891 ATGAAGAATTTGATTCAGGCTGTGCTGCTGTTTGAAGTCATGCTTTGCTTGGAGAA 950
    ||||| : : : : : ||||| : : : : : |||||
Db LeuLeuValIlePheIleValLeuValAsnSerThrIleGlnSerLeuThrLeuGlyThr 254
QY 951 TTTTGAAGAATGAGAACTTTGAAAGCTTTGACAAATCTGCTCTAGAGGCTGTGCAAT 1010
    ||||| : : : : : ||||| : : : : : |||||
Db PheGluAspMetAspAsp--GluAspIleSerProAlaValPheGluGlyLeuValCysGlu 273
QY 1011 TTGACCACTTGAAGATTCGATTTAGACATTAAGTACACTGACCTGATATTAATTTAG 1070
    ||||| : : : : : ||||| : : : : : |||||
Db MetSerValGlnSerIleAsnLeu--GlnValHisTyrPhePheAsnIleSerSerAsn 292
QY 1071 TTAATTAATTTGTTGACAAATGTTTCTTCATTTCCCTGGTGAAGTGAATTTGAAGG 1130
    ||||| : : : : : ||||| : : : : : |||||
Db ThrPheIleCysPheSer----- 298
QY 1131 GTTAAAGACTTTTCTTAATTAATTTGCGATGCGCAATTTAGAACTTAACTGAATTT 1190
    ||||| ||||| : : : : : |||||
Db GlyLeuGlnGluLeuAspLeuThrAlaThrHisLeu 310
QY 1191 GGAAGATTTCCACA-----TTGAACCTCAAACTCTCAAGGCTTACTTTCACTTCC 1244
    ||||| : : : : : ||||| : : : : : |||||
Db SerGlnLeuProSerGlyLeuValGlyLeuSerThrLeuValSerValLeuSerAla 330
QY 1245 AACAAAGTGGGAAT-----GCTTTTTCAGAAATGATCTTACCAAGCTTTGAGTTT 1295
    ||||| ||||| : : : : : ||||| : : : : : |||||
Db AsnIlePheGluAsnLeuValCysGlnIleSerAlaSerAsnThrProSerLeuThrHisLeu 350
QY 1295 ----- 1295
Db SerIleLeuGlyAsnThrIleValArgLeuGluLeuGlyThrGlyCysLeuGluAsnLeuGlu 370
QY 1296 -----CTAAGTCTCAGTGAAGAAATGCTGAGTTTCAAAAGTTCTGTCTGCA 1343
    ||||| ||||| : : : : : ||||| : : : : : |||||
Db AsnLeuValGlyLeuValLeuSerHisAspAspIleGluThrSerAspCysAsnLeu 390
QY 1344 AGTGAATTTTGGCAACAACGCTTAAGATTAATTTAGATTTGAGCTTCAATGTGTTAATACC 1403

```

```

Db 391 GlnLeuArgAsnLeuSerHisIleGlnIleSerLeuAsnLeuSerTyrAsnGluProLeuSer 410
    : : : : : || : : : : : || : : : : : || : : : : : || : : : : : || : : : : : ||
QY 1404 ATGAGTTCAAC-----TTCTTGGGCTTTAGAAACAATGAAACATCTGATTTCCAGACTTCC 1460
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db LeuValThrGluAlaPheLeuValCysValProGlnIleGluLeuLeuValPheThr 430
QY 1461 AATTGAACAATAGTAGTAGTTTTCAGTATCTCTATCACTGACAGAACTCAATTTACCTT 1520
    ||||| ||||| : : : : : ||||| : : : : : |||||
Db ArgLeuValValValAspAlaGlnSerProPheGlnAsnLeuHisIleLeuLeuValValLeu 450
QY 1521 GACATTTCTCATATCTACACACAGATGCTTCAATGAGCATCTTCAATGGCTTTGCTCAAT 1580
    ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db AsnLeuSerHisIleSerLeuLeuValPheSerSerGlnIleLeuPheAspIleValProAla 470
QY 1581 CTGCAAGCTTTGAAATGCTGCTGCAATTTCTTTCCAGAAACTCTT-----CCAGAT 1634
    ||||| ||||| : : : : : ||||| : : : : : |||||
Db LeuGlnHisIleValAsnLeuGlnIleValAsnHisPheProGlyValAsnIleGlnValThrAsn 490
QY 1635 ATCTTCACAGAGCTGAGAACTTTGACCTTCTGAGACCTTCTGAGTCACTGAGAGAG 1694
    ||||| ||||| : : : : : ||||| : : : : : |||||
Db SerLeuGlnThrLeuGlyValArgLeuGluIleLeuValLeuSerPheCysAspLeuSerSer 510
QY 1695 TTGTCTTCAACACATTTTAATCACTCACTGCTTCAAGTCTTCAAGTCAATTAATGAGCCACAAC 1754
    ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db IleAspGlnHisAlaPheThrSerLeuValMetMetAsnHisValAspLeuSerHisAsn 530
QY 1755 AACTTTTCTTCATGATGATGCTTCTCTTAAAGTGTCTGAACCTCTCCAG-----GTT 1808
    ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db Arg-----LeuHisSerSerSerIleGluAlaLeuSerHisIleValValLeuValGlyIleTyr 547
QY 1809 CTGATTAACAGCTCAATCACTCAATTAATGACTTCCAAAAACAGAACTACAGACTTTTCA 1868
    ||||| ||||| : : : : : ||||| : : : : : |||||
Db LeuAsnLeuAlaSerAsnHisIleSerIleIle-----LeuPro 560
QY 1869 AGTATCTAGCTTTCTTA-----AATCTTACTCAGATGACTTTGCT 1910
    ||||| ||||| : : : : : ||||| : : : : : |||||
Db SerLeuLeuProIleLeuSerGlnGlnArgThrIleAsnLeuArgGlnAsnProLeuAsp 580
QY 1911 TGTACTTGAACACACAGATTTCTGCAATGATGATCAAGACAGACAGGAGCTTTGGTG 1970
    ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db CysThrCysSerAsnIleTyrPheLeuGluTyrTyrGlyValMetGlnIleValSerGlu 600
QY 1971 GAAAGTTGAACGAAATGATGTCACAACCTTCAATTAACAGAGGACGCTGTGCTGAGT 2030
    ||||| ||||| : : : : : ||||| : : : : : |||||
Db AspThrGluAspThrLeuValCysGluAsnProProLeuLeuValArgGlyValArgLeuSerAsp 620
QY 2031 TTGAATATCACCTGTCAAGTGAATTAAGACCAATCAATTTGATGTGCTGCTCAAGTGTCT 2090
    ||||| : : : : : ||||| : : : : : ||||| : : : : : |||||
Db ValThrLeuSerCysSerMetAlaAlaValGlyIlePhePheLeuIleValPheLeuLeu 640
QY 2091 GTTATCTGTGTGTAGCACTTCTGTGCTTAAGTCTAT 2129
    ||||| : : : : : ||||| : : : : : |||||
Db ValPheAlaIleLeuLeuIlePheAlaValIleTyrPhe 653

RESULT 2
T08664
Toll protein-like receptor DKFZp547I0610.1 - human
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence__revision 11-Jun-1999 #ext_change 09-Jul-2004
C/Accession: T08664
R/Pousterka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A/Reference number: Z16466
A/Accession: T08664
A/Molecule type: mRNA
A/Residues: 1-786 <POU>
A/Cross-references: UNIPROT:O15399; EMBL:AL050262
A/Experimental source: fetal brain; clone DKFZp547I0610
A/Note: DKFZp547I0610.1

Alignment Scores:

```



```
Db      662  GlnGlyMet-----GlnIleCysLeuHISgluAArgAsnDheValProGlyLysSer 678
QY      2316  ATGTGTCGCAACATCATTCATGAAGTTTCCATTAAGCCGAAGAGGATGTTGTGGGTC 2375
Db      679  ILeValGlnAsnIleLe--ThrCysIleGlnLysSerTrpLysSerIlePheValLeu 697
QY      2376  TCCCAACACTTCATTCAGAGCCGCTGGTATCTTGAATGATGAGATTGCTGACCTG 2435
Db      698  SerProAsnDheValGlnSerGlnTrpCysHISGlyGlnLysTrpHISAsnVal 717
QY      2436  CAGTTTTCAGACAGCTGCTGTGATCATCTTATCTGCTGACAGAGTG--GAGAG 2492
Db      718  LeuPheHISgluLysSerAsnSerLeuIleLeuIleLeuGlnProIleProGlnTrp 737
QY      2493  ACCCTGCTACGAGACAGCTGAGCTGTATCCGCTTCTGACGAGAACCTTACCTGAG 2552
Db      738  SerIleProSerSerTrpHISLysLysLysSerLeuMetAlaArgHISTrpLysGln 757
QY      2553  TGGAGAGACAGTCTCTGGGCGGACATCTTCTGAGACGACTGACAGAAAGCCCTG 2609
Db      758  TrpProLysgluLysSerLysTrpGlyLeuPheTrpAlaAsnLeuArgAlaIle 776

RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A29943
R:Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A:title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, an
A:Reference number: A29943; PMID:88135760; PMID:2449285
A:Accession: A29943
A:Molecule type: DNA
A:Residues: 1-1097 <HAS>
A:Cross-references: UNIPROT:P08953; GB:M1969; GB:J02682; NID:G158640; P1DN:AAA28941.1;
C:Genetics:
A:Gene: FLYBase:FL
A:Cross-references: FLYBase:FBgn0003717
C:Keywords: Transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-1097/Product: Toll protein #status predicted <MAT>

Alignment Scores:
Pred. No.: 5 37e-26 Length: 1097
Score: 454.00 Matches: 219
Percent Similarity: 38.97% Conservative: 129
Best Local Similarity: 24.52% Mismatches: 291
Query Match: 6.75% Indels: 254
DB: 2 Gaps: 43

US-09-396-985b-3 (1-3811) x A29943 (1-1097)
QY      267  AATATTACTTATCATGATGAGCTGATTTCTACAAA--ATCCCGCAACCTTCCCC 323
Db      270  AsnValThrAspIleAsnLeuSerAlaAsnLeuPheArgSerLeuProGlnGlyLeuPhe 289
QY      324  TTCTCAACCAAGACTGAC-----CTGAGCTTTAAT-----CCCTGAGGCAT 368
Db      290  AspHISAsnLysHISLeuAsnGlnValArgLeuMetAsnAsnArgValProLeuAlaThr 309
QY      369  TTGAGGAGTATAGCTTCTTCCAGTTTCCGAGATCGAGCTGAGCTTATTCAGGTG 428
Db      310  LeuProSerArgLeuPheAlaAsnGlnProGlnLeuGlnIleLeuArgLeu--ArgAla 328
QY      429  GAATCCAGCAATGTAAGATGGGCGCATATCAGAGCTTAAGCCACTTCTACCTTATA 488
Db      329  GlnLeuGlnSerLeuProGlyAspLeuPheGlnHISerThrGlnIleThrAsnIleSer 348
QY      489  TTGACAGAAACCCCATCAGAGTTTACCCCTGGAGCCCTTTCTGACATCAAGTTTA 548
Db      349  LeuGlyAspAsnLeuLeuLysTrpLeuProAlaThrLeuGlnHISGlnValAsnLeu 368
```

```
QY      549  CAGAACTGTCGCTGTGGAGACAATATGATCTTACAGAACTTCCCAATTGGACAT 608
Db      369  LeuSerLeuAspLeuSerAsnAsnArgLeuThrHISLeuProAspSerLeuHISAsn 388
QY      609  CTCAAAACCTTGAAGAACTTAATGTCGCTCAAAATCTTATCCAACTTTCAAAATTA 668
Db      389  ThrThrAsnLeuThrAspLeuArgLeuAsnValAsnLeuLeuThrGlyLysSer--Gly 407
QY      669  GAGTATTTTCTTAATTCGCAATCTAGAGCACTTGACCTTCCAGCAAGAAATTTCA 728
Db      408  AspIlePheSerAsnLeuLysAsnLeuValThrLeuValMetSerArgAsnArgLeuArg 427
QY      729  AGTATT-----TATTGACAGACTTGGCGGTTCTACAT----- 761
Db      428  ThrIleAspSerArgAlaPheValSerThrAsnGlyLeuAsnHISLeuHISLeuAsnHIS 447
QY      762  -----CAAAATGCCCTTACAAATCTCTTTTACACCTTCCCTGAAC-- 803
Db      448  AsnAspIleAspLeuGlnInProLeuAspIleMetLeuGlnThrGlnIleAsnSer 467
QY      804  CCTATGAACTTATTCCAACCAAGTGCATTTAAAGAAATTAAGCTTCATAGTCACTTA 863
Db      468  ProPheGlyTrpMetHIS-----GlyLeuLeuThrLeuAsnLeu 480
QY      864  AGAATTAATTTGATGATGTTAATGTAATGAATACTTGATTCAGAGCTGCTGGTTTA 923
Db      481  ArgAsnAsn-----SerIleLe----- 486
QY      924  GAAGTCCATCGTTGGTCTGTGGAGAAATTGACAAATGAAGAAACTTGGAAAGTTTGAC 983
Db      487  -----PheValTrpAsnAspTrpLysAsn----- 494
QY      984  AATTCGCTAGAGGCGCTGTGCAATTGACACATTTGAAGATTCGATAGATACTTA 1043
Db      495  -----ThreLeuGlnLeuAspGlnLeuAspLeuSerLys--- 506
QY      1044  GACTACTACCTGATGATGATTAATGACTTATTAATTTGACAAATGTTTCTTCATTT 1103
Db      507  -----AsnAsnIleSerSerLeu 512
QY      1104  TCCCTG-----GTGAGTGTGACTATTGAA 1127
Db      513  GlyTrpGlyAspLeuAlaPheLeuSerGlnAsnArgLeuHISValAsnMetThrHISAsn 532
QY      1128  AGGTTAAAGACTTTTCT-----TATATTTCCGA 1157
Db      533  LysIleArgArgIleAlaLeuProGlnAspValHISLeuGlyGlnGlyTrpAsnAsnAsn 552
QY      1158  TGGCAACATTTGAATTA-----GTTAACTGTAAATTTGGACAGTTT 1199
Db      553  LeuValHISValAspLeuAsnAspAsnProLeuValCysAspCysThrIleLeuTrpPhe 572
QY      1200  CCCCACTTG-----AAACTCAAACTT 1220
Db      573  ILeGlnLeuValArgGlyValHISLysProGlnTrpSerArgGlnPheLysLeuArgThr 592
QY      1221  CTCAAAAGGCTTACTTCACTTCCAA--AAAGTGGGAAGCTTTTCAAGAGTTGAT 1277
Db      593  AspArgLeuValCysSerGlnProAsnValLeuGlnGlyTrpProValArgGlnIleGln 612
QY      1278  -----CTACCAAGCTTGAGTTCTAGATCTCAGTGAAGAAATGGCTTGAGTTTC 1325
Db      613  ProGlnThrLeuIleLysProLeuAspPheSerAspAspProArgLysArgLysCysPro 632
QY      1326  AAGGTTC--TGTTCTCAAGATGATTTTGGACAAACAGCCATAAGTATTAGATCTG 1382
Db      633  ArgGlyCysAsnCysHISValArgThrTrpAsp-----LysAlaLeuValIle 648
QY      1383  AGCTTCAATGCGTTTATTACATGATTCAACTTCTGGGCTTGAACAACATGAACAT 1442
Db      649  AsnCysHIS-----SerGlyAsnLeuThrHISValArgProArgLeuProAsn 663
```

QY 1443 CTGATTTCCAGCATTCCTCAATTTGAAAACAATGAGTGGTTTCAGTATTCCTATCATC 1502
 DB Leu-----HslyAsnMetGlnLeuMetGlu-----LeuHsleu 675
 QY 1503 AGAAACCTCATTTGACATTTCTCATATCTACACCCAGAGTTGCTTTCATATGAGCATC 1562
 DB GluAsnAsnThrLeuLeuArgLeuProSerAlaAsnThr----- 688
 QY 1563 TTCATGGCTTGTCTGCTGCAAGTCTTGAAAATGCTGGCAATTCCTTCCAGGAAAC 1622
 DB 689 ---ProGlyTyrGluSerValThrSerLeuHsleuGlnArgLysn----- 702
 QY 1623 TTCCTTCCAGATATCTTCCAGAGCTGAGAAACTTGAACCTTCTGAGACTCTCTCAGT 1682
 DB 703 -----AsnLeuHsThrSerIleAspValAspGlnLeu 712
 QY 1683 CAATGAGCAGATTTGTCTCCAAACGATTTAACTCACTCTCCAGCTTTCAGGTACTAAAT 1742
 DB 713 -----ProThr-----Asn 715
 QY 1743 ATGAGCCACAACAACCTTTTCATTTGATACGTTTCTTATAAGTGTGAACTCCCTC 1802
 DB 716 LeuHsThrHis----- 718
 QY 1803 CAGGTTCTTGTATTCAGTCTCAATCATATATGACTTCCAAAAACAGAACTACAGCAT 1862
 DB 719 -----LeuAspIleSerTrpAsnHsleu-----GlnMetLeuAsn--- 720
 QY 1863 TTTCCAGATGACTAGCTTTCTTAAAT-----CTTACT 1895
 DB 731 ---AlaThrValLeuGlyPheLeuAsnArgThrMetLysTrpArgSerValLysLeuSer 749
 QY 1896 CAGATGACTTGTCTGTACTGTGGAACACCAAGAGTTCTCTGCAATGATCAAGAGCAG 1955
 DB 750 GlyAsnProThrMetCysAspCysThrAlaLysProLeuLeuLeuPheThrGlnAspAsn 769
 QY 1956 AGCAGACTTGTGTGGAAGTGAACGAAATGGAATGTGCAACCTTCATGATTAAGCAGGAC 2015
 DB 770 PheGlnArgIleGlyAspArgAsnGlnMetCysValAsnHsleuGlnMetProThrArg 789
 QY 2016 ATGCTCTGTGCTGATTTGAATATCATCCTGTCAAGATGAATTAAGCAATC---ATTGCTGTG 2072
 DB 790 MetValGlnLeuSerThrAsnAspIleCysAspProAlaGlnLysGlyValPheIleAlaLeu 809
 QY 2073 TCGGTC-----CTCAGTGTGCTGTAGTATCTGTGTGAGAGTTCGGCTTAATAG 2123
 DB 810 AlaValValIleAlaLeuThrGlnGlyLeuLeuAlaGlyPheThrAlaAlaLeuTyrLys 829
 QY 2124 TTC-----TATTTTCACTGATGCTTCTTGTGCTGCTGCATAT 2159
 DB 830 PheGlnThrGlnIleLysIleTyrPheLysAlaHsleuLeuLeu----- 845
 QY 2160 AAGTATGTAGAGGTGAAAATC-----TATGATGCTTTGTATATAC 2204
 DB 846 TrpPheValThrGlnGlnAspLeuAspLysAspLysPheAspAlaPheIleSerTyr 865
 QY 2205 TCAAGCAGATGAGAGCTGGTGAAGAAAGAGTATTAAGATTTGAAGAAGAGGCTG 2264
 DB 866 SerHisLysAspGlnSerPheIleGlnAspLysLeuValProGlnLeuGlnHsleuPro 885
 QY 2265 CTTCACTTTCAGTCTGCTTCACTACAGAGACTTTATTCCTCGGTGGGCAATTTGCTGC 2324
 DB 886 GlnLysPheGlnLeuCysValHsleuArgAspTrpLeuValGlnGlyHsleuProGln 905
 QY 2325 AACATCATCATGAAGGTTTCCATAAAAGCCGAAAGGATGTTGTGTGTGCTCCAGAC 2384
 DB 906 AsnIleMet---ArgSerValAlaAspSerArgArgThrIleIleValLeuSerGlnAsn 924
 QY 2385 TTGATCCAGAGCCGCTGTATCTTGAATATGAGATTTGCTCAGACTGGCAGTTCTG 2444
 DB 925 PheIleLysSerGlnTrpAlaArgLeuGlnPheArgAlaAlaHsleuSerAlaLeuAsn 944
 QY 2445 AGCAGTGTGTCTGTATCATCTTCATCTGTC-----CTGCAGAAAGTGAGAAAGAC 2495

DB 945 GlnGlyArgSerArgIleIleValIleIleTyrSerAspIleGlyAspValGlnLys--- 963
 QY 2496 CTGCTCAGCAGAGAGGTGAGAGCTGTACCGGCTTCTCAGCAGAAACCTTACCTGAGTGG 2555
 DB 964 ---LeuAspGlnGlnLeuLysValAlaTyr-----LeuLysMetAsnThrTyrLeuLysTrp 980
 QY 2556 GAGACAGTGTCTGTGGGCGGACATCTTCTGTGAGACGACTCAGAAAAGCCTGTGGAT 2615
 DB 981 GlyAspPro-----TrpPheTrpAspLysLeuArgPheAlaLeuProHis 995
 QY 2616 GGTAAATCATGAAATCCAGAGGACAGTGGGTACAGA 2654
 DB 996 ArgArg-----ProValGlnAsnIleGlyAsnGly 1005
 RESULT 4
 T13852
 gene wheeler protein - fruit fly (Drosophila melanogaster)
 C/Species: Drosophila melanogaster
 C/Date: 20-Sep-1999 #sequence_rev1sion 20-Sep-1999 #text_change 09-Jul-2004
 R/Accession: T13852
 R/Eidom, E.; Kooyer, S.; D'everlym, D.; Duman, M.; Lawinger, P.; Bocas, J.; Belien, H.
 Development 120, 885-899, 1994
 A/Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simi
 A/Reference number: Z17796; PMID:95324375; PMID:7609965
 A/Accession: T13852
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1389 <ELD>
 A/Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:9415682; PID:G1019104; PID:AAA792
 A/Genetic: C/Gene: wheeler
 A/Cross-references: FlyBase:FBgn0004364
 Alignment Scores:
 Pred. No.: 2.16e-24 Length: 1389
 Score: 433.00 Matches: 217
 Percent Similarity: 39.93% Conservative: 138
 Best Local Similarity: 24.41% Mismatches: 356
 Query Match: 6.44% Indels: 178
 DB: 2 Gaps: 34
 US-09-396-985b-3 (1-3811) x T13852 (1-1389)
 QY 339 CTGAGACTGAGCTTATATCCCTGAGGACATTTAGCAGCATATGCTTTCAGTTTCCCA 398
 DB 338 LeuAsnLeuSerAsnAsnAlaLeuThrArgIleGlySerLysThrPheLysGlnLeuTyr 357
 QY 339 GAAGTCAAGTGTGATTTATCCAGGTGGAATCCAGCAATTTGAAGATGGGCAATAT 458
 DB 358 PheLeuGlnIleLeuAspMetArgAsnAsnSerIleGlyHsleuGlnGlnAlaPhe 377
 QY 459 CAGAGCTTAAGCCACTCTTCACTTAATATTAAGCAGAAACCCATGAGCTTAAGCC 518
 DB 378 LeuProLeuTyrAsnLeuHsThrLeuAsnLeuAlaGlnAsnArgLeuHsThrLeuAsp 397
 QY 519 CTGGAGCCTTTTCTGCACTATATCAAGATTTACAGAACTGTGCTGTGAGCAAAATCTA 578
 DB 398 AsnArgIlePheAsnIleLeuTyrValLeuThrLysLeu---ThrLeuAsnAsnLeu 416
 QY 579 GCATCTCTA---GAGAACTTCCCATTTGAGCATCTCAAAACTTGAAGAAGATTAAATGTG 635
 DB 417 ValSerIleValGlnSerGlnAlaPheArgAsnCysSerAspLeuLysGlnLeuAspLeu 436
 QY 636 GCTCACAATCTTAATCCAAATCTTCAATTAATCACTGATATTTTCTAATGTGACCAATCTA 695
 DB 437 SerSerAsn-----GlnLeuThrGlnValProGlnAlaValGlnAspLeuSerMetLeu 454
 QY 696 GAGACTTGTGACCTTTTCCAGCAACAAGATTTCAAGATTTATTTATGACAGACTTGGGGTT 755
 DB 455 LysThrLeuAspLeuGlnLysGlnGlnIleSerGlnPheLysAsnAsnThrPheArgAsn 474
 QY 756 CTACATCAATGAGCCCTTCAATCTC-----CTGCAGAAAGTGAGAAAGAC 782

[illegible]

Db	824	Asn1aSerAsnLeuMetThrLeuGlnAsnGlySer-----	835
QY	1629	CSAGATATCTTTCACAGAGCTGAGAACTTGAACCTTCCSGAGACCTTCTCAGTCAATG	1688
Db	836	-----Leu1aGlnLeuValAsnLeuArgValLeuThrIleLeuGlnAsnLeuLeu	852
QY	1669	GAGCAGTTGTCTCCACAGCACTTTAACTCACTCTCCAGTCTTCCAGGATCTTAAATATGAC	1748
Db	853	Thr1aLeuGlnGlyThrGlnPheArgSerLeuGlyLeuLeuArgGlyLeuLeuTyrLeuIle	872
QY	1749	CACAAACAACCTCTTTTCATTTGAGTACGTTTCCCTTAAGTAGTCTGAACCTCCCTCCAGTT	1808
Db	873	AsnMetLeuThrTrpIleSerAsnAlaThrPheIuProLeuValSerLeuGlnVal	892
QY	1809	CTTGATTAACAGTCAATCAATATGATCACTTCCAAAAACAGAACTACAGCATTTTCCA	1868
Db	893	LeuArgLeuAspAsnAsnArgLeuSerSerLeuProIleLeuGlnTyrArgIle-----	910
QY	1869	AGTAGTCTAGCTTTCTTAACTTTACTCAGATCACTTTGCTGTACTTGAACAC---	1925
Db	911	---SerLeuGlnGlyLeuThrLeuGlyArgAsnAlaTrpSerCysArgCysGlnGlnLeu	929
QY	1926	CAGAGTTTCCSGCAATGGATGATCAAGACGACGAGCGACTTTCGGTAGAGTTGAACGATG	1985
Db	930	ArgGluLeuAlaGlnPheValSerAspAsnAlaMetValValArgAspAlaHisAspIle	949
QY	1986	GAATGTGCACACCTTACAGATTAAGCAGGCGCATCGCTGTGCTG-----	2027
Db	950	TyrCysLeuAspAlaGlyIleLeuArgGluLeuLeuIleGlyAsnLeuAlaAsnGly	969
QY	2028	-----AGTTGAATATCACTGTCAATGCAATTAAG	2057
Db	970	ProAspCysSerAspLeuLeuAspAlaSerAlaSerAsnIleSerSerGlnAspLeu	989
QY	2058	ACC---ATCATTTGCT-----GTGCGGCTCCAGTGTCTTGTAGTA	2096
Db	990	AlaGlyAlaIleGlyCysProCysTrpProAlaValLeuValLeuIlePheLeuValVal	1009
QY	2097	TCTGTGTAGACAGTTCGTGCTTAAAGTTCTATTATTCACGTAGCTTCTTGCTGCTGC	2156
Db	1010	ValLeuIleIleValPheValPheArgGluSerValArgMetTrpLeuPheAla-----	1027
QY	2157	ATTAAGTATGCT-----AGAGGTGAAC-----ATTATGAT	2189
Db	1028	---HisTyrGlyValArgValCysGluProArgPheGlnAspAlaGlyIleValTyrAsp	1046
QY	2190	GCCTTTGTATCTACTCAAGCCAGAGACGAGACCTGGTAGAGATGAGCTAGTAAAGAT	2249
Db	1047	AlaIleIleLeuHisSerGlnValAspTyrGluPheValCysArgAsnIleAlaIleGlu	1066
QY	2250	TTAGAAGAGGGGTGCTCCATTTCACTCTGCCTTCACTACATACAGACTTTATATCCCGGT	2309
Db	1067	LeuGlnHisGlyAlaGlyProPheArgLeuCysIleGlnGlnArgAsp---LeuProPro	1085
QY	2310	GTGGCCATTTGTGCCAACATCATCAATGAAGGTTTCATAAACCCGAAGCTGATTTGT	2369
Db	1086	Gln1aSerThrIleLeuGlnLeuVal---GlnGlyAlaArgAlaSerArgIleIleLeu	1104
QY	2370	GTGGTGTCCCAAGCACTTATCAAGACCGCTGTGTATCTTTGAATATGAGATTGCTCAG	2429
Db	1105	ValLeuThrArgAsnLeuLeuAlaThrGluTrpAsnArgIleGlnPheArgAsnAla---	1123
QY	2430	ACCTGCGCACTTCTGACGAGCTCGGTGGTATCATCTTCATTCCTGCGACAGAC-----	2483
Db	1124	-----PheHisGlySerLeuArgGlyLeu-----AlaGlnIleLeuVal	1136
QY	2484	---GTGAGAGAGACCTGTCTCAGGACGAGCTGAGCTGTATCCGCTTCTCAGAGAAC	2540
Db	1137	IleIleGlnGlnThrSerValSerAlaGlnAlaGlnAspValAlaGluLeuSer-----	1154
QY	2541	ACTTAACCTGAGTGGAGAGACAGTGTCTCGGGCGGCAATC-----	2582
Db	1155	ProTyrLeuLeu-----SerValProSerAsnArgLeuLeuThrCysAspArgTyr	1171

[illegible]

RESULT 6
T15864
hypothetical protein C56E6.6 - *Caenorhabditis elegans*
C1:Species: *Caenorhabditis elegans*
C1:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T15864
R:Pulmon, L.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C56B6.
A:Reference number: S69019
A:Accession: T15864
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1066 <Full>
A:Cross-references: UNIPROT:Q18902; EMBL:U03996; NID:g1055114; PID:g1055120; PIDN:AAA81C
C:Genetics:
A:Gene: CESP:C56B6.6
A:Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3; 950/3
Alignment Scores:
Pred. No.: 3,14e-22
Score: 404.00
Percent Similarity: 41.17%
Best Local Similarity: 25.21%
Query Match: 6.01%
DB: 2
Gaps: 29
Length: 1066
Matches: 177
Conservative: 112
Mismatches: 268
Indels: 145

US-09-396-985B-3 (1-3811) X T15864 (1-1066)

QY	44	GATGATGTCGTGCGCCGCTGGAGCTGATCCAGGACGCTTCCTCCG	103
Db	11	AsnAsnLeuSerValIleProThrTyrAlaLeuThrTyrLeuHisSerLeuGlnIleLeu	30
QY	104	CGT---GAGACCAAGAGCTGGAGACCCGCGCTGGA-----	136
Db	31	HisLeuGlnAsnAsnArgIleAspValLeuArgSerAsnThrPheAspIuThrGlnLeu	50
QY	137	-----GACTTGGCC	145
Db	51	AsnAsnLeuGlnPheLeuTyrLeuAspAsnAsnGlnLeuArgIleIleProAsnLeuAla	70
QY	146	CTAAACCCAC-----ACGAAGAGCTGGCATGAACCA	178
Db	71	PheAsnHisLeuArgLeuValValLeuMetLeuAlaAsnAsnArgIleThr-GluIleGln	90
QY	179	GAGCTTTCAGACTCCGGAGACCTCAGCCCTTC-----ACCC	214
Db	90	HisMetSerLeuProGlnThrLeuLysPheLeuValLeuAspAsnAsnLeuLeuThrGln	110
QY	215	GATTCATCTGCTCTT-----GCTTAATGCTCCGCTTATGACGAGGTGGTCC	265
Db	110	HisProTyrValAlaLeuAsnAspLeuLysThrLeuGlnSerIleAspLeuGlnGlyAs	130
QY	266	TAATTTACTTTCATGATGATGAGCTGAATTTCTACAAAAATCCCGACAACTCCCTT	325
Db	130	AsnIleThrHis---LeuMetAspThrAsnIleValThrPheGlnSerGluMetLysVal	149
QY	326	CTCAACCAAGAACCTGGACCTGAGCTTAAATCCCGTAGAGCACTTATGAGCATATAGCTT	385
Db	149	IleLeuArgAsn-----AsnLysValArgAlaGluAspLysHisSerPhe	164
QY	386	CTTCAGTTTCCGAACCTGACAGTGTGATTTACAGGTGTGAATCCAGACAAATGGA	445
Db	164	eArgSerPheArgLysIleArgGlnLeuAspIleSerTyrAsnGlnIleGlnThrValGln	184
QY	446	AGATGGGCGCATATCAGAGCTTACGCCACTCTCTACCTTAATATTGACAGAAACCCCAT	505
Db	184	HisPheSerSerPheGlnThrValGlnHisMetGlnSerLeuAspLeuSerTyrLysArgIle	204
QY	506	CCAGAGTTTAGGCCCTGGAGACCTTTTCGAGACTATCAATTTTACAGAGCTGTGGCTGT	565
Db	204	eAlaTyrLeuProArgGly-----	210
QY	566	GGAGCAAAATTCAGATCTCTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAAGA	625
Db	211	-----MetLeuLysAsnPhe-----AlaLysThrLeuLysThr	221
QY	626	ACTTAATGTGCTCAACATCTTATCCAACTTTTCAAAATTAAGCTGAGTATTTTCTAATCT	685

```

Db      221  rleuylsleuilaqlusnmetlehlala-----ThrProGluIalaLeuArgAspLe 239
Oy      686  GACAACTGAGAGCACTTCAGCAACATTTCAGCAATTCAGTAAT-----734
Db      239  uatgashneuthrhlsleuhsnleuasnlgylasnllyleuasnargllleapglasparva 259
Oy      735  -----TATTGCACAGACTTCGCGGTTCTCATCAATGACCCCTACTCAATCTCTCTT 787
Db      259  lleuylsleuylcyserthrleuval-----GluLe 270
Oy      788  AGACCTGCTCCCTGATGACCTTATGCAACAGGTCATTTAAGAAATGAGCT 847
Db      270  upheilealasnasyrleuugluhlsileProhlsleuylleuyserylmetls-- 289
Oy      848  TCATTAAGCTGACTTAAGAAATATTTGATAGTTTAATGATGAAATCTTATATCA 907
Db      290  -----GlnleuGluHlsleuasprileserylsnlyslle 302
Oy      908  AGGCTGAGCTGTTTAGAAGTCATCGTTGTTCTGGAGAAATTTGAATGAAGAA 967
Db      302  tserleu-----lyslyspProthrse 309
Oy      968  CTTCGAAAAGTTGACAAATCTGCTTAGAGGCGCTGCAATTTGACATTTGAAGAAAT 1027
Db      309  rleuhserylthrlysgluGluThrserThrValArgArgleuhsnleuilaGlyAs 329
Oy      1028  CCGATTGACACTACTAAGCTACTCTCGATGATATTTAGCTTATTTATTTGAC 1087
Db      329  nargllleasnhsnmetserasprryleu-----llephelGluHlsnecProleuLeuth 347
Oy      1088  AAATGTTTCT--TCATTTTCCCTGAGTGAAGTGAATGAAGGTTAAAGACTTTTC 1144
Db      347  rlyrValaspvalserpheasnarglleargpheilleserProkrghalpheGluylsle 367
Oy      1145  TTATATTTGGATGGACAACTTATGATTAATTTGAATTTGACAGTTTCCAC 1204
Db      367  ulysasnleu-----GlnserleuPhelGlnAsnandlnleuHlsnephProse 385
Oy      1205  ATTG--AAACTCAAACTCTCAAAAAGCTTACTTCACTTCACAA-----AAGG 1252
Db      385  rleuPhearglsnleuasprrylsleuasnlgylsleuMetleuAsnasnlnleuGlnlysl 405
Oy      1253  TGGGAATGCTTTTCAAGAGTTGATCTACCAAGCTTGAAGTTTATGATCTCACTAATAA 1312
Db      405  eaaphsn---PheaserleuHlsnleuProlylsleuGlnHlsleuSerleuHlsnleu 424
Oy      1313  TGGCTTGAAGTTTCAAGAGTTGCTGTTCTCAAGATGATTTGGGCAACAGC----- 1364
Db      424  nglnleuaspriLe-----llethrGluAsnMetPheGlyserSerSerSerSergl 441
Oy      1365  -CTTAAGTATTTAGATCTGAGCTTCAATGGTGTATTATTCATGATTCGA---AACTTCTT 1420
Db      441  ulyseryserleuhsnleuHlsnleuasnlgylsleuHlsnleuSerleuSerleuSerleu 461
Oy      1421  GGGCTTGAACAATAGATCAATCTGAGTTTCAGCATTTCAATTTGAACAAATGATGTA 1480
Db      461  rAspleuAspAsnleuGlnleuHlsnleuArgleuSerHlsnAspAsnlnleuThrleu 481
Oy      1481  GTTTTCAATTTCTTATCTAGCAAAAATCTTATTTACCTTGAATTTCTCATCTACAC 1540
Db      481  rmetThr---PheaserasnleuArgleuHlsnleuArglyleuAspserleuHlsnleu 500
Oy      1541  CAGAGTTGCTTTCAATGAGCATTTCAATGGCTTTCAGAGTCTGCAAGCTTGAAGAAATGCG 1600
Db      500  eileuylsleuProseralaleuylrglnleuProalaleuasprrylleuHlsnleu 520
Oy      1601  TGGCAATTTCTTCCAGAAAATCTTCCAGATATCTTCAACAGAGTGAAGAACTTGAC 1660
Db      520  pHlsnAsnleuasnleu---lleapArgAspAlaPheArgserPheaserAspLeuG 539
Oy      1661  CTTCCTGAGCTCTCTGAGTGTCAACTGAGCACTTGTCTTCAACAGACTTAACTCACT 1720

```

```

Db      539  nserleuylsleuSerHlsnleuAlaPheArgArgPheSerCysGluPheleuGlyseril 559
Oy      1721  CTCAGCTCTCAGACTACTTAATATGAGCCCAACAATCTTCTTTCATGATGATGCTTCC 1780
Db      559  eserGlnvalHlsnleuAsnleuSerSerHsnGlnHlsnGluHlsnleuSerleu 578
Oy      1781  TTTAAAGTCTG---AACTCCCTCAGGTTCTTGAATGATGATCTCAATCAATGATGAC 1837
Db      579  -----CysleAlaArgglyleuArglylsleuSerleuAlaSerHsnSerValGlu 596
Oy      1838  TTCAAAAAAGAGAACTACGACATTTTCCAGTACTGCTTCTTAAATCTTACTCA 1897
Db      596  slleasnarglyleuLeuHlsnasp---AlathrGluLeuThrserleuHlsnleuSerH 615
Oy      1898  GAAT-----GACTTGGCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 1936
Db      615  asnGlylleleaspvalaspseraspAlaPheCysGluCysArglylsleuSerHlsn 635
Oy      1937  GCAA 1940
Db      635  elys 636

RESULT 7
A29944
chaoptin precursor - fruit fly (Drosophila melanogaster)
N/Alternate names: photoreceptor cell-specific membrane protein
C/Species: Drosophila melanogaster
C/Date: 15-Dec-1988 #sequence, revision 15-Dec-1988 #text_change 09-Jul-2004
C/Accession: A29944; A21123
R/Reinke, R.; Krantiz, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988
A/Title: Chaoptin, a cell surface glycoprotein required for Drosophila photoreceptor ce
A/Reference number: A29944; PMID:88135762; PMID:3124963
A/Accession: A29944
A/Molecule type: DNA
A/Residues: 1-1134 <REI>
A/Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19010; GB:M19011; GB:M190
R/Zipursky, S.L.; Venkatesh, T.R.; Teplow, D.B.; Benzer, S.
Cell 36, 15-26, 1984
A/Title: Neuronal development in the Drosophila retina: monoclonal antibodies as molecu
A/Reference number: A21123; PMID:84106810; PMID:6420071
A/Accession: A21123
A/Molecule type: protein
A/Residues: 31-43, 'HX', 46-49, 'H' <ZIP>
C/Genetics:
A/Gene: FlyBase:chp
A/Cross-references: FlyBase:FBgn0000313
A/Intons: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
C/Superfamily: chaoptin; leucine-rich alpha-2-glycoprotein repeat homology
C/Keywords: cell adhesion; glycoprotein; membrane protein
F/1-29/Domain: signal sequence #stratus predicted <SIG>
F/30-1134/Product: chaoptin #stratus predicted <MAT>
F/80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
F/103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F/128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F/152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
F/177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
F/201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F/226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F/250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F/279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F/303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F/326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F/351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F/375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F/401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F/428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F/453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F/477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F/502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F/527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F/551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
F/577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>

```

Alignment Scores:	
Pred. No.:	6.55e-17
Score:	333.50
Percent Similarity:	37.74%
Best Local Similarity:	22.9c%
Query Match:	4.96%
DB:	1
US-09-396-985B-3 (1-3811) x A29944 (1-1134)	
	Length: 1134
	Matches: 177
	Conservative: 114
	Mismatches: 299
	Indels: 221
	Gaps: 30

OY	312	TAACAACCTCCCTCTTCAACCAAGAACTGGACCTGAGTTTAAATCCCTGAGGACATTTA	371
Db	346	AspSerLeuValAsnSerLeuGlnIleuAspLeuSerGlyValAsnAsnLeuThrIlyLeu	365
OY	372	GGCAGCTATAGCTTCTTCAGTTTCCCGACAACTGCAGATG	410
Db	366	HisHisIyLeuPheHisAsnIlePheAspValIleLeuAlaGlyAlaIleSerMetArgAspAsnIly	385
OY	411	-----CTG	413
Db	386	IleIyValIleGlnIyPheThrGlnIyThrPheAsnAlaValAlaIleTyThrIleuLeuIyLeu	405
OY	414	GATTATATCC-----AGGTGTGAATTCGACGAATGAAATGAGTGGGCA	455
Db	406	AspLeuSerGlyAspArgHisAspProThrAsnLeuGlnIleThrIleuArgAsnMetHisArg	425
OY	456	-----TATCAGAGCCTAAGC-----	470
Db	426	MetArgAsnMetArgSerLeuSerIleSerArgLeuGlyIySerSerSerValGlyProGln	445
OY	471	-----CACTCTCTACTTAAATATTTGACAGAAACCCCATCCAG	509
Db	446	AspPheIyAspPheGlyValGlnIyLeuGlnIyAspLeuGlnIleThrArgAlaSerLeuSer	465
OY	510	AGTTTAGCCCTGGAGCCCTTTCTGGACATATCAAGTTTACAGAAAGCTGTGGCTGGAG	569
Db	466	GlyIleGlnSerHisIleAlaPheLeuHisIyValAlaGlyIyLeuIyAlaGlyLeuAspPheSerGln	485
OY	570	ACAAATCTTACGATCTCTTAGAAGAC-----TTCCCATTTGGACATCTCAAAACTTTG	620
Db	486	AsnGlyIleSerSerIleGlnIyAsnArgAlaPheHisIyGlnIleGlnIyHis-----SerLeu	503
OY	621	AAAGAACTTAATGTGGGTCAACATCTTATTCGAATCTTTCAATATTCCTGAGTATTTTCT	680
Db	504	IleSerLeuIyMetSerHisIyGlyIySerGlySerAlaLeuProAlaIyProLeuAlaG	523
OY	661	AATGTGACCAATCTAGAGCACTTGGACCTTTGCACAGAAACAGATTCMAAGTATTTAATTC	740
Db	524	HisLeuThrSerLeuGlnIyLeuAspPheSerAsnAsnHisIleSerSerMetSerAsp	543
OY	741	ACAGACTTGGGGTTCTACATCAAAATGCCCTTACATCTCTCTTTAGACCTGTCCGCG	800
Db	544	ThrSerPheHisPheLeuIyAsnLeuAlaGlu-----IleuIyLeuHisAsp	559

```

Oy      1047  TACTACCTGCAGTATTT-----ATTGACTTATTTATTTGTTCAGAAAGTT 1094
Db      655  MetAlaPhehngInIuProAhnPheasnPheaspIyrrPheaspGInValGlyThlieu 674
Oy      1095  TCCTTCATTTTCCCGTGGAGTGAGTGACATTTGAAAGGTTAAAGACTTTCTTATTAATTC 1154
Db      675  Serhnsneuhn---ValasnValSerhIsasnGInIleargInIuMetTyAsnSer 693
Oy      1155  GGATGGCAACATTTAGATTAGTTAACTGTAAATTTGGACAGTTTCCACATTTGAAATC 1214
Db      694  SerTrp----- 695
Oy      1215  AAATCTGCAAAAGCTTACTTTCACTTCCACAAGAGTGAGATGCTTTTCAGAAAGT 1274

```

```

Db      696 -----SerGlyrAaGlnHLeGlyMet 704
QY      1275 GATTCACCAAGCCTTGAGTTTCAGTATCTCAGTAAAGAAATGCGTGAAGTTTC-----AAA 1328
Db      705 TyrHisSerSerIleLeuAspSerHisAsnIleLeuIleHisIlePro 724
QY      1329 GGTGGCTGTTCTCAAGATGATTTGGGACAACC----- 1361
Db      725 GLyTyrPheArgProAlaGluIleSerLeuThrHisIleuHisIleuGlyTyrAsnSerLeu 744
QY      1362 -----AGCCCTAAAGTATTTAGATCTGAGC 1385
Db      745 MetAsnThrThrIraGArValPheGlyAsnMetProHisIleuGlnThrLeuAspLeuSer 764
QY      1386 TTCATGGGTGTATTATACCATGAGTTCAAC---TTCCTGGGCTTAAAGACAATGACAT 1442
Db      765 TyrAsnThrPrIleHisGluLeuAspPheAspAlaPheLeuAsnThrIleuGlnLeu 784
QY      1443 CTGGAATTTCCAGACATTCGCATTTGAAACAAATGAGTAGTTTCAGTATTCATCACTC 1502
Db      785 ValPheHeGlyHisAsnTyrLeuSerAspIleProGln---AspIlePheLeuProAl 803
QY      1503 AGAAACCTCATTTACCTTGACATTTCTCATCTACACACAGA---GTTCGTTCAATGGC 1558
Db      804 GlnIleuArgIleValAspPheSerHisIleuHisIleuArgIleuProAspAsnLeu 823
QY      1560 ATCTTCATAGGC----- 1571
Db      824 PheTyrAsnGlyMetGlyuLeuAspValSerHisIleuMetMetLeuLeuIlePro 843
QY      1572 -----TTGTCAGCTCGAGAGCTCTGAAATAGCGTCGACATTTCTTCACAGAAAC 1622
Db      844 SerSerSerLeuSerSerLeuAlaIleuThrIleuGlyuLeuHisIleuSerAspAsn 863
QY      1623 TTCCTTCCA-----GATATCTTCAACAGAGCTGAGAAACTTGACCTTCCTG 1667
Db      864 PheIleSerThrIleHisSerMetAspLeuSerIleuAspPheArgSerLeuAlaTyrIleu 883

```


QY 1308 AGA---AATGGCTTGAATTTCAAGGTGCTGT-----TCTCAAGGAT 1349
 Db 387 LyeLnuHISerLeuHISleuGIuGIySerCySeuGIyArgILearProHISThrPhe 406
 QY 1350 TTTGGACAACCAAGCCTAAAGATTAGATCTGAGCTTCAATGGTGTATTACCAAGAT 1409
 Db 407 AlAGILyLeuSerLISleuArgLLeuPheLysAspAsnLISleuValIGILyLeu 426
 QY 1410 TCAAACTTCTTG---GGCTTAGAAACAATGAAATCTGATCTTCCAGCTTCCAAATTG 1466
 Db 427 GluHISerLeuTrpGILyLeuAlAGILyLeuHISleuHISleuSPrLeuThrSerAsnGILyLeu 446
 QY 1467 AAACAATGAGTGGTTTTCAGTATTCTTATCTCATCTCAAGAAACCTTATTTACTTGACAT 1526
 Db 446 ----- 446
 QY 1527 TCTCATACTCACACCAAGAGTGTCTTTCATATGCAATCTTCAATGGCTTGTCCAGTCTGAA 1586
 Db 447 -----ThrHISleuPro-----HISGILyLeuPheGILyLeuGILyLeuGILy 461
 QY 1587 GTCTTGAATAATGGCTGGCAATCTTCTTCCAGGAAACTCTTCTCA---GATATCTTACA 1643
 Db 462 TyLISleuLeuSerHISAsnArgLLeuAlAGILyLeu-----LeuProAlAspAlAsp 479
 QY 1644 GAGCTGAGAACTTGAACCTTCTCTGAGACCTCTCTCAGTGCACCTGAGAGAGTGTCTCCA 1703
 Db 480 ProLeuGILyArgAlAspHISleuPheLysAspValSerHISAsnArgLLeuAlAspProGILy 499
 QY 1704 ACAGCATTTAATCTTCACTCTTCCAGCTTTCAGGATCTTAATATGAGCCACAACCTTCTTT 1763
 Db 500 SerLeuLeuAlAspSerLISleuGILyArgLLeuArgTyLISleuAsnLISleuArgAsn 516
 QY 1764 TCAATGATACGTTTCTTCTTAAAGTGTCTGAACCTCCAGTCTTGTGATTAACAGTCTC 1823
 Db 517 SerLeuArgThrPheThrProGILy----- 524
 QY 1824 AATCATATATGACTTCTCAAAAAACAGAACTACAGCATTTTCCAGATTTAGTCTTTC 1883
 Db 525 -----ProGILyLeuGILyArg 530
 QY 1884 TTAATCTTACTCAGAAATGACTTGTCTTGTACTTGTGAACCAAGCT----- 1931
 Db 531 LeuTrpLeuGILyLeuAsnProTrpAspCySerCySerProLeuLysAlAspArgAspPhe 550
 QY 1932 -----TTCCTGCAATGATC-----AAGAGC 1952
 Db 551 AlAspLeuGILyAsnProSerAlAspAlProArgPheValGILyAlAspCysGILyAspAsp 570
 QY 1953 CAGAGCAGCTCTTGTGTGAAGTTGAACGAATGGAATGCAACACTTCCAGATTAAGCAG 2012
 Db 571 CysGILyProValArgLISleuThrTyLISleuAsnLISleuThrCysAlAspSerProGILyValAlAsp 590
 QY 2013 GGCATGCTGTGCTGAGTTTG 2033
 Db 591 GILyLeuAspLeuArgAspLeu 597
 RESULT 9
 T17461
 disease resistance protein D - tomato
 C/Species: Lycopersicon esculentum (tomato)
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T17461
 R/Parniske, M.; Jones, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 96, 5850-5855, 1999
 A/Title: Recombination between diverged cluters of the tomato Cf-9 plant disease resist
 A/Reference number: Z18801; MUID:99254130; PMID:10318973
 A/Accession: T17461
 A/Status: preliminary; translated from GB/EMBL/DBDut
 A/Molecule type: DNA
 A/Residues: 1-853 <P&R>
 A/Cross-references: UNIPROT:Q9ZS82; EMBL:AF119040; NID:94235640; PID:94235641; PIDN:ADN1
 C/Genetic:
 A/Gene: NLOD

Alignment Scores:
 Prd. No.: 9,94e-16 Length: 853
 Score: 317.50 Matches: 204
 Percent Similarity: 37.57% Conservative: 115
 Best Local Similarity: 24.03% Mismatch: 311
 Query Match: 4.72% Indels: 219
 DB: 2 Gaps: 38
 US-09-396-985B-3 (1-3811) x T17461 (1-853)
 QY 84 GCCATGGCTTCTCTCC-----TGGTGAACCAAGAACTGGAGCCC 128
 Db 33 AlAspAlAspLeuGILyLeuGILyLeuHISleuAsnMetPheThrValAsnProAspAlAspTrpTyL 52
 QY 129 TGGTGAAGACTTGGCTTAAACCAACAGAAAGCTGGCATGAAACCAAGACTTTCAG 188
 Db 53 CysGILyPheSerHISleuProLysThr-----ArgSerTrpAsnLysSer----- 66
 QY 189 ACTCGGAGCCCTCAGCCCTTCAACCCGATTCATGTCTTGTAAATGCTGCCGTTT 248
 Db 67 -----ThrAspCysSerTrp 72
 QY 249 ATCAGCAGAGTGGTTCCTAATATTAATTAATCAATGATGAGCTGATTTCTAC----- 302
 Db 73 AspGILyValHIScysAspAsnThrThrGILyGILyValILISleuLeuAspLeuArgCysSer 92
 QY 303 -----AAAATCCCAACAACCTCCCTTC-----TCAACAGAAAC 338
 Db 93 GILyLeuGILyLISleuHISleuSerHISleuSerSerLeuPheGILyLeuSerAsnLISleuArg 112
 QY 339 CTGACCTGAGCTTAAAT-----CCCTGAGGACTTTAGCAGCTTACG 383
 Db 113 LeuAspLeuSerLISleuAsnPheThrArgLISerProLISer-----SerProLys 128
 QY 384 TTCTTCAATTTCCAGAACTGCAAGCTGTGATTTATCCAGGTGTAATCCAGACAATT 443
 Db 129 PheGILyLISleuSerAsnLISleuThrHISleuAspLeuPheAspSerAsnPheThrGILyLe 148
 QY 444 GAAAGATGGGACATATAGAGCCTTAAGCCACTCTCTCACTTAATATGACAGAAACCC 503
 Db 149 ILISerSerGILyLISleuSerHISleuSerLISleuValLeuArgThrSerThrAspTyL 168
 QY 504 ATCCAGATTTAGCCCTGGGA-----GCCTTTCTGACATTAACAAT 545
 Db 169 ProTyLISleuSerLISleuProHISAsnPheGILyLeuLeuLeuLISleuLysAsnLISleuTrpGILy 188
 QY 546 TTACAGAGCTGTGCTGTGAGACAAATTAAGCATCTTAAGAACTTCCCATTTGA 605
 Db 189 LeuArgGILyLeuAsnLISleuTyLISleuValAsnLISerSer-----ThrLISerSerAsn 206
 QY 606 CATCTCAAACTTTGAAGAATTAATGTGGCTCAGACATCTTAATCAATCTTTCAATT 665
 Db 207 PheSerSerHISleuThrAsnLISleuArgLLeuAlAspTyLISleuGILyLeuArgLISleu 225
 QY 666 CTGAGATATTTTCTAATCTGAACCAATCTAGAGCACTTGAACCTTCCAGCAACAGATT 725
 Db 226 ProGILyArgPhePheHISleuSerAsnLISleuLISleuSerLeuAspLeuPheAsnProGILy 245
 QY 726 CAAGATTTAATTTGACAGACTTGCAGGTTTCAATCAATATGCCCTACTCAATCTCTCT 785
 Db 246 LeuThrValArgPheProThrThrLISleuTrpAsnSerSerAlAspLISleuValAsnLISleuTyL 265
 QY 786 TTAGACCTGCTCTGAACCTTATGAACCTTATTCACAGAGGTCATTTAAAGAAATTAAG 845
 Db 266 Leu---AlAGILyValAsnLISleuAlAspArgLISleu---ProGILySerHISleuSerHISleu 282
 QY 846 CTTCATAGCTGACTTAAGAAATATTTTGAATGTTTAAATGATGAAGAACTGTATT 905
 Db 282 ----- 282
 QY 906 CAGGTCTGGCTGTTTGAAGTCAATCGTTGGTCTGGAGCAATTTGAATGAAGGA 965
 Db 906 ----- 965

F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>

Alignment Scores:

Pred. No.:	6,82e-15	Length:	605
Score:	306.00	Matches:	160
Percent Similarity:	38.25%	Conservative:	94
Best Local Similarity:	24.10%	Mismatches:	258
Query Match:	4.55%	Indels:	152
DB:	2	Gaps:	24

US-09-396-985B-3 (1-3811) x AA1915 (1-605)

```
QY 219 CCATTGCTCTTCTTAATGCTGCGCTTTATACAGAGGTGGTCTTCAATATATCTTAT 278
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 39 ProAlaCyseProAlaIaIaCyseValCyseSerTyAspAspAspAlaAspGluLeuSerVal 58
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 279 CAATGATGAGAGTGAATTTCTACAAATCCCGACACCTCCCTTCCTCAACCAAGAAC 338
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 59 PheCyseSerArgAsnLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAla 78
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 339 CTGACACTGAGCTTTATATCCCTGAGCATTTAGGACGATATGCTTTCAGATTCCCA 398
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79 LeuTrpLeuAspGlyAsnAsnLeuSerSerValProProAlaIaIaPheGlnAsnLeuSer 98
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 399 GAACTGCAAGTGTGATTTATCCAGGTGTGAATCCAGACAAATTGAAGATGGGCAATAT 458
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 99 SerLeuGlyPheLeuAsnLeuGlnGlyGlyGlnLeuGlySerLeuGlnProGlnAlaLeu 118
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 459 CAGAGCTTAAGCACTCTCTACTTATATTTGACAGAAACCCCTCCAGATTATAGCC 518
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 119 LeuGlyLeuGlnAsnLeuCyHisLeuHisLeuGlnArgAsnGlnLeuArgSerLeuAla 138
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 519 CTGGAGACCTTTCT-----GACATATCAAGTTTACAGAACTGTGGCTGTG 533
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 139 LeuGlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeu 158
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 534 -----GACATATCAAGTTTACAGAACTGTGGCTGTG 566
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 159 SerArgLeuGlnAspGlyLeuPheGlnGlyLeuGlySerLeuTrpAspLeuAsnLeuGly 178
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 567 GACACAATCTACACTCTAGAGAACTCCCATTTGAGCATCTTCAAACTTGGAAAGA 626
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179 TrpAsnSerLeuAlaValLeuProAspAlaAlaPheArgGlyLeuGlySerLeuAspGln 198
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 627 CTTAATGTGGCTCACATCTTATCTCAATCTTTCAATACCTGAGATTTTCTAATCG 686
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 199 LeuValLeuAlaGlyAsnArgLeu---AlaTyLeuGlnProAlaLeuPheSerGlyLeu 217
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 687 ACCAATCTAGAGCACTTGACCTTTCCAGACACAAAGATTCAAAGTATTTATGACACAG 746
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 218 AlaGlnLeuArgGlyLeuLeuPheLeuSerArgAsnAlaLeuArgAlaIle-----Lys 234
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 747 TTGCGGGTTCTATACATAATGCCCTACTCAATCTCTTTACACTGTGCCCTGAACCT 806
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 235 AlaAsnValPheValGlnLeuProArgLeuGln--LysLeuTyLeuAspArgAsnLeu 253
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 807 ATGACCTTATCCACACAGGTGCATTTAAAGAAATTAGG---CTTATAAGCTGACTCTTA 863
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 254 IleAlaIaValAlaProGlyAlaPheLeuGlyLeuIleAsnArgTrpLeuAspLeu 273
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 864 AGAATAATTTTGTATGATTAAATGTAAATGAAAATTGATTCAGAGTCTGGCTGTGTTA 923
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 274 SerHisAsn---ArgValAlaGlyLeuLeuGlnAspThrPheProGlyLeuLeuGlyLeu 292
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 924 GAAATCCATCGTTTGGTCTCGGAGAAATTGAAGAAAGAACTTGGAAAAATTGGT 983
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 293 ArgValLeuArgLeu-----Ser 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 984 AAATGCTTAGAGGGCTGTGCAATTGACCATTTGAGAGAAATTCGATTAGCATCTTA 1043
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 HisAsnAlaIleAlaSerLeuArgProArgThrPheIleAspLeu----- 313
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1044 GACTACTACCTCGATGATATATATGACTTATTTAATGTGTCAAATGTTTCTCATTT 1103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 314 ---HisPheLeuGlnGluLeu----- 319
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1104 TCCCTGTGAGTGTGACTATTTGAAGGGTAAAGAACTTTCTTATATTTGGATGGCA 1163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 320 GlnLeuGlyHisAsnArgGlyLeuArgGlnLeuAlaGlnArgSerPheGln--GlyLeuGly 338
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1164 CATTTAGAATTAGTTAATCTGTAATTTGGACAGTTTCCACATTTGAATCTCAATCTCTC 1223
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 339 GlnLeuGlnValLeuThrLeuAspHisAsnGlnLeuGlnGlnValIleValAlaPhe 358
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1224 AAAAGCTTACTTCACTTCC-----AACAAAGGTGGAAATGCTTTTCAAGATTGAT 1277
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 359 LeuGlyLeuThrAsnValAlaValIleAsnLeuSerGlyAsnCyLeuArg-----Asn 376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1278 CTACAGAGCTTGAGTTTCTATACCTCAGTAGA---AATGGCTTGAAGTTCAAGGTTCC 1334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 377 LeuProGlnGlnValPheArgGlyLeuGlyIleValHisSerLeuHisLeuGlnGlySer 396
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1335 TGT-----TCTCAAGTGAATTTTGGGACACACAGCCTAAAGTATTAGAT 1379
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 397 CyLeuGlyArgGlyLeuArgProHisThrPheThrGlyLeuSerGlyLeuArgArgLeuPhe 416
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1380 CTGAGCTTCAATGTGTATTATACATGAGTTCAAACTTCTTG--GGCTTGAACAACATA 1436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 417 LeuIleAspAsnGlyLeuValGlyIleGlnGlnGlnSerLeuTrpGlyLeuAlaGlnLeu 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1437 GAACATCTGGAATTTCCAGATCTCCAAATTTGAACAAGATGAGTTTCAATATTTCTTA 1496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 437 LeuGlnLeuAspLeuThrSerAsnGlnLeu----- 446
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1497 TCACCTCAGAAACCTATTTACTTGAATTTCTCACTACTCACACACAGATGTTCTTCAAT 1556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 447 -----ThrHisLeuPro-----His 451
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1557 GGCATCTTCAATGTGCTGTGCTGACGTCCAGATCTTGAAGAACTGTGGCAATCTTCCAG 1616
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 452 ArgLeuPheGlnGlyLeuGlyIleLeuGlnGlyIleLeuLeuSerArgAsnArgLeuAla 471
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1617 GAAAACCTCTCTCC---GATATCTTCAACAGAGCTGAGAAATTTGACCTTCCAGACCTC 1673
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 472 Gln-----LeuProAlaAspAlaLeuGlyProLeuGlnAlaGlyAlaPheTrpLeuAspVal 489
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1674 TCTCAGTGTCACTGAGAGCACTGTGTCTCCACAGCAATTTAATCTCACTCTCCAGTCTTCCAG 1733
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 490 SerHisAsnArgLeuGlnAlaLeuProAsnSerLeuLeuAlaProLeuGlyArgLeuArg 509
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1734 GTACTTAATATAGCCACACAACTTCTTTTATTGATAGCTTTCTTATAAGTGTCTG 1793
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 510 TyLeuSerLeuArgAsnAsn-----SerLeuArgThrPheThrProGln----- 524
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1794 AACTCCCTCCAGTTCTTGATTACAGTCTCATCATATATGACTTCCAAAAACAGAA 1853
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 524 ----- 524
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1854 CTACAGCATTTTCCAAGTAGTCTAGCTTTCTTAATCTTACTCAGAAATGACTTGTCTGT 1913
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 525 -----ProProGlyLeuGlnArgLeuTrpLeuGlnGlyAsnProTrpAspCys 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1914 ACTTGTGAACACCAAGATTTCTGCAATGATCAAGAC----- 1952
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 GlyCysPro-----LeuIleValIleuArgAspPheAlaLeuGlnAsnProSer 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1953 -----CAGAGCAGCTCTGTGTGGAAGTTGACGAATGGAATGTGCAACAGCTTCAGAT 2006
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 557 AlaValProArgPheValGlnAlaIleCysGlnGlyAspAspCysGlnProProGlyValTy 576
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2007 AAGCAGGGCATCTGTGCTGAGTTGATTAATATCACTGTCCAGATGAATTAAGCAGCATAT 2066
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 577 ThrTyTrpAsn-----AsnIleThrCysAlaSerProProGlnValVal 590
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2067 GGTGTGTGGTCT 2078
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```


QY 1575 TCCAGCTCGGAATCTTTGAAAATGGCTGGCAATCTTTCCAGGAAAATCTCTTCCAGAT 1634
 Db ::::::::::::::::::::-ValProArg 539
 QY 521 AasnSerLeuArgValIleSerLeuHieGlyAasnLySerLeuThrGlyLys- 539
 Db 1635 ATCTTCACAGAGCTGAGAAATCTTGAACCTCTGGACCTCTGCAGTGTCAACTGGAGCAG 1694
 QY 540 SerLeuIleasnGlySerLyThrLeuThrLeuLeuasnProGlyAasnArgIleuasnPro 559
 Db 1695 TTGTCTCCACACAGCATTTAACTCACTCTCCAGTCTTCAGGTAAGTAATATGACCAAC 1754
 QY 560 ThrPheProasnThrLeuGlyAasnLeuSerGlnLeuLySileLeuAasnLeuArgSerA 579
 Db 1755 -----AACTCTTTTCA----- 1766
 QY 580 LysLeuHieGlyProIleLysSerSerGlyAasnThrAasnLeuPheThrArgLeuGlnIle 599
 Db 1767 TTGGAT-----ACGTTTCTTAAAGTGTGTAACCTCCCTC 1802
 QY ::::::::::::::::::::- 619
 Db 600 LeuAspLeuSerSerHengIlyPheSerGlyAasnLeuProGluSerIleLeuGlyAasnLeu 619
 QY 1803 CAGGTTCTT-----GATTACAGT 1820
 Db ::::::::::::::::::::- 639
 QY 620 GlnAlaMetLysLysIleAspGluSerThrArgThrProGluTyrIleSerAspIleTyr 639
 QY 1821 CTCGAATCACATA-----ATGACTTCCAAAACAGAGAA-----CTACAGCATTTT 1865
 Db ::::::::::::::::::::- 659
 QY 640 TyrAsnThrLeuThrThrIleThrThrLysGlyGlnAspTyrAspSerValArgIlePhe 659
 QY 1866 CCAAGTAGTCTAGCTTTCTTAAATCTTACTCAGATGACTTTGCTGTGTAAGTGTGAACAC 1925
 Db ::::::::::::::::::::- 676
 QY 660 ThrSerAsnMet---IleIleHieLeuSerLysAasnArgPheGluGlyArgIle----- 676
 QY 1926 CAGAGTTTCCCTGCAMATGATCMAGAACCCAGGAGCCTTTGGTGAAGTTGAACGATG 1985
 Db ::::::::::::::::::::- 696
 QY 677 ProSerThrIleGlyAspLeuValGlyLeuArgThrLeuAasnLeuSerHisAasnValLeu 696
 QY 1986 GAATGTGCACACCTTCAAGTATAGCAGGAGGATCGCTGTGCTG----- 2027
 Db ::::::::::::::::::::- 716
 QY 697 GluGlyHisIleProAlaSerPheGlnAasnLeuSerValIleGluSerLeuAspLeuSer 716
 QY 2028 AGTTGAATTCACCTGTCAGATGATATAGACCATCATTTGGTGTGCGCTCCAGCTGG 2087
 Db ::::::::::::::::::::- 736
 QY 717 SerAasnLysIleSerGlyAlaIleProGlnIleuAlaSerLeuThrPheLeuGluVal 736
 QY 2088 CTGTAGATATCTGTTGTAGCAGTTCGTGCTATATAGTTCTATTTTCCACCTGATCTTCT 2147
 Db ::::::::::::::::::::-HisAasnIleLeuVal----- 745
 QY 737 LeuAasnLeuSer----- 745
 QY 2148 GCTGCTGCATTAAGTATGCTAGAGCTGAAAACATCTATGATGCTTTGTTATCTACTCA 2207
 Db ::::::::::::::::::::- 761
 QY 746 ---GlyCysIlePheProLysGlyLysGln-----PheAspSerPheGlyAasnSerSer 761
 QY 2208 AGCCAGGATAGAGCTGGTATAG 2231
 Db 762 TyrGlnGlyAasnAspGlyLeuArg 769
 RESULT 12
 T24315
 hypothetical protein T01G9.3 - Caenorhabditis elegans
 CSpecies: Caenorhabditis elegans
 CDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 CAccession: T24315
 RLeppard, N.
 submitted to the EMBL Data Library, July 1996
 AReference number: Z19874
 AAccession: T24315
 AStatus: preliminary; translated from GB/EMBL/DDBJ
 A.Molecule type: DNA
 A.Residues: 1-603 <WTL>
 A.Cross-references: UNIPROT:Q20275; EMBL:Z75713; PDB: CAB00050.1; GSPDB: GN00019; CESP: TC
 A.Experimental source: clone T01G9
 CGenetics:
 A.Gene: CESP:T01G9.3

A:Map position: 1			
A:Introns: 68/3; 346/1; 407/3; 450/3; 486/3			
Alignment Scores:			
Pred. No.:	2.3e-14	Length:	603
Score:	299.00	Matches:	170
Percent Similarity:	42.46%	Conservative:	117
Best Local Similarity:	25.15%	Mismatches:	225
Query Match:	4.45%	Indels:	164
DB:	2	Gaps:	35
US-09-396-985B-3 (1-3811) x T24315 (1-603)			
QY	426 TGTGAAATCCGACAACTTGAAGATGGGCGATATCGAGCGTAAAGCAACCTCTCTACCTTA	485	
DB	41 Cysatgylsvallelleasnsprrhrleryralagluile-----Leuenglnleu	58	
QY	486 ATATTGACAGAAACCCCATCGAGATTTTAAAGCCCTGGAGACCTTTTTCGACTATCAAGT	545	
DB	59 Proleuthr-----LeuargserleuhsillegnProProserhsanrgllegly	75	
QY	546 TTACAGAACTGGTGGCTGTGGAGCAAAATCTAGCATCTCTAGAGAACTTCCCATTTGA	605	
DB	76 Seranlylsvallelrgtrpasmnp-----Asnilleasnarphe-----Ala	89	
QY	606 CATCTCAAAACCTTGAAGAACTTATGNG---GCTCAAACTCTATCCATCTTTCACA	662	
DB	90 Glnleuargvalleuargleuileasnysglnleproalamehserrargserllearg	109	
QY	663 TTACCTGAGTATTTTCTAATCTGACCAATCTTAGACACTTGGACCTTTCAGCAACAG	722	
DB	110 Leupro-----Serleuqlvalleuasprenhserrhsana	122	
QY	723 ATTCAAGATTTTANTGACAGACTGGGGGTTTACATCAAAATGCCCTACTCAATCTC	782	
DB	123 lleglunhsalathmetserasn-----PheglglymepProlysbuargval	139	
QY	783 TCTTTAGACCTGTCCTGACCCCTTGAACCTTATTCACACGAGGTCATTTAAGAAATT	842	
DB	140 ---LeuaprlenseSerhsnhsileuasnilleuoprothgllyvalphenrlyrleu	158	
QY	843 AGG---CTTCATTAAGCTGACCTTGAAGAAATATTTTGATAGTTTAAATGTAAGAACT	899	
DB	159 Argalaleuargserleuhserrhsanhsenanthrlleaser---Aspreuhserrhsan	177	
QY	900 TGTATTCAAGGCTGGCGCTTTAGAAGTCCATCGTTTGGTCTCTGGAGAAATTTAGAAAT	959	
DB	178 Leuileuargllyleuasnserleuargvalleuargleu-----	190	
QY	960 GAAGGAAACCTTGAAAGTTGACAAATCTGCTCTAGAGGGCGCTGNCATTTTGACATT	101	
DB	191 -----Asprarganpro-----lleprolle	197	
QY	1020 GAAGATTCGATAGCACTATGACATCTAGCATCTGATGATATTAATTGATTTTAAT	107	
DB	198 Glnhsilleasngluleuphenrthasrvalserglnleuargluleuylrleuhsnhs	217	
QY	1080 TGTTTGACAAATGTTCTTCATTTTCCCTGGAGAGTGATCATATGAAAGGTAAGAAAGC	113	
DB	218 Cys-----Asnleuser-----serlleylserleuallleuhsprgllleprogn	233	
QY	1140 TTT---TCTTAATAATTCGATGGCAACATTTAGAAATTTGTTAACTGTTAAATTTGGACAG	119	
DB	234 Leuargglnleucllyllellyllysnanleuylmeval-----	247	
QY	1197 TTTCACAACTGAAATCTCAAAATCTTCAAAAGCTTACTTTCATTTCCAAAGAGGTGG	125	
DB	248 ---Prothlyrglleuargserleuoprognleuser---Valleuhsprleuhsnhs	265	
QY	1257 AATGCTTTTTCGAAGTGTATCTA-----CCAAGCTTGAAGTTCTTGAAT	130	
DB	266 Annsrllleeglnghlillethralacysalaphesysasnthhsnilleserlyrleuhspr	285	

QY	1302	CTCAGTACAAAT	-----GGCTTGAGCTTCAAGAGTCTGTCTCAAGAGTAACTTGGG	1355S
Db	286	LeuSerHisAsnLeuLeuGlyIleSerIysAspSerProPheAsnGlnAspAlaPheArg	305	
QY	1356	ACAAACCAAGCCAAAGTAAATTTAGATGTGAGCTTCAATGGTGTAAATTAACATGATTTCAAC	1415S	
Db	306	ThrMetProLeuArgHisLeuAspSerPheAsnHisMetAsnAspPheAspSerIys	325	
QY	1416	TTCTTTGGC-----TTGAACAACACTGAACATCTGGATTTCCAGCATTTCCAAATTTGAA	1469S	
Db	326	TrpLeuGlyTrpAlaGlnGlnLeuLeuThrSerIleAlaLeuSerGlyAsnPheLeuIys	345	
QY	1470	CAATAGATGAGTTTTCAGTATCTCTACATCCAGAAACCTTACCTAGCATTTCT	1529S	
Db	346	AsnPheGlnGln-----SerTrpThrIyrThrIeuIysSerLeuIleHisLeuGlnLeu--A	364	
QY	1530	CATACTCACACAGAGTTGCTTTCATAGGACCTTCATGGCTGTCTCAGTCCGAACTC	1589S	
Db	364	IeTyAsnHis-----	367	
QY	1590	TTGAATAATGGCTGGCAATTTCTTCCAGAAAACTTCCAGATATCTTCAAGAGCTG	1649S	
Db	368	-----IleIysPheIleProValGlnLeuProSerArgIyrHisIleu-----	382	
QY	1650	AGAAACTTGACCTTCTGGACCTCTCTCAGTGTCACTGAGACAGTGTCTTCCAAACAGA	1709S	
Db	382	-----	382	
QY	1710	TTTAACGACCTCCAGCTTCAGGTACTAA-----TATGAGCCACAAACTTTCTT	1763S	
Db	383	-----IleSerLeuAsnIleSerGlyAsnGlnLeuThrTyrLeuPro--AspAsnIleAsn	400	
QY	1764	TCATTGATACGTTTCTTATATAGTGTGAACTCCCTCAGAGTTCTTGAATTAAGTCTC	1823S	
Db	401	ThrIeu-----LeuProAsnValIysThrPheAspIleHrxAla	413	
QY	1824	AATGACATTAAGACTTCCAAAAACAGAACTACAGCAATTTTCCAAAGTACTAGCTTC	1883S	
Db	414	AsnArgPheHisThr-----PheSerHis-----ThrAspLeuAlaPhe	426	
QY	1884	TTAAATCTTACTCAG-----AATGACTTTCCTGACTTGTGACAC	1925S	
Db	427	LeuAsnAsnValGlnGlnValIyrValAspGlyAsnProTrpAspCysSerCysAlaIle	446	
QY	1926	CAGATTTCTGCAATGATCAAGACCAAGGACGCTC-----TTGGTGAAGTTGAA	1979S	
Db	447	GlnGlyLeuGlnValHisMetCysArgSerArgIyrAlaMetArgHisIleLeuAsnTyrAsp	466	
QY	1980	CGAATGAAATGTGCACACCTTCAGATTAAGCAGGCACTGCTGTCTGATGTTGAATATC	2039S	
Db	467	AsnValArgCysAlaThrProSerLeuValGlnGlyHisSerValLeuAlaIleHr--	485	
QY	2040	ACCTGACATGAATTAAGACCATCTT-----GGTGTGGGTCTC	2081S	
Db	486	-----AspValAsnAspCysAlaValIleuPheGlyAlaArgIyrGlyLeuThrGlnThr	503	
QY	2082	AGTGCTTGTAAGTATCTGTTGTAGACAGTCTGTGCTAATGTTTATTTTCCACCTGATG	2141S	
Db	504	SerGlnMetLeuIleLeuLeuAlaGlyValIleuLeu-----PheAlaAlaLeuLeuLeu	521	
QY	2142	CTTCTTGCTGCTGATAAAGTATGTAAGAGGTGAAAACTATATGATGCTTGTGTATC	2201S	
Db	522	MetIleLeuGlyCysIleTyrPheLeuArg--GlnArgGlnIyrGlySerTyrVal	540	
QY	2202	TACTCAACCCAGAGATCGGGTAAAGATGAGCTAGTAAGATTTTGAAGAAGG	2261S	
Db	541	ThrArgLeuHisSerArgThrProLeuThrMetAla-----	552	
QY	2262	GTGCTTCATTTTCACTGCTGCTTCACTACAGAGACTTATTTCCGGTGTGGCCA-----	2318S	
Db	553	AsnThrHisSerCysSerSerSerThrAsnAspHisIleGlyProLeuSerProProH	572	
QY	2317	-----TTGCTGCCAACATCATTCATGAAGTTTCC	2346S	

Score: 298.00 Matches: 186
Percent Similarity: 38.87% Conservative: 95
Best Local Similarity: 25.73% Mismatches: 258
Query Match: 4.43% Indels: 184
DB: 2 Gaps: 35

US-09-396-985B-3 (1-3811) x S42799 (1-662)

```

QY 240 TGGCGTTTATCAGGAGGAGTTCCTAATATTAATCAATGAGAGGAGTTC 299
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 26 Cyslyshetvalaaplysllyseval-----SerCysglinalleuglyleu 40
QY 300 TACAAATCCCGCAACATCCCTCTTCAACCAAGAACTGAGCTTAAATCC 359
    :|...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 41 LeuglnvalproservalleuProproksphrthgluthrleuapleuSerCylAsnln 60
QY 360 CTGAGGCAATTAGGAGCTATAGCTTCTTCAAGTTCCAGAACTGAGAGTCTGATTTA 419
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 61 LeuArgserlileuAlaserProleuglyPheTyThrAlaleuArgHileuAsprleu 80
QY 420 TCCAGGCTGAATCCAGCAATGAAGATGGGGATTCAGAGCTTACGACCTCTCT 479
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 81 SerThranglulleserPheleuglnProglYalAphelglinalleuThrHileugln 100
QY 480 ACCTTAATATTCAGAGAAACCCATCCAGAGTTTACGCTTCTTCTGAGTA 539
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 101 HisleuSerleuAlahleuAsnArgleuAlametalathrAlaleuSerAlaglyCylleu 120
QY 540 TCAAGTTTACAGAACTGGCTGCTGTGAGACAAATCTAGCATTT----- 584
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 121 GlYProleuProArgvalThrSerleuAsprleuSerGlyAsnSerleuTySerGlyleu 140
QY 585 CTAGAGAACTCCCATTTGCAATCTCAATCTGAAAGAACTTAATAGTGGCTCACAT 644
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 141 LeuAluArgleu---LeuglyGlualAProserleuHleuHleuSerleuAlaGlualsn 159
QY 645 CTATTCGAATCTTCAATATCTAGAGTAT---TTTCTATCTGACCAATCTAGAGAC 701
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 160 SerleuThr-----ArgleuThrArgHleuThrPheArgAspMetProAlaleuGluln 177
QY 702 TTGAGCTTTTCAGCAACAGATTCAAGATTATTAATTCAGACAGCTTGGGGTCTACAT 761
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 178 LeuAsprleuHleuSerAsnvalleuMetAsprlleuGlualAsprlyAlaPheglulYleuPro 197
QY 762 CAATGCCCTACTCAATCTCTCT----- 785
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 198 ArgleuThrHleuAsnleuSerArgAsnSerleuThrCysIleSerAspPheSerleu 217
QY 786 -----TTAGACCTGTCCCTGAACCCCTATGAACCTTATTC----- 818
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 218 GlnglnleuArgvalleuAsprleuSerCysAsnSerlleuGlualAphelglnThrAlaser 237
QY 819 CAACAGGTGATTTAAAGAAATTAGGCTTCATAGCTTCACTTAAAGAAATAT----- 872
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 238 GluProglinala-----GluPheglleuThrTrpleuAsprleuArgGlualsnlyleu 255
QY 873 -----TTGATAGTTTAATGTATGAAAACTGTATTCAGAGCTTGGCTGGTTTGAA 926
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 256 LeuHleuPheProAsprleuAlaleuProArgleuIleTyIleuAsnleuSerAsnAsn 275
QY 927 GTCCATGCTTTGGTTCTGGGAGATTAGAAAT----- 959
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 276 LeuIleArgleuProthrglyProProglinspserlyseglyIleHleuAlaProserGlu 295
QY 960 -----GAGGAAACTTGGAAAGATTGACAAATCT 989
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 296 GlYTrpserAlaleuProleuSerAlaProserGlyAsnAlaserGlyArgProleuSer 315
QY 990 GCTTAAAGGCGCTGTGCAATTTGACATTCAGAAATTCGATTTAGCATTAAGTAC 1049
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 316 GluIleuAsnleu---AsprleuSerTyAsnGlnIleGlnleu---IleProAspser 333
QY 1050 TACCTGATGATATTATTAATTT-----AATTTGTTGACAAAT 1091

```

```

DB 334 PheleuGlulHleuThrSerleuCysPheleuAsnleuSerArgAsnCysleuArgThr 353
QY 1092 GTTTCCTTCATTTTCCCTGGAGCTGTACATTTGAAAGGTTAAAGACTTTCTTATAT 1151
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 354 PheglulAlaArgArgleuGlySerleuProCysleuMetleuAsprleuSerHleuAsn 373
QY 1152 TTGGAGGAGCAACTTTAGAAATTAGTTAAGTGAATTTGGACAGTTTCCACATTTGAA 1211
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 374 ---AlaleuGlulThrleuGluleuGlyAlaArgAlaleuGlySerleuArgThrleu 392
QY 1212 CTCAATCTCTCAAAAAGCTTACTTCTTCACTTCCAAAGAGTGGAAATGCTTTTTCAGAA 1271
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 393 LeuGln-----GlyAsnAlaleuArgAsp 400
QY 1272 GTT-----GATCTACAAAGCTTGAATTTCTAGATCTCAGTGAAT 1313
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 401 LeuProProTyThrPheAlaAsnleuAlaserleuGlnArgleuAsnleuGlnlyAsn 420
QY 1314 GGCCTGAGT-----TTCAAAGGCTGCTGTTCACAAAGT 1346
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 421 ArgvalSerProCysglyTyProAspGluProglYProserGlyCysvalAlaPheSer 440
QY 1347 GATTTGGGACAAACAGCTTAAAGTATTAGTCTGAGCTTCAATGGTGTATTATACATG 1406
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 441 ---GlyIleThrSerleuArgSerleuSerleuValAspAsnGlnIle----- 455
QY 1407 AGTTCAAACTTTCTGGGCTTAAAGCAACTGAAACATCTGAGATTTCCAGCATTCCAATTG 1466
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 456 -----GluIleuLeuArgAlaGlyAlaPheleuHleuThrProleu 468
QY 1467 AAACAATGAGTGAATTTTCAATTTCTTCACTCACTGAAAAACCTTACCTTGAATAT 1526
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 469 ThrGln-----LeuAsprleu 473
QY 1527 TCTCATACTACACACAGAGTTGCTTTCATAGGCATCTTCAATGGCTTG---TCCAGTCTC 1583
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 474 SerSerAsnProglYleuGlnvalAlaThrCylAlaleuGlyleuGlnAlaSerleu 493
QY 1584 GAACTCTTGAATAATGGCTGCAATCTTTTTCAG-----GAAAATCTTCTCCAGATATC 1637
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 494 GluValleuAlaleuGlnGlnlyAsnGlyleuMetValleuGlnvalleuAsprleuProCysPhe 513
QY 1638 TTCACAGAGCTGAGAAACTTGACCTTCTTGAGCTCTCTCAGTGTCAATCTGAGAGCACTTG 1657
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 514 IleCys-----LeuTyArgleuAsnleuAlaGlnAsnArgleuSerHleu 529
QY 1698 TCTCAACAGCAATTTAACTCACTCTCCAGCTTCAGGATCTAAATATAGACCAACAAAC 1757
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 530 -----ProAlaThrPthrGlnAlaValSerleuGlnvalleuAsprleu---ArgAsnAsn 546
QY 1758 TCTTTTCATTTGATAGCTTCTTCTTAAAGTGTCTGAACCTCCGAGGTTCTTGATTAAC 1817
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 547 SerPheSerleu-----LeuProGlySerAlameCylglyleuGln----- 560
QY 1818 AGTCTCAATCAATATGACTTCCAAAAAAGAGAACTACAGCATTTTCCAAGTACTTA 1877
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 561 -----ThrSerleu 563
QY 1878 GCTTCTTAATCTTACTCAGATGACTTGTGTTGACTTGTGAACACAGAGTTTCTGT 1937
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 564 ArgArgleuTyIleuGlnGlyAsnProleuSerCys---CysGlyAsn----- 578
QY 1938 CAATGATCAAGAGCAG---AGCAGCTCTGTGTGAAGTTGAACGAAATGAA----- 1988
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 579 GlYTrpIleuAlaGlnleuHleuHleuGlnlyArgValAsprValaThrAlaThrAlaAsprleu 598
QY 1989 ---TGTCAACACCTTCAATAGACAGGAGGATGCTGTGAGTTGAAATATACAC--- 2042
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|
DB 599 IleCysArgPheSerSerGlnGln-----ValSerleuSerHleuValArg 614
QY 2043 -----TGTCAAGTGAAT-----AAGACATCATTTGGTGTGCTGCTCAGGCTG 2087
    |||...:|...:|...:|...:|...:|...:|...:|...:|...:|...:|

```

Db 615 ProGluAspCysgluylslyleuylAsnIleAsnleuIlelleuThrPhe 634
 QY 2088 CTGTGATCTGTGTAGAGAGTTGGTCTATTAAGTTCTATTTCACCGTAGCTTCTT 2147
 Db 635 IleValSerAlaIleLeu-----LeuThrThrLeu 645
 QY 2148 GCTGGCTGC 2156
 Db 646 AlaAlaCys 648
 RESULT 15
 T42218
 silt-1 protein homolog - rat
 N:Alternate names: MEGF4 protein
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T42218
 R:Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 A>Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: Z14126; MUID:98360089; PMID:9693030
 A:Accession: T42218
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1531 <NAK>
 A:Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:G3449289; PIDN:BAA32460.1; PID:G3
 A:Experimental source: strain Sprague-Dawley; brain
 C/Genetics:
 A:Gene: MEGF4
 C/Superfamily: fruit fly salt protein; BGF homology; leucine-rich alpha-2-glycoprotein
 Alignment Scores:
 Pred. No.: 3,31e-14 Length: 1531
 Score: 298.00 Matches: 164
 Percent Similarity: 35.05% Conservative: 94
 Best Local Similarity: 22.28% Mismatches: 254
 Query Match: 4.43% Indels: 225
 DB: 2 Gaps: 26
 US-09-396-985b-3 (1-3811) x T42218 (1-1531)
 QY 282 TGCATGAGAGTGAATTTCTACAAATGCCGACACCTCCCTTCACCAAGAACTG 341
 Db 295 CysArgGlyLysGlyLeuThrAlaIleProAlaAsnLeuProGluThrIle 314
 QY 342 GACCTGAGCTTATCCCTCGAGGCAATTAGGCAAGCTTCTTCACCTTCCCGAGA 401
 Db 315 ArgLeuGluLeuAsnGlyIleLysSerIleProProGlyAlaPheSerProIlyrArgLys 334
 QY 402 CTGCAGGTGCTGATTTATTCAGAGTGAATCCAGACAACTTGAAGATGGGCATATCAG 461
 Db 335 LeuArgArgIleAspLeuSerAsnAsnGlnIleAlaGluIleAlaProAspAlaPheGln 354
 QY 462 AGCCTAAGCACCCTCTTCACTTAATATTAAGACAGAAACCCATCCAGAGTTAGCCCTG 521
 Db 355 GlyLeuArgSerLeuAsnSerLeuValLeuIlyrGlyAsnLysIleThrAspLeuProArg 374
 QY 522 GGAAGCTTTCTGTGACATATCAAGTTTACAGAAGCTGTGGCTGTGGAGACAAATCTAGCA 581
 Db 375 GlyValPheGlyGlyLeuIlyrThrLeuGlnLeuLeu----- 387
 QY 582 TCTCTAGAAACTTCCCATTTGACATCTCAAAACTTGAAAGACTTAAATGGGCTCAC 641
 Db 388 -----LeuAsnAla----- 390
 QY 642 AATCTTATCCAACTTTCAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGAGCAC 701
 Db 391 AsnLysIleAsnCysIleArg---ProAspAlaPheGlnAspLeuGlnAsnLeuSerLeu 409
 QY 702 TTGGACCTTTCCAGCAACAAGATTCAAGATT-----TATTGCACAGACTTGGG 752
 Db 410 LeuSerLeuIlyrAspAsnLysIleGlnSerLeuAlaLysGlyThrPheThrSerLeuArg 429

QY 753 GTTCTACATCAAAATGCCCTACTCAATCTCTGTTAGACSTGTCCSTGAAACCTATAGAAC 812
 Db 430 AlaIleGln-----ThrLeuIleLeuAlaGlnAsnPro----- 440
 QY 813 TTTATCCAAACAGGTGCAATTTAAGAAATTAGAGCTTCATAGCTGATTAAGAAATAT 872
 Db 441 PheIleCysAspCysAsnLeuIlyrThrLeuAla-----Asp 452
 QY 873 TTTGATAGTTTAAATGTATGAAACTGTATTAACAAGTCTGGCTGTTTAAAGTTCAT 932
 Db 453 PheLeuArgThrAsnProIleGluThr-----ThrGlyAlaArgCysAlaSerProArg 470
 QY 933 CGTTTGCTT-----CTGGAGAAATTATGAATGAAGAAACTTGAAAGTTTGAC 983
 Db 471 ArgLeuAlaAsnLysArgIleGlyGlnIleLysSer-----LysLysPheArg 486
 QY 984 AATGTGCTCTAGAGGCGCTGTGCATTTGACCATTAAGAAATCCGATTAGCATATCTTA 1043
 Db 487 CysSerAlaLysGlu-----GlnIlyrPheIleProGlyThrGlu 499
 QY 1044 GACTACTACTGAT-----GATATTATGACTTATTATTATTTGAC 1088
 Db 500 AspTyrHisLeuAsnSerGluCysThrSerAspValAlaCysProHisLysCysArgCys 519
 QY 1089 AATGTTCTTCATTTTCCCTGGTGAAGTGAATTAAGAAAGGTTAAAGACTTTCTTAT 1148
 Db 520 GluAlaSerValValGluCysSerGlyLeuLysLeuSerLysIleProGlu---ArgIle 538
 QY 1149 AATTTGCAATGGCAACATTTAGAAATTAGTTAACTGTAATT----- 1190
 Db 539 ProGlnSerThrThrGluLeuArgLeuAsnAsnGlnIleSerIleLeuGlnAlaThr 558
 QY 1191 GCAACATTTCCCACTGAATGAATCCAAATCTCAAAAGGCTTACTTCATCCACAA 1250
 Db 559 GlyLeuPheLys-----LysLeuSerHisLysLysLysIleAsnLeuSerAsnLys 576
 QY 1251 GGTGGAAATGCTTTTTCAGAAAGTGAATCTACAAAGCTTGAGTTCTAGATCTCACTAGA 1310
 Db 577 -----ValSerGluIleGluAspGlyThrPheGlu----- 586
 QY 1311 AATGCTTAGTTCAAAAGGTGCTGTCTCAAAAGTATTTGGCAACACGCTTAAG 1370
 Db 587 -----GlyAlaThrSerValSer 592
 QY 1371 TATTAGATCTGAGCTTCAATGAGTGTATTATCCATGATTCAAAC---TTCCTGGGCTTA 1427
 Db 593 GluLeuHisLeuThrAlaAsnGlnLeuGlnSerValArgSerGlyMetPheArgGlyLeu 612
 QY 1428 GAACAACTAGAACATCTGGAATTTCCAGACTTCCAAATTTGAAACAAATGAGTAGTTTCA 1487
 Db 613 AspGlyLeuArgThrLeuMetLeuArgAsnAsnArgIleSerCysIleHisAsnAspSer 632
 QY 1488 GTATTCCTATCTAGAAACCTGATTTACCTTGAATTTCTCAATCTCACACCAAGATT 1547
 Db 633 ---PheThrGlyLeuArgAsnValArgLeuLeuSerLeuIlyrAspAsnHisIleThrThr 651
 QY 1548 GCTTTCAATGGCATCTTCAATGAGCTTGTCCAGTCTGGAAGTCTTGAATAATGCTGGCAAT 1607
 Db 652 IleSerProGlyAlaPheAspThrLeuGlnAlaLeuSerThrLeuAsnLeuAlaAsn 671
 QY 1608 TCTTTCAGAGAAACTTC----- 1625
 Db 672 ProPheAsnCysAsnLysGlnLeuAlaThrPheGlyAspThrLeuArgLysArgLysIle 691
 QY 1625 ----- 1625
 Db 692 ValThrGlyAsnProArgCysGlnAsnProAspPheLeuArgGlnIleProLeuGlnAsp 711
 QY 1625 ----- 1625
 Db 712 ValAlaPheProAspPheArgCysGluGluGlyGlnGluGluValGlyCysLeuProArg 731
 QY 1625 ----- 1625

```
Db      732 ProGlnCysProGlnGlnCysAlaCysLeuAspThrValValArgCysSerAsnIleHis 751
QY      1626 -----CTTCCAGATATCTCCACAGAGCTG-----1649
Db      752 LeuGlnAlaLeuProIysGlyIleProIysAsnValThrGlnLeuTyrlLeuAspGlyAsn 771
QY      1650 -----AGAACTTGACCTTCCTGACCTC 1673
Db      772 GlnPheThrIleuValProGlyGlnLeuSerThrPheIysTyrlLeuGlnLeuValAspLeu 791
QY      1674 TCTCAGTGCAGCTGAGAGCTGTGTCACACAGCATTTAACTCACTCTCCAGCTTTCAG 1733
Db      792 SerAsnAsnIysIleSerSerLeuSerAsnSerSerPheThrAsnMetSerGlnLeuThr 811
QY      1734 GTACTAAATATGACCCACACAACTTTCTTTCATGTGATACGTTCTCTTAATAGTCTG 1793
Db      812 ThrLeuIleLeuSerTyrlAsnAlaLeuGlnCysIleProProLeuAlaPheGlnGlyLeu 831
QY      1794 AACCTCCCTCCAGGTTCTTGATTACAGTCTCAATGCATATGACATTTCCAAAAACAGAA 1853
Db      832 ArgSerLeuArgLeuLeuSerLeuHisGlyAsnAspValSerThrLeuGlnGlyIle 851
QY      1854 CTACAGCATTTTCCAGTAGCTAGCTTTCTTAAATCTTAATCTCAAGATGACTTGTCTGT 1913
Db      852 PheAlaAspVal---ThrSerLeuSerHisLeuAlaIleGlyAlaAsnProLeuTyrlCys 870
QY      1914 ACTTGTGAACACACAGATTCTCTGCAATGATCAAGACACAGAGCAGCTGTGGTGA 1973
Db      871 AspCysHisLeuArgIleuSerSerSerTrpValIleThrGlyTyrlCys-----Gln 887
QY      1974 GTTGAACGATGGAATGTGCACACACTTCAGATAGAGGAGCATGCCGTGCTGAG---- 2029
Db      888 ProGlyIleAlaArgCysAlaGlyProProGlnMetGlnGlyIleValLeuLeuThrThr 907
QY      2030 -----TTTGAATATCACTGTCAATGATGATAGACCATCATTTGCTGTCTG 2077
Db      908 ProAlaIysIysPheGln-----CysGlnGly 916
QY      2078 CCT-----CAGTGTGCTTGTAGTATCTGTGTAGCAGT 2110
Db      917 ProProSerLeuAlaValGlnAlaIysCysAspProCysIleSerSer 932
```

Search completed: March 29, 2005, 17:33:36
Job time : 100.695 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:30:23 ; Search time 205.959 Seconds
(without alignments)
18950.714 Million cell updates/sec

Title: US-09-396-985B-3

Perfect score: 6724
Sequence: 1 accagggccactgctgtctac.....ttctactgacaggaacta 3811

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+ n2p model -DEV=xjh
-Q=/cgn2_1/USFTO_spool/US0939685/Runat_28032005_155743_21146/app_query.fasta_1.85098
-DB=UniProt_03 -QFMT=faatan -SUFMT=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bloum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US0939685 @CGN 1.1 5213 @Runat_28032005_155743_21146 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEDUTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03.*

1: uniProt_sprot.*
2: uniProt_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4325	64.3	839	TLR4_HUMAN	O00206 homo sapien
2	4311	64.1	839	TLR4_PANPA	Q9ctn0 pan paniscu
3	4290	63.8	837	Q8SP88	O8sp88 gorilla gor
4	4162	61.9	828	TLR4_PONPY	O8sp89 pongo pygma
5	4013	59.7	826	TLR4_PAPAN	Q9tsp2 papio anubi
6	3312	49.3	843	TLR4_HORSE	O9mpy3 equus cabal
7	3291.5	49.0	841	TLR4_BOVIN	Q9g155 equus cabal
8	3288.5	48.9	841	Q8SQS5	O8sg55 bos taurus
9	3286.5	48.9	841	Q8WCD5	O8wcd5 bos taurus
10	3283.5	48.8	833	TLR4_FELCA	P58727 felis silve
11	3277.5	48.7	841	Q6WCD4	O6wcd4 bos taurus
12	3167.5	47.1	841	TLR4_PIG	O68y66 sus scrofa
13	3072.5	45.7	839	Q8MTQ2	Q8mtq2 cycotilegus
14	2987	44.4	838	TLR4_CRIGR	Q9qkx5 ratius norv
15	2850.5	42.1	835	TLR4_RAT	Q9kx25 mus musculu
16	2822	42.0	835	Q8K2T5	

17	2817	41.9	835	1	TLR4_MOUSE	Q9quk6 mus musculu
18	2206	32.8	636	2	Q8SQH3	O8sqh3 canis fami1
19	1828.5	27.2	843	2	Q7ZTG5	Q7ztg5 gallus gall
20	1276.5	19.0	819	2	Q6TS41	O6ts41 brachydanio
21	1265.5	18.8	817	2	Q6NV08	O6nv08 brachydanio
22	834.5	12.4	258	2	Q70EK4	Q70ek4 sus scrofa
23	693	10.3	945	2	Q76CT9	Q76ct9 parailichthy
24	686	10.2	945	2	Q80IF9	O80if9 carassius a
25	685	10.2	940	2	Q8T753	O8t753 branchiost
26	685	10.2	961	2	Q76CT7	Q76ct7 parailichthy
27	667.5	9.9	991	2	Q6R5N8	Q6r5n8 mus musculu
28	656.5	9.8	661	1	C180_MOUSE	Q62192 mus musculu
29	641.5	9.5	784	2	Q6YU02	Q6yug2 ratius norv
30	638.5	9.5	661	2	Q8CC21	O8cc21 mus musculu
31	633.5	9.4	973	2	Q6KCC7	Q6kcc7 oncohychnu
32	619.5	9.2	661	1	C180_HUMAN	Q99467 homo sapien
33	617.5	9.2	784	1	TLR2_HUMAN	Q9qu77 mus musculu
34	616.5	9.2	784	2	Q8K3D9	O8k3d9 mus musculu
35	613.5	9.1	784	2	Q811T5	O811t5 mus musculu
36	602.5	9.0	784	1	TLR2_HUMAN	O60603 homo sapien
37	601.5	8.9	661	2	Q7YRL4	Q7yrl4 sus scrofa
38	601.5	8.9	785	2	Q761Z4	Q761z4 sus scrofa
39	600.5	8.9	785	2	Q6TN21	Q6tn21 sus scrofa
40	597	8.9	784	2	Q6T752	Q6t752 equus cabal
41	595.5	8.9	784	1	TLR2_MACFA	Q95m53 macaca fasc
42	591.5	8.8	784	1	TLR2_CRIGR	Q9t1f8 cricetus
43	580.5	8.6	1032	1	TLR2_MOUSE	P58682 mus musculu
44	577.5	8.6	785	2	Q689D1	Q689d1 canis fami1
45	576	8.6	781	1	TL22_CHICK	Q9dgb6 gallus gall

ALIGNMENTS

RESULT 1
TLR4_HUMAN STANDARD; PRT; 839 AA.
AC O00206; Q9UK78; Q9UM57;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Toll-like receptor 4 precursor (Toll).
GN Name=TLR4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RC TISSUE=Brain;
RC TISSUE=Spleen;
RX MEDLINE=97379437; PubMed=9237759; DOI=10.1038/41131;
RA Medzhitov R., Preston-Hurlburt P., Janeway C.A. Jr.
RT "A human homologue of the Drosophila Toll protein signals activation
RT of adaptive immunity.";
RT Nature 388:394-397(1997).
RN [2]
RP SEQUENCE OF 41-839 FROM N.A.
RC TISSUE=Retal liver, lung, and Placenta;
RX MEDLINE=98118556; PubMed=9435236; DOI=10.1073/pnas.95.2.586;
RA Rock F.L., Hardiman G., Timans J.C., Kastelein R.A., Bazan J.F.;
RT "A family of human receptors structurally related to Drosophila
RT Toll.";
RN Proc. Natl. Acad. Sci. U.S.A. 95:586-593(1998).
RN [3]
RC SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.
RX MEDLINE=20558910; PubMed=11104518;
RA Shulimova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
RT locus (TLR4).";
RN Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
RN [4]
RC SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.
RX MEDLINE=20296622; PubMed=10635634; DOI=10.1038/76048;
RA Atbour N.C., Lorenz E., Schutte B.C., Zahner J., Kline J.N., Jones M.,

FT VARIANT 299 299 /FtId=VAR_018730.
 D -> G (in allele TLR4*B; reduced LPS-
 response; dbSNP:4986790).
 FT VARIANT 329 329 /FtId=VAR_012739.
 N -> S
 FT VARIANT 399 399 /FtId=VAR_018731.
 T -> I (in allele TLR4*B; reduced LPS-
 response; dbSNP:4986791).
 FT VARIANT 443 443 /FtId=VAR_012740.
 F -> L
 FT VARIANT 474 474 /FtId=VAR_018732.
 E -> K
 FT VARIANT 510 510 /FtId=VAR_018733.
 O -> H
 FT VARIANT 694 694 /FtId=VAR_018734.
 K -> R

Alignment Scores:
 Pred. No.: 0 Length: 839
 Score: 4325.00 Matches: 839
 Percent Similarity: 95.45% Conservative: 0
 Best Local Similarity: 64.32% Mismatches: 0
 Query Match: 64.32% Indels: 40
 DB: 1 Gaps: 1

US-09-396-985B-3 (1-3811) x TLR4_HUMAN (1-839)

QY 45 ATGATTCGCGCCGCGCCGCGCTGGAGCTGTGATCCCAAGCATGGCGCTTCTCTCTGC 104
 1 MetMetSerLaserTrgleuAlaGlyThrLeuIleProIleMetAlaPheLeuSerCys 20
 QY 105 GTGAGACCAAGAAAGCTGGAGCCCTGTGGAGAGACTTGGCCCTAAACACACAGAAAGAGC 164
 21 ValArgProGluSerTrpGluProCysVal----- 30
 QY 165 TGGCATGAACCCAGAGCTTTCAGACTCCGAGCTTCAGCCCTTCACCCCGATTCCATTG 224
 30 ----- 30
 QY 225 CTTCTGCTAAATGCTGCCCTTTATCAGGAGGTGGTCTTAATATTACTTATCAATGC 284
 31 -----GluValValProAsnIleThrTyrglnCys 40
 QY 285 ATGAGAGTAATTTCTACAAATATCCCGACCAACTCCCTTCTCAACCAAGAACTGAGC 344
 41 MetGluLeuAsnPheTrpIleProPheAsnLeuProPheSerThrTyrsAsnLeuAsp 60
 QY 345 CTGAGCTTAATCCCTGAGGAGATTAGGAGCTATAGCTTCTCAGTTTCCCAAGACTG 404
 61 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPheSerPheProGluLeu 80
 QY 405 CAGGTCTGATTTATCCAGGTGTGAATCCAGACAAATTGAGATGGGGCATTCAGAGC 464
 81 GluValLeuAsnPheSerArgCysGluIleGlnThrIleGluAsnGlyAlaTyrglnSer 100
 QY 465 CTAAGCACCTCTCTAATATTGACAGAGAAACCCATCCAGAGTTTAAAGCCCTGGGA 524
 101 LeuSerHisLeuSerThrLeuIleuInnGlyAsnProIleGlnSerLeuAlaLeuGly 120
 QY 525 GCGTTTTCGACTATCAAGATTACAGAGCTGGTGGCTGTGGAGCAAAATCTAGCATCT 584
 121 AlaPheSerGlyLeuSerSerLeuGlnTyrsValAlaValGluThrAsnLeuAlaSer 140
 QY 585 CTAGAGAACTTCCCACTTGACACTTCAAAATTGAAAGAACTTATGTGGCTCAAT 644
 141 LeuGluAsnPheProIleGlyHisLeuTyrsThrLeuIleGluLeuAsnValAlaHisAsn 160
 QY 645 CTTATCCAACTTTTAAATTAACCTAGTATTTTCTAATCTGACCAATCTAGAGCACTTG 704
 161 LeuIleGlnSerPheTyrsLeuProGluTyrsPheSerAsnLeuThrAsnLeuGluHisLeu 180
 QY 705 GACCTTTCAGACAAAGATTCAAGATTATTTGACAGACTTGGGGTCTTACATCAA 764
 181 AspLeuSerSerAsnIleGlnSerIleTyrsCysThrAspLeuArgValLeuHisGln 200
 QY 765 ATGCCCTCTCAATCTCTTATAGACCTGTCCCTGACACCTTGAACCTTATCAACCA 824
 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 825 GGTGATTTAAAGAAATTGAGCTTCAAGCTGACTTGAAGAAATATTTGATAGTTTA 884
 221 GlyAlaPheLeuSerIleLeuArgLeuHisTyrLeuThrLeuArgHisAsnPheAspSerLeu 240
 QY 885 AATGTATGAAAATTGTATTCAGGCTGGCTGTTTGAAGATCCATGCTTGGTCTTG 944
 241 AsnValMetLeuThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 260
 QY 945 GGAGAAATTTAGAAATGAGAAACTTGAAAAATTGACAAATCTGCTCAGAGGGGCTG 1004
 261 GlyGluPheArgAsnGluGlyAsnLeuGluTyrsPheAspTyrsSerAlaLeuGluGlyLeu 280
 QY 1005 TGCATTTTGAACCTTGAAGAAATTCGATTAGCATACTTACACTACCTGATGATATT 1064
 281 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrsLeuAspTyrsTyrsLeuAspAla 300
 QY 1065 ATGACTTATTTAATGTTTGAACAAATGTTTCTCATTTTCCCTGTGAGTGTGACTATT 1124
 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
 QY 1125 GAAAGGTAAAGACTTTTCTTATATTTCCGATGGCAACATTGAATTAAGTAACTGT 1184
 321 GluArgValTyrsPheSerSerTyrsAsnPheGlyTrpGlnHisLeuGluLeuValAsnCys 340
 QY 1185 AAATTGACAGATTTCCCACTTGAACCAATCTGCAAAAGCTTACTTCACTTCC 1244
 341 TyrPheGlyGlnPheProThrLeuTyrsLeuTyrsSerLeuTyrsArgLeuThrPheTrpSer 360
 QY 1245 AACAAAGTGGGAATGCTTTTTCAGAAAGTTGATCAACAAAGCTTGAGTTTCAAGATCTC 1304
 361 AsnTyrsGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluIlePheLeuAspLeu 380
 QY 1305 AGTAAAGATGCTTGAATGCTTCAAGGTTTCTGTTTCAAGACATTTTGGGACAAACACAGC 1364
 381 SerArgAsnGlyLeuSerPheLeuGlyCysCysSerGlnSerAspPheGlyThrTrpSer 400
 QY 1365 CTTAAAGTATTTGATGATGCTTCAATGATGTTATTAACATGATGTTCAACTTCTGGGC 1424
 401 LeuTyrsTyrsLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
 QY 1425 TTGAAACAACTGAACATGTGATTTCCAGACTTCCAAATTTGAAACAAATGAGTGAATT 1484
 421 LeuGluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuTyrsGlnMetSerGluPhe 440
 QY 1485 TCAATTTCTTATCACTGAGAAACCTCATTTACCTTGACATTTCTGATCTCACACCA 1544
 441 SerValPheLeuSerLeuArgAsnLeuIleTyrsLeuAspIleSerHisThrHisTrpArg 460
 QY 1545 GTTGCTTTCAATGGGATCTTCAATGGCTTGTCCAGCTGCAAGTCTTGAAGAAATGGCTGAC 1604
 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuTyrsPheAlaGly 480
 QY 1605 AATTTCTTCCAGAGAAACTTCTCCAGATATCTTCAACAGACTGAGAAATGACCTTC 1664
 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgHisAsnLeuThrPhe 500
 QY 1665 CTGAGACTTCTCAAGTGTGAATCTGAGACAGTTGTCTCAACAGCAATTTAATCACTCTGC 1724
 501 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 520
 QY 1725 AGCTTCAAGGTACTAATATGAGCCAAACAATCTTTCAATGGATAGTTCCTTAT 1784
 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeuAsnSprThrPheProTyrs 540
 QY 1785 AAGTCTGTAATCTCCCTCAGGTTCTTGATTAACGTTCAATCAATATGACATTCACAA 1844
 541 TyrsCysLeuAsnSerLeuGlnValLeuAspTyrsSerLeuAsnHisIleMetThrSerTyrs 560

Db 181 AspLeuSerSerAsnIleGlnSerIleTyrsCysThrAspLeuArgValLeuHisGln 200
 QY 765 ATGCCCTCTCAATCTCTTATAGACCTGTCCCTGACACCTTGAACCTTATCAACCA 824
 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 825 GGTGATTTAAAGAAATTGAGCTTCAAGCTGACTTGAAGAAATATTTGATAGTTTA 884
 221 GlyAlaPheLeuSerIleLeuArgLeuHisTyrLeuThrLeuArgHisAsnPheAspSerLeu 240
 QY 885 AATGTATGAAAATTGTATTCAGGCTGGCTGTTTGAAGATCCATGCTTGGTCTTG 944
 241 AsnValMetLeuThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 260
 QY 945 GGAGAAATTTAGAAATGAGAAACTTGAAAAATTGACAAATCTGCTCAGAGGGGCTG 1004
 261 GlyGluPheArgAsnGluGlyAsnLeuGluTyrsPheAspTyrsSerAlaLeuGluGlyLeu 280
 QY 1005 TGCATTTTGAACCTTGAAGAAATTCGATTAGCATACTTACACTACCTGATGATATT 1064
 281 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrsLeuAspTyrsTyrsLeuAspAla 300
 QY 1065 ATGACTTATTTAATGTTTGAACAAATGTTTCTCATTTTCCCTGTGAGTGTGACTATT 1124
 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
 QY 1125 GAAAGGTAAAGACTTTTCTTATATTTCCGATGGCAACATTGAATTAAGTAACTGT 1184
 321 GluArgValTyrsPheSerSerTyrsAsnPheGlyTrpGlnHisLeuGluLeuValAsnCys 340
 QY 1185 AAATTGACAGATTTCCCACTTGAACCAATCTGCAAAAGCTTACTTCACTTCC 1244
 341 TyrPheGlyGlnPheProThrLeuTyrsLeuTyrsSerLeuTyrsArgLeuThrPheTrpSer 360
 QY 1245 AACAAAGTGGGAATGCTTTTTCAGAAAGTTGATCAACAAAGCTTGAGTTTCAAGATCTC 1304
 361 AsnTyrsGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluIlePheLeuAspLeu 380
 QY 1305 AGTAAAGATGCTTGAATGCTTCAAGGTTTCTGTTTCAAGACATTTTGGGACAAACACAGC 1364
 381 SerArgAsnGlyLeuSerPheLeuGlyCysCysSerGlnSerAspPheGlyThrTrpSer 400
 QY 1365 CTTAAAGTATTTGATGATGCTTCAATGATGTTATTAACATGATGTTCAACTTCTGGGC 1424
 401 LeuTyrsTyrsLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
 QY 1425 TTGAAACAACTGAACATGTGATTTCCAGACTTCCAAATTTGAAACAAATGAGTGAATT 1484
 421 LeuGluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuTyrsGlnMetSerGluPhe 440
 QY 1485 TCAATTTCTTATCACTGAGAAACCTCATTTACCTTGACATTTCTGATCTCACACCA 1544
 441 SerValPheLeuSerLeuArgAsnLeuIleTyrsLeuAspIleSerHisThrHisTrpArg 460
 QY 1545 GTTGCTTTCAATGGGATCTTCAATGGCTTGTCCAGCTGCAAGTCTTGAAGAAATGGCTGAC 1604
 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuTyrsPheAlaGly 480
 QY 1605 AATTTCTTCCAGAGAAACTTCTCCAGATATCTTCAACAGACTGAGAAATGACCTTC 1664
 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgHisAsnLeuThrPhe 500
 QY 1665 CTGAGACTTCTCAAGTGTGAATCTGAGACAGTTGTCTCAACAGCAATTTAATCACTCTGC 1724
 501 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 520
 QY 1725 AGCTTCAAGGTACTAATATGAGCCAAACAATCTTTCAATGGATAGTTCCTTAT 1784
 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeuAsnSprThrPheProTyrs 540
 QY 1785 AAGTCTGTAATCTCCCTCAGGTTCTTGATTAACGTTCAATCAATATGACATTCACAA 1844
 541 TyrsCysLeuAsnSerLeuGlnValLeuAspTyrsSerLeuAsnHisIleMetThrSerTyrs 560

QY 1845 AAACAGAACTACAGATTTTCCAGATGCTGATCTTTCTTAATCTTACCTGAGATGAC 1904
 DB 561 LysGlnGlnLeuGlnIlnIspheProSerSerLeuAlaPheLeuGlnLeuIlnIlnAsnAsp 580
 QY 1905 TTTGCTTGTACTTGTGAGACACAGAGTTTCTTGCAATGATGACAGACAGAGCAGCTC 1964
 DB 581 PheAlaCysThrCysGlnIlnIlnSerPheLeuGlnIlnIlnIlnIlnIlnIlnIlnIln 600
 QY 1965 TTGGTGGAGTTGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2024
 DB 601 LeuValGlnValGlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIln 620
 QY 2025 CTGAGTTTGAATATCACTGCTGAGATGAGATGAGATGAGATGAGATGAGATGAG 2084
 DB 621 LeuSerLeuGlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIln 640
 QY 2085 GTGCTTGTAGTATCTGTTGAGAGTCTGCTGATGATGATGATGATGATGATGATG 2144
 DB 641 ValLeuValValSerValValAlaValLeuValTyrLysPheThrPheHisLeuMetLeu 660
 QY 2145 CTTCCTGCTGCTCAATAAGTATGATGAGAGTGAAGAGATCATGATGCTTGTATCTAC 2204
 DB 661 LeuAlaGlyCysIleLysIleTyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIleTyr 680
 QY 2205 TCAGCCAGAGATGAGAGCTGGGTAAGAGATGAGATGAGATGAGATGAGATGAGAGG 2264
 DB 681 SerSerGlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIln 700
 QY 2265 CCTCATCTTCACTCTGCT 2324
 DB 701 ProProPheGlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIln 720
 QY 2325 AACATCATCATGATGAGTTTCCATTAAGCCGAAAGAGTATGTTGTGCTGCTCCAGC 2384
 DB 721 AsnIleIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIln 740
 QY 2385 TTTCATCCAGAGCCGCTGCTGATCTTGAATATGATGATGATGATGATGATGATGAT 2444
 DB 741 PheIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIln 760
 QY 2445 AGCAGCTGCTGCTGATCATCTTCAATGCTCTGAGAGAGTGAAGAGAGCCTGCTCAG 2504
 DB 761 SerSerArgAlaGlyIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIln 780
 QY 2505 CACGAGGTGAGAGCTGATCCGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2564
 DB 781 GlnGlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIln 800
 QY 2565 GTGCTGGGGGGGAGCATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2624
 DB 801 ValLeuGlyArgIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIln 820
 QY 2625 TGGATTCAG 2681
 DB 821 TrpAsnProGlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIlnIln 839
 RESULT 2
 TLR4_PANPA
 ID TLR4_PANPA STANDARD; PRT; 839 AA.
 AC O9TND;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE TOLL-like receptor 4 precursor.
 GN Name=TLR4;
 OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 OC NCBI_TaxID=9597;
 RX MEDLINE=20558910; Pubmed=11104518;

RA Smitnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
 RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
 RT locus (TLR4)";
 RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.101(2000).
 CC -1- FUNCTION: Cooperates with MyD88 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TIRAP.
 CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; AF179220; AA05320.1; -.
 DR EMBL; AF179218; AA05320.1; JOINED.
 DR EMBL; AF179219; AA05320.1; JOINED.
 DR HSSP; Q15399; LFV.
 DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045576; P:macrophage activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
 DR GO; GO:0045362; P:negative regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-13 biosyn. . .; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR_12.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_TYP; 2.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 DR GlycoProtein; Immune response; Inflammatory response;
 KW leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 839
 FT DOMAIN 24 631
 FT TRANSMEM 632 652
 FT DOMAIN 653 839
 FT REPEAT 52 76
 FT REPEAT 77 100
 FT REPEAT 101 124
 FT REPEAT 128 149
 FT REPEAT 150 173
 FT REPEAT 174 197
 FT REPEAT 203 225
 FT REPEAT 228 252
 FT REPEAT 277 303
 FT REPEAT 307 330
 FT REPEAT 332 350
 FT LRR 11.

FT REPEAT 351 372 LRR 12.
 FT REPEAT 373 398 LRR 13.
 FT REPEAT 400 421 LRR 14.
 FT REPEAT 422 445 LRR 15.
 FT REPEAT 447 469 LRR 16.
 FT REPEAT 470 494 LRR 17.
 FT REPEAT 495 518 LRR 18.
 FT REPEAT 520 541 LRR 19.
 FT REPEAT 543 566 LRR 20.
 FT REPEAT 568 592 LRR 21.
 FT DOMAIN 672 818 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 282 282 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 624 624 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 630 630 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 839 AA; 95637 MW; 3B328C5682127D37 CRC64;

Alignment Scores:

Pred. No.: 0 Length: 839
 Score: 4311.00 Matches: 836
 Percent Similarity: 95.34% Conservative: 2
 Best Local Similarity: 95.11% Mismatches: 1
 Query Match: 64.11% Indels: 40
 DB: 1 Gaps: 1

US-09-396-985b-3 (1-3811) x TLR4_PANPA (1-839)

QY 45 ATGATGCTGCTGCGCCCTGGCTGGAGACTGTATCCAGCGCATGCGCTTCTCTCTGC 104
 |||||
 DB 1 MeMeSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 105 GTGAGACGAGAAAGCTGGAGCCCTGGCTGGAGACTGTGCGCCCTTAACACACAGAGAGC 164
 |||||
 DB 21 ValArgProGlnSerTrpGlnProCysVal----- 30
 QY 165 TGGCATGAAACCCAGAGCTTTCAGACTCCGAGCGCTCAGCCCTTACCCGATTCATG 224
 |||||
 DB 30 ----- 30
 QY 225 CTTCTGCTAAATGCTGCGCTTTTATACGAGAGTGCTTCTTAATATTACTTATCAATGC 284
 |||||
 DB 31 -----GluValValProAsnIleThrTyGlnCys 40
 QY 285 ATGAGCTGAATTTCTACAAATGCCGAGCAACCTCCCTTTCACACAGAAACCTGAGC 344
 |||||
 DB 41 MetGluLeuAsnProPheTyLysIleProAsnLeuProPheSerThrLysAsnLeuAsp 60
 QY 345 CTGAGCTTAAATCCCTGAGGACTTTAGGAGCTATAGCTTCTTCACTTCCCGAAGTGC 404
 |||||
 DB 61 LeuSerPheAsnProLeuAlaGlnIleSerTySerPhePheSerPheProGlnLeu 80
 QY 405 CAGGCTGTGATTTATTCAGAGGTGAATCCAGCAATTGAAGTGGGGCATATCAGAGC 464
 |||||
 DB 81 GluValLeuAsnLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyGlnSer 100
 QY 465 CTAGACCACTTCTTACTTAATATTGACAGAAACCCCATCCAGATTTAGCCCTGGAG 524
 |||||
 DB 101 LeuSerIleLeuSerThrLeuIleLeuThrGlyAsnProIleGlnIleSerLeuAlaLeuGly 120
 QY 525 GCCTTTCTGAGACTATCAAGTTTACAGAAAGCTGTGGCTGTGAGAGCAAAATCTAGACT 584
 |||||
 DB 121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGluThrAsnLeuAlaSer 140
 QY 585 CTAGAGAACTTCCCATTTGACATCTGAAAATTGAAAGAACTTAAATGTGGCTACAAAT 644
 |||||
 DB 141 LeuGluAsnProIleGlyIleLeuIleLeuThrLeuIleGluLeuAsnValAlaIleAsn 160

QY 645 CTTATCCAACTTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTG 704
 |||||
 DB 161 LeuIleGlnSerPheIleuSerProGlnIlePheSerAsnLeuThrAsnLeuGlnIleu 180
 QY 705 GACCTTTCCAGAACCAAGATTCAAGATTTATTTGACAGACTTGGCGGTTCTACATCAA 764
 |||||
 DB 181 AspLeuSerSerAsnIleGlnIleSerIleTyCysThrAspLeuArgValIleAsnIleGln 200
 QY 765 ATGCCCTTACTCAATCTCTTTAGACCTGCTCCCTGAGACCCCTTAAGCTTTATCCAGCA 824
 |||||
 DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 825 GTGCACTTTAAAGAAATTAAGCTTCAAGCTGACTTAAGAAATAATTTGATAGTTTA 884
 |||||
 DB 221 GlyAlaPheIleGlnIleArgLeuIleIleLeuThrLeuArgAsnAsnPheAspSerLeu 240
 QY 885 AATGTAATGAATCTGTATTCAGAGCTGTGGCTGTGTTAGAGTCCATCGTTGGTTCTG 944
 |||||
 DB 241 AsnValMetIleIleThrCysIleGlnIleLeuAlaGlyLeuGluValIleAspLeuValLeu 260
 QY 945 GAGAAATTTGAATGAAGAGAACTTGGAAAGTTTGACAAATCTGCTCTTGAAGGGGCTG 1004
 |||||
 DB 261 GlyGluPheArgAsnGluGlyAsnLeuGluIlePheAspIleSerAlaLeuGluGlyLeu 280
 QY 1005 TGCAATTTGACCAATGAGAAATTCGATTAAGTACTTACTTACTTACTTACTTACTTACT 1064
 |||||
 DB 281 CysAsnLeuThrIleGlnIlePheArgLeuAlaIleTyLeuAspIle 300
 QY 1065 ATTGACTTATTTAATGTTTGAACAAATGTTTCTTCAATTTTCCCTGGTGAAGTGAATTT 1124
 |||||
 DB 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
 QY 1125 GAAAGGTGAATGAACTTTCTTAATTTGGANNGCAATTTGAATTAAGTAACTGT 1184
 |||||
 DB 321 LysSerValIleAspPheSerIleTyAsnPheGlyTrpGlnIleIleuGluLeuValAspCys 340
 QY 1185 AAATTTGACAGATTTCCCATTTGAATGAATCTGCTCAAAAGCTTACTTACTTACTTCC 1244
 |||||
 DB 341 LysPheGlyGlnPheProThrLeuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 360
 QY 1245 AACAAAGTGGGAATGCTTTTTCAGAAAGTTGATTCACAAAGCTTGAATTTCTAGATTC 1304
 |||||
 DB 361 AsnIleGlyIleAsnIlePheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
 QY 1305 AGTGAATATGCTTGAATTTCAAAAGTGTGCTGTTCTCAAGTATTTGGAGCAACAGC 1364
 |||||
 DB 381 SerArgAsnIleuSerPheIleuGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1365 CTAAAGTATTTAGATCGAGCTTCAATGAGTGTATTTACATGAGTCAAACTTCTGGGC 1424
 |||||
 DB 401 LeuIleTyIleuAsnLeuSerPheAsnGlyValIleIleIleIleIleIleIleIleIleIle 420
 QY 1425 TTAGAACACTAGAACATCTGATTTTCAGCATTTCCAAATTTGAAACAAATGAGTGAAT 1484
 |||||
 DB 421 LeuGluGlnIleuGlnIleuAspPheGlnIleSerAsnLeuIleuGlnIleMetSerGluPhe 440
 QY 1485 TCAGTATTTCTATACCTGACAAACCTGATTTACTTCACTTCACTTCACTTCACTTCACT 1544
 |||||
 DB 441 SerValPheLeuSerLeuArgAsnLeuIleTyLeuAsnIleSerIleIleIleIleIleIleIle 460
 QY 1545 GTTGCTTTCAATGAGCATTTCAATGAGCTTTCAGAGTCTGCAAGTCTTGAATGAGTGGC 1604
 |||||
 DB 461 ValIlePheAsnIleIlePheAsnGlyLeuSerSerLeuGluValIleuIleuIleuIleuIleu 480
 QY 1605 AATTTCTTCCAGAGAAATCTTCCATGATATCTTCCAGAGCTTGAGAGAACTTGACCTTC 1664
 |||||
 DB 481 AsnSerPheGlnIleuAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
 QY 1665 CTGAGACTTCTCTCAAGTCACTGAGAGCACTGTCTTCCAAACACATTTAATCACTCTCC 1724
 |||||
 DB 501 LeuAspLeuSerGlnCysGlnIleuGluGlnIleuSerProThrIlePheAsnSerLeuSer 520
 QY 1725 AGTCTTCAAGGTACTTAATATGAGCCCAACAACTTCTTTCAATGATAGTTCCTTAT 1784

```

Db      521 SerLeuGlnValIleuSerMetSerHisAsnAsnPhenSerLeuSerThrProTyr 540
QY      1785 AAGTGTCTGAATCCTCCAGGTTCTTGATTACAGTCTCATATGACTTCCAA 1844
Db      541 LysCysLeuAsnSerLeuGlnValIleuAspTyrSerLeuAsnHisIleMetThrSerLys 560
QY      1845 AAACAGGAATATACAGATTTTCCAGAGTCTGAGCTTTCTTAATCTTACTACGAAATGAC 1904
Db      561 LysGlnIleuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuTrpGlnAsnAsp 580
QY      1905 TTTGCTTTGATCTTGTGAACACAGAGTTTCTGCAATGATGACAGACAGAGGAGCTC 1964
Db      581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnAspGlnLeu 600
QY      1965 TTGGTGAAGTTGAACGATGGAATGTGCACACCTTCAGATAGCAGGGGAGCTGTGTG 2024
Db      601 LeuValGlnValIleuArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProVal 620
QY      2025 CTGAGTTTGAATATCACTGTCAAGTGAATAGACCATTCATGGTGTGTGCTCTGAGT 2084
Db      621 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 640
QY      2085 GTGCTGTGATCTATCTGTGTGAGCAGTTCTGCTATAGTTCTATTTTCACTGATCTT 2144
Db      641 ValLeuValIleuSerValIleuAlaValIleuValIleuValIleuValIleuVal 660
QY      2145 CTTCGTGCTGTCATTAAGTATGTTGAGGAGGAAAAACCTATGATGCTCTTGTATGTAC 2204
Db      661 LeuAlaIleuValIleuValIleuValIleuValIleuValIleuValIleuValIleu 680
QY      2205 TCAAGCCAGATGAGCCTGGTGAAGGATGAGTATTAAGATTTTGAAGAAAGGGGTG 2264
Db      681 SerSerIleuArgIleuAspTrpValArgAsnIleuValIleuValIleuValIleuVal 700
QY      2265 CTTCCATTTGAGCTCTGCTCTTCACTACAGAGACTTTATTCCTCCGCTGTGAGCATTTG 2324
Db      701 ProProheGlnIleuValIleuValIleuValIleuValIleuValIleuValIleu 720
QY      2325 AACATCATCAATGAAGGTTTCCATTAAGACCGGAAAGGTATGTTGTGTGCTCCAGAC 2384
Db      721 AsnIleIleuValIleuValIleuValIleuValIleuValIleuValIleuValIleu 740
QY      2385 TTATTCAGAGCCGCTGATCTTGAATATGATGATGATGATGATGATGATGATGATGAT 2444
Db      741 PheIleIleuSerArgTrpCysIlePheGlnIleuValIleuValIleuValIleuVal 760
QY      2445 AGCAGTGTGCTGATCATCTTTCATTTCTGTCAGAGAGTGAAGAACCTGCTCAGG 2504
Db      761 SerSerArgAlaGlyIleIlePheIleValIleuGlnIleuValIleuValIleuVal 780
QY      2505 CAGAGAGTGAAGCTGTACCCGCTTTCAGCAGAGAACCTTACCTGAGGTGAGAGAGACGT 2564
Db      781 ArgGlnValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 800
QY      2565 GTCTCTGGGGGGGACATCTTCTGAGAGACATCGAAGAACCCCTGAGTGAATGATCA 2624
Db      801 ValIleuValIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 820
QY      2625 TGGATTCAGAGAGAACAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2681
Db      821 TrpAsnProGlnIleuValIleuValIleuValIleuValIleuValIleuValIleu 839

```

```

OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX      NCBI_TaxID=9593;
RN      [1]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=21405531; PubMed=11514453;
RA      Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RT      "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
RL      in humans".
RL      Genetics 158:1657-1664(2001).
RN      [2]
RN      SEQUENCE FROM N.A.
RA      Beutler B., Smirnova I., Hamblin M.T., McBride C., Di Rienzo A.;
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RL      EMBL; AF497565; AAM18617.1; -;
DR      EMBL; AF497563; AAM18617.1; JOINED.
DR      EMBL; AF497564; AAM18617.1; JOINED.
DR      HSSP; O60603; 1077.
DR      GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR      GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR      GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR      GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR      GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR      GO; GO:0042116; P:macrophage activation; ISS.
DR      GO; GO:0045576; P:macrophage activation; ISS.
DR      GO; GO:0045571; P:negative regulation of osteoclast different. . .; ISS.
DR      GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR      GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR      GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR      GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR      GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR      InterPro; IPR001611; LRR_Cterm.
DR      InterPro; IPR000483; LRR_Cterm.
DR      InterPro; IPR003591; LRR_Typ.
DR      InterPro; IPR000157; TIR.
DR      Pfam; PF01463; LRCT; 1.
DR      Pfam; PF00560; LRR_1; 10.
DR      Pfam; PF01582; TIR_1.
DR      PRINTS; PR00019; LEURICHRPT.
DR      SMART; SM00082; LRCT; 1.
DR      SMART; SM00369; LRR_TYP; 2.
DR      SMART; SM00255; TIR; 1.
DR      PROSITE; PS50104; TIR; 1.
KW      Receptor.
SQ      SEQUENCE 837 AA; 95497 MW; 5A177BAB341396DD CRC64;

```

Alignment Scores:

```

Pred. No.: 0 Length: 837
Score: 4290.00 Matches: 832
Percent Similarity: 94.99% Conservative: 3
Best Local Similarity: 94.65% Mismatches: 2
Query Match: 63.80% Indels: 42
DB: Gaps: 1

```

US-09-396-985b-3 (1-3811) x Q8SPB8 (1-837)

```

QY      45 ATGATGTCTGCTTCGCGCTGCTGAGACTCTGATCCAGCAATGGCTTCTCTCTGTC 104
Db      1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY      105 GTGAGCCGGAAGAGCTGGAGCGCTCGTGAAGACTTGCCCTTAACACAGAGAGAGC 164
Db      21 ValArgProGlnIleSerTrpGlnProCys----- 29
QY      165 TGGCATGAAGAACCCAGAGCTTTCAGACTCCGAGCCTCAGCCTTCAACCCGATTCATTG 224
Db      29 ----- 29
QY      225 CTTCCTGCTTAATGCTGCGCTTTTATCAAGAGGTGGTTCCTTAATATTACTTATCAATGC 284
Db      30 -----ValValProAsnIleThrTyrGlnCys 38

```

QY 285 ATGAGCTGAATTCTACAAATCCGACAACTCCCTTCTCAACCAAGACCTGAC 344
Db MetGluLeuAenPheYrLysIleProAsnLeuProPheSerThrLysAsnLeuAsp 58
QY 345 CTGAGCTTATCCCTGAGGACATTGAGCAGCTATAGCTTCTTCACTTCCCGAAGCTG 404
Db LeuSerPheAenProLeuArgHisLeuGlySerYrSerPhePheSerPheProGluLeu 78
QY 405 CAGGTGCTGATTTATCCAGGTGTGAATCCAGCAATTTGAAGATGGGGCATTCAGAGC 464
Db GlnAlaLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaIleYrGlnSer 98
QY 465 CTAAAGCACTCTCTCACTTAATATGACAGAGAAACCCCATCCAGATTGACCTGGA 524
Db LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 118
QY 525 GCCCTTTCTGACATATCAAGTTTACAGAAAGCTGGTGGTGGAGACAAATCTAGCATCT 584
Db AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSer 138
QY 585 CTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAAGAACTTAATGTGGCTCACACT 644
Db LeuGluAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 158
QY 645 CTATCCAACTTTCAATTAACCTGAGTATTTTCTAATCTGACCAATCTGAGCACTTG 704
Db LeuIleGlnSerPheLysLeuProGluIleYrPheSerAsnLeuThrAsnLeuGluIleLeu 178
QY 705 GACCTTTCCAGCAACAAAGATTCAAAAGTATTTATGACAGACAGCTGGGGTCTTCAATCA 764
Db AspLeuSerSerAsnLysIleGlnSerIleYrCysThrAspLeuArgValLeuHisGln 198
QY 765 ATGCCCTTACATCTCTCTTTAGACCTGTCCCTGAAACCTTAGAACTTTATTCACACA 824
Db MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetThrPheIleGlnPro 218
QY 825 GGTGCACTTAAAGAAATTAAGCTTCATAGCTGACTTAAAGAAATTAATTTGATAGTTTA 884
Db GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu 238
QY 885 AATGTATGAAAACTTGTATTTCAAGGCTGTGGCTGGTTTGAAGTCCATCGTTGGTTCTG 944
Db AsnAlaMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValAlaGArgLeuValLeu 258
QY 945 GGAGAACTTTGAAATGAAGGAACTTGAAGAAAGTTTACAAATGTGCTTAGAGAGGCTG 1004
Db GlyGluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu 278
QY 1005 TGCAATTTGACATTTGAAGAATTCGATAGCATATTAAGACTTACCTGATGATATT 1064
Db CysAsnLeuThrIleGluGluPheArgLeuAlaIleYrLeuAspIle 298
QY 1065 ATTGACTTATTTAATGTTTGAACAATGTTTCTTCAATTTCCCTGGTGAAGTGTGACTATT 1124
Db IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 318
QY 1125 GAAAGGCTAAAGAACTTTCTTAATTTGGAAGGGAACAATTGAATTAAGTAACTGT 1184
Db GlnArgValLysAspPheSerYrAsnPheGlyTyrGlnHisLeuGluLeuValAsnCys 338
QY 1185 AAATTTGACAGTTTCCCATTTGAATTCGAATCTCTCAAAAGGCTTACTTCACTTCC 1244
Db LysPheGluGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 358
QY 1245 AACAAAGGTGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAAGTTTCTAGATCTC 1304
Db AsnLysGlyGlyAsnAlaPheSerGluValAlaAspLeuProSerLeuGluPheLeuAspLeu 378
QY 1305 AGTAGAAATGGCTTGAAGTTTCAAAAGTTGCTTCTCAAGTAAATTTTGGAGCAACAGC 1364
Db SerThrArgAsnGlyLeuSerPheLysGlyCysCysSerIleAspPheGlyThrThrSer 398
QY 1365 CTAAAGTATTTAGATCTGAGCTTCAATGATGTTATTAACATGAGTTCAAACTTCTTGGGC 1424

Db 399 LeuYrYrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 418
QY 1425 TTAGAACAATTAAGACATCTGAGATTTCCACATTTCCAAATTTGAAACAAATGAGAGATT 1484
Db LeuGluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 438
QY 1485 TCAGTATTTCTATCACTCAGAGAAACCTTATTAACCTTGAATTTCTCATTACTCAACAGCA 1544
Db SerValPheLeuSerLeuAlaArgAsnLeuIleYrLeuAspIleSerHisThrHisThrArg 458
QY 1545 GTTGCTTTCAATGAGCATCTTCAATGAGCTTGTCCAGTGTGAAAGTCTTGAATGAGCTGAC 1604
Db ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 478
QY 1605 AATCTTTCCAGAGAAACCTTCCCTCCAGATATCTTCAACAGAGCTGAGAGAACTTACCTTC 1664
Db AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 498
QY 1665 CTGAGACCTCTCAGTGTCAACTGAGACAGTGTCTCCAAAGCAAGCTTAACTCACTCTCC 1724
Db LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 518
QY 1725 AGTCTTCAAGTAAATTAATGAGCAACAACTTCTTTCAATTGATGATGATGATCTTAT 1784
Db SerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeuAspThrPheProTyr 538
QY 1785 AAGTGTGAACTCCCTCCAGGTTCTTGATTACAGTCTCAATCAATCAATGACTTCCAA 1844
Db LysCysLeuAsnSerLeuAlaArgValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 558
QY 1845 AAACAGGAATTAACGACTTTTCAAGATGTAGTCTTCTTAATCTTACTCCGAATGAC 1904
Db LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 578
QY 1905 TTGCTTGACTTGTGAACACAGAGTTTCTGCAATGATGATCAAGACAGAGGACCTG 1964
Db PheAlaCysThrCysGluHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeu 598
QY 1965 TTGCTGGAATTTGAAGAAATGGAATGTGCAACCTTCAATTAAGACAGGAGTCCCTGTG 2024
Db LeuValGluValAlaLysArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 618
QY 2025 CTGAGTTTGAATATCACTCTGTCAGATGAATPAACCATCTTGGTGTGGTCTGACT 2084
Db LeuSerLeuAsnLleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 638
QY 2085 GTGCTGTAGTATCTGTTGAGCAGTTCTGGTCTATTAAGTTTCACTGATGCTT 2144
Db ValLeuValValSerValValAlaValLeuValTyrLysPheYrPheHisLysMetLeu 658
QY 2145 CTGCTGGCTGCAATTAAGTATGAGTGAAGTGAAGCAATCTATGATGCTTGTATCTAC 2204
Db LeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnValTyrAspAlaPheValIleYr 678
QY 2205 TCAAGCGAGATGAGACCTGGGTAAGAAATGACTGTAAAGAAATTAAGAAAGAGGCTG 2264
Db SerSerGlnAspGluAspIlePheValArgAsnGluLeuValLysAsnLeuGluGlyVal 698
QY 2265 CTTCCATTTCAAGCTGTGCTTCACTACAGAGCTTATATCCCGGTGGGCACTTGTGCGC 2324
Db ProProPheGlnLeuCysLeuHisTyrYrArgAspPheIleProGlyValAlaIleAlaAla 718
QY 2325 AACATCAATCAAGATTTCCATAAAGCCGAAGGTGATGTTGTGTGCTCCAGAC 2384
Db AsnIleIleHisGluGluPheHisLysSerArgLysValIleValValValSerGlnHis 738
QY 2385 TTGATCAAGACCGCGTGTATCTTGAATTAAGATGCTTCAAGCTGCGGAGTTTCTG 2444
Db PheIleGlnSerIleTyrPyrCysIlePheGluTyrGluIleAlaGlnThrTyrGlnPheLeu 758
QY 2445 AGCAGTGTGCTGATTCATCTTCAATGTCTGACAGAGGTGAGAGACCTGTCTCAGG 2504

Db 759 SerSerArgAlaGlyIleIleIleValleuGlnValGluValGlyThrLeuLeuArg 778
 QY 2505 CACAGGTGAGGTGATGACCGCTTCTCAGCAGGAACCTTACCTGAGTGGAGACAGT 2664
 Db 779 GlnGlnValGlnIleuLeuThrArgLeuLeuSerArgPheThrThrLeuGlnTrpGlnLeuSer 798
 QY 2565 GTCTGTGGGGCGGACATCTTCTGAGAGCAGTCAGAAAGCCCTGTGATGGTAAATCA 2624
 Db 799 ValIeuGlnIlyrghIlePheTTPArgArgLeuArgGlyAlaLeuLeuArgGlyLysSer 818
 QY 2625 TGGATTCAGAAAGAACAGTGGGTACGATGCAATTCGAGAGAGAACATCATC 2681
 Db 819 TrpAsnProGlnGlnThrValGlnThrGlyCysAsnTrpGlnGlnAlaThrSerIle 837
 RESULT 4
 ID TLR4_PONPY STANDARD; PRT; 828 AA.
 AC QSPSP9;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
 ON NCBI_TaxId=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=1405531; PubMed=11514453;
 RA Shitrova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
 RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
 in humans.";
 RL Genetics 158:1657-1664(2001).
 CC -|- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -|- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TIRAP via
 CC binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
 CC their respective TIR domains (By similarity).
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -|- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -|- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
 CC -|- SIMILARITY: Contains 1 TIR domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; AF497562; AAM18616.1; .
 CC EMBL; AF497560; AAM18616.1; JOINED.
 CC EMBL; AF497561; AAM18616.1; JOINED.
 CC HSP; O66003; 1PTW.
 DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004688; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0005958; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045576; P:mast cell activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
 DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.

DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Tyr.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR; 12.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICRPT.
 DR SMART; SM00369; LRR_TYR; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KW Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 828 Toll-like receptor 4.
 FT DOMAIN 24 629 Extracellular (potential).
 FT TRANSMEM 630 650 Potential.
 FT DOMAIN 651 828 Cytoplasmic (potential).
 FT REPEAT 50 74 LRR 1.
 FT REPEAT 75 98 LRR 2.
 FT REPEAT 99 122 LRR 3.
 FT REPEAT 126 147 LRR 4.
 FT REPEAT 148 171 LRR 5.
 FT REPEAT 172 195 LRR 6.
 FT REPEAT 201 223 LRR 7.
 FT REPEAT 226 250 LRR 8.
 FT REPEAT 275 301 LRR 9.
 FT REPEAT 325 348 LRR 10.
 FT REPEAT 349 370 LRR 11.
 FT REPEAT 371 396 LRR 12.
 FT REPEAT 398 419 LRR 13.
 FT REPEAT 420 443 LRR 14.
 FT REPEAT 445 467 LRR 15.
 FT REPEAT 468 492 LRR 16.
 FT REPEAT 493 516 LRR 17.
 FT REPEAT 518 539 LRR 18.
 FT REPEAT 541 564 LRR 19.
 FT REPEAT 566 590 LRR 20.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 33 33 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 171 171 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 203 203 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 280 280 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 307 307 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 524 524 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 573 573 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 622 622 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 628 628 N-linked (GlcNAc...) (potential).
 SQ SEQUENCE 828 AA; 94340 MW; 51AC094AE5970PDE CRG64;
 Alignment Scores:
 Pred. No.: 828
 Score: 8.2e-306 Length: 828
 Percent Similarity: 4162.00 Matches: 808
 Best Local Similarity: 93.79% Conservative: 8
 Query Match: 92.87% Mismatches: 12
 DB: 61.90% Indels: 42
 Gaps: 1
 US-09-396-985b-3 (1-3811) x TLR4_PONPY (1-828)
 QY 45 ATGATGTGCTGCTGCGGCTGAGGAGCTGATCCAGCCATGAGGCTTCTCTCTGCG 104
 Db 1 MetMetSerAlaSerArgLeuAlaGlyThrIleIleProAlaMetAlaPheLeuSerCys 20
 QY 105 GTGAGACCAAGAAAGCTGGAGCCCTGCGGAGACTTGCCCTTAACCAACAGAAAGAGC 164
 Db 21 ValArgProGlnIleuThrTrpGlnProCys----- 29
 QY 165 TGGCATGAAGAACCCAGAGCTTTTCAGACTCCGAGAGCTCAGCCCTTACCCGATTCATTG 224
 Db 29 ----- 29

QY 225 CTTCTGCTAAATGCTGCCGTTTATACAGAGGTGGTTCCTAAATATTACTTATCATATGC 284
 Db 30 -----ValValProAsnIleThrTyGlnCys 38
 QY 285 ATGAGAGCTGAATTTCTACAAATCCCGACAACTCCCTTCTCACCAGAAAGCTGGAC 344
 Db 39 MetGluLeuAsnProPheTyrIleProAsnLeuProPheSerThrTyrAsnLeuAsp 58
 QY 345 CTGAGCTTATCCCTGAGGACTTTAGCAGCTATACCTCTTCAGTTCCCGAAATG 404
 Db 59 LeuSerPheAsnProLeuArgIleLeuGlySerTyrSerPhePheSerPheProGluLeu 78
 QY 405 CAGGTGCTGAATTTATCCAGGTGTGAATCCAGCAATTTGAAGATGGGGCATTCAGAGC 464
 Db 79 GlnValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaIleTyGlnSer 98
 QY 465 CTAGGCCACTCTCTCACTTATATTTGACAGAGAAACCCCATCCAGAGTTTACCCCTGGGA 524
 Db 99 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnAsnLeuAlaLeuGly 118
 QY 525 GCCCTTTCTGACATCAAGTTTACAGAGCTGGTGGTGGAGCAAACTAGCATCT 584
 Db 119 AlaPheSerGlyLeuSerSerLeuGlnLeuValAlaValGluThrAsnLeuAlaSer 138
 QY 585 CTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAGAATTGAGTGCACAAAT 644
 Db 139 LeuGluAsnProIleGlyHisLeuIleThrLeuIleGluAsnValAlaHisAsn 158
 QY 645 CTTATCCAACTTTCAAAATTACTGAGTATTTTCTAATCTGACCAATCTAGACACTTG 704
 Db 159 LeuIleGlnSerPheIleuProGluTyrPheSerAsnLeuThrAsnLeuGlnHisIleu 178
 QY 705 GACCTTCCAGCAACAAGATTCAAGATTATTTGACAGACTTGGCGGCTCTACATCA 764
 Db 179 AspLeuSerSerAsnIleGlnIleThrCysIleAspLeuGlnValLeuHisGln 198
 QY 765 ATGCCCTACTCAATCTCTCTTAGACCTGTCCTGAACCTTATGAATTTATCCAAACA 824
 Db 199 MetProLeuAsnLeuSerLeuAspLeuSerLeuAsnAlaMetAsnPheIleGlnPro 218
 QY 825 GGTCACTTAAAGAAATTAAGCTTCATAGCTGACTTTAAGAAATTAATTTGATAGTTTA 884
 Db 219 GlyAlaPheIleGlyIleArgLeuHisIleLeuThrLeuArgAsnSerPheAspSerLeu 238
 QY 885 AATGTATGAATACTGTATTCAGAGTCTGCTGGTTTGAAGTCCATCGTTGGTCTG 944
 Db 239 AsnValMetCysIleGlnGlyLeuAlaGlyLeuGlnValAlaHisIleLeuValLeu 258
 QY 945 GGAGAAATTTGAAGAACTTGAAGAACTTGAAGAACTTGCCTTAGAGAGGCTG 1004
 Db 259 GlyGluPheArgAsnGluIleAsnLeuGluIlePheAspThrSerAlaLeuGlnGlyLeu 278
 QY 1005 TGCATTTGACCATTTGAAGAACTTCGATAGCATACTAGCTACTACCTCGATGATATT 1064
 Db 279 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 298
 QY 1065 ATTGACTTATTTAATTTTGAACAATGTTTCTCATTTTCCCTGGAGTGTGACTAATT 1124
 Db 299 IleAspLeuPheAsnCysLeuAlaAsnValSerSerPheSerLeuValSerValThrIle 318
 QY 1125 GAAAGGCTAAAGACTTTCTTATATTTCCGATGAGCAACTTTAGAATTAGTAATGT 1184
 Db 319 LysSerValIleAspPheSerTyrAsnPheGlyTyrProIleHisIleGluIleValAsnCys 338
 QY 1185 AATTTGAGACATTTCCCATTTGAACCTCAAACTCTCAAAAGCTTACTTTCACTTCC 1244
 Db 339 LysPheGlyGlnPheProThrLeuGluLeuIleSerLeuIleAspGlyLeuThrPheThrAla 358
 QY 1245 AACCAAGGTGGAAATGCTTTTTCAGAGTTGATTTACCAAGCTTGAAGTTTCTAGATCTC 1304
 Db 359 AsnIleGlyGlnAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 378

QY 1305 AGTAAATGCTTGAGTTTCAAAAGTGTCTGTTCTCAAAAGTATTTTGGACAAACGAC 1364
 Db 379 SerArgAsnGlyLeuSerPheIleGlyCysGlySerGlnSerAspPheGlyThrThrSer 398
 QY 1365 CTTAAAGTATTTAGATCTGAGCTTCAATGCTGTTTATACCATGAGTTCAAACTTTGGGC 1424
 Db 399 LeuIleTyrLeuAspLeuSerPheAsnAspValIleThrMetGlySerAsnPheLeuGly 418
 QY 1425 TTAGAACACTAGAAACATCGGATTTCCAGATTTCCAAATTTGAACAATGAGGAGTTT 1484
 Db 419 LeuGluGlnLeuGluHisIleuAspPheGlnHisSerAsnLeuIleGlnMetSerGluPhe 438
 QY 1485 TCAGTATTTCTATCACTCAGAAACCTCATTTTACCTTACATTTCTCATCTCAGACAGA 1544
 Db 439 SerValPheLeuSerLeuAsnArgAsnLeuIleTyrLeuAspIleSerHisIleThrArg 458
 QY 1545 GTTGCTTTCAATGGCATCTTCAATGCTTGTCCAGTCTCGAAGTCTTGAAGTGGTGGC 1604
 Db 459 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuIleValLeuIleMetAlaGly 478
 QY 1605 AATTCCTTCCAGAAACCTTCCCTCCAGATATCTTCAAGAGCTGAGAACTTGACCTTC 1664
 Db 479 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 498
 QY 1665 CTGAGCCTCTCTCAGTGTCAACTGAGACAGTGTGTCTCAACAGCATTTAACTCACTCTCC 1724
 Db 499 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 518
 QY 1725 AGTCTCAGGTACTAAATATGAGCCACACAACTTCTTTTCATTTGATGATGATGCTTAT 1784
 Db 519 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 538
 QY 1785 AAGTGTGAACTCCCTCCAGGTTCTTGATTTACAGTCTCAATCACAATAAGACTTCCAA 1844
 Db 539 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 558
 QY 1845 AAACAGAGAACTACAGACTTTTCCAAAGTCTAGCTTTCTTAAATCTTACTCAGAAATGAC 1904
 Db 559 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 578
 QY 1905 TTTGCTTGATCTTGGAACACAGAGTTTCTGCAATGATCAAGACACAGAGGACCTC 1964
 Db 579 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleIleAspGlnArgGlnLeu 598
 QY 1965 TTGGTGAAGTTGAACAAATGGAATGTGCAACCTTCAATTAAGACGGGACATGCTGTG 2024
 Db 599 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnIleMetProVal 618
 QY 2025 CTGAGTTTGAATATCACTGTCCAGATGAATGAAGCACTCATTTGGTGTGGTCTCAGT 2084
 Db 619 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrValIleGlyValSerValPheSer 638
 QY 2085 GTGCTGTGATATCTGTGTGAGCAGTTCTGGTCTATTAAGTTCTAATTTTCACTGATGCTT 2144
 Db 639 ValLeuValIleSerValValAlaValLeuValTyrLysPheTyrPheHisIleuMetLeu 658
 QY 2145 CTGCTGTGGCTGCAATAAGTATGTAAGTGTGAAGAAACATCTATGATGCTTTGTATTTAC 2204
 Db 659 LeuAlaGlyCysIleLeuTyrGlyArgGlyGluAsnThrTyrAspAlaPheValIleTyr 678
 QY 2205 TCAAGCCAGATGAGACTGGTGAAGAAATGAGCTGTGAAGAAATTTAGAAGAGGGGTG 2264
 Db 679 SerSerGlnAspGluAspTyrPheValArgAsnGluLeuValLysAsnLeuGlnGlyVal 698
 QY 2265 CTTCAATTTCAAGCTTGCCTTCACTACAGAGACTTATTTCCCGGTGGCATTTGCTGCC 2324
 Db 699 ProThrPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaAla 728
 QY 2325 AACATATCCATAAGTTTCCATTAAGACCCGAAAGTGATTTGTGTGTGCTCCAGCAC 2384
 Db 719 AsnIleIleHisGlnIlePheHisLysSerArgLysValIleValValIleSerGlnHis 738
 QY 2385 TTCATCCAGAGCGGTGTGTATCTTTGAATATGAGATTGCTCAGACCTGGCAGTTTCTG 2444

```

Db      739 PheIIgISeArgrtrpCysIlePegIuTrpGIuIleIaGInhrtrpGInPheIeU 758
QY      2445 AGAGTCGTCGTCGTATCATCTTCATTTCTCCAGAGGTGAGAAAGCCCTGCTCAGG 2504
Db      759 SeSeArgrAlaIylIleIlePheIleValIleGInIyValGIuIyThrIleuArG 778
QY      2505 CACAGGTGAGGCTGACCGCTTCCTCAGAGGAAACCTTACCTGAGTGGAGAGCAGT 2564
Db      779 GInGIuValGIuIeUTrpArGleuIeUSeArgrArSnrThrIyIeUgluTrpGIuAepSer 798
QY      2565 GTCTGGGGGGGACATCTTCTGAGAGCAGTCAGAAAGCCCTGCTGATGGTAATCA 2624
Db      799 ValIeUGIyArGIstIlePheTrpArGrIeUArGIyAlaIeUleuAepGIyLySer 818
QY      2625 TGGAAATCCAGAGAAACAGTCGGTACAGCA 2654
Db      819 TrpArSnrProGIuGIyThrValGIyThrGIy 828

RESULT 5
TIR4_PAPAN STANDARD; PRT; 826 AA.
ID TIR4_PAPAN
AC 9YTSF2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name-TIR4;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20558910; PubMed=11104518;
RA Smitnova I., Poltorak A., Chan B.K.L., McBride C., Beutler B.;
RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
RT locus (TIR4)".
RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TIR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
CC their respective TIR domains (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by, and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF180964; AAF07059.1; -.
DR EMBL; AF180962; AAF07059.1; JOINED.
DR EMBL; AF180963; AAF07059.1; JOINED.
DR HSSP; Q15399; LFV.
DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO; GO:0016046; P:detection of fungi; ISS.
DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR GO; GO:0042116; P:macrophage activation; ISS.
DR GO; GO:0045576; P:mast cell activation; ISS.

```

```

DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Tyr.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 13.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PRO00019; LEURICRPT.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KW Glycoprotein; Immune response; Inflammatory response;
KW Leucine-rich Repeat; Receptor; Signal; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 826
FT DOMAIN 24 631
FT TRANSMEM 632 652
FT DOMAIN 653 826
FT REPEAT 53 76
FT REPEAT 77 100
FT REPEAT 101 124
FT REPEAT 128 149
FT REPEAT 150 173
FT REPEAT 174 197
FT REPEAT 203 225
FT REPEAT 228 252
FT REPEAT 277 303
FT REPEAT 327 350
FT REPEAT 351 372
FT REPEAT 373 398
FT REPEAT 400 421
FT REPEAT 422 445
FT REPEAT 447 469
FT REPEAT 470 494
FT REPEAT 495 518
FT REPEAT 520 541
FT REPEAT 543 569
FT REPEAT 571 592
FT DOMAIN 672 818
FT CARBOHYD 35 35
FT CARBOHYD 173 173
FT CARBOHYD 205 205
FT CARBOHYD 282 282
FT CARBOHYD 309 309
FT CARBOHYD 497 497
FT CARBOHYD 526 526
FT CARBOHYD 575 575
FT CARBOHYD 624 624
FT CARBOHYD 630 630
SQ SEQUENCE 826 AA; 94678 MW; 42277731855F1769 CRC64;

Alignment Scores:
Pred. No.: 1.52e-294
Score: 4013.00
Percent Similarity: 92.48%
Best Local Similarity: 89.81%
Query Match: 59.68%
DB: 1
Length: 826
Matches: 776
Conservative: 23
Mismatch: 25
Indels: 40
Gaps: 1

US-09-396-985b-3 (1-3811) x TIR4_PAPAN (1-826)
QY 45 ATATATGTGCGCTCGGCGCTGCTGAGTTCGATCCAGCAATGCGCTTCTCTCTG 104
Db 1 MetThrSerIleuArGIeUArGIyThrIleIleProIaIeUArIaPheIeUSeArCys 20
QY 105 GTGAGACAGAAAGCTGGAGCCCTGCTGAGAGACTTGCGCCCTTAACACACAGAGAGC 164

```

```

Db      21 ValArgProGluSerThrGluProCysVal-----30
QY      165 TGGCATTGAAGAACGAGCTTTCAGACTCCGGAGCCTCAGCCCTTCAACCCGATTCCATTG 224
Db      30 -----30
QY      225 CTCTCTGTAATAGCTGCCGTTTATACAGAGAGTGCTTCTATATATTACTTCAATGC 284
Db      31 -----GluValValProAsnIleThrTyrGlnCys 40
QY      285 ATGAGCTGAATTTCTACAAATATCCCGACACCTCCCTTCTCAACCAAGAACTTGGAC 344
Db      41 MetGluLeuAsnThrGlyIleProAspAsnIleProPheSerThrIleuAsnLeuAsp 60
QY      345 CTGAGCTTAAATCCCTGAGGAGCTTATAGAGCTATAGCTTCTTCAAGTTCCAGAACTG 404
Db      61 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPheLeuArgPheProGluLeu 80
QY      405 CAGGTCTGGAATTTATCCAGAGTGTGAATCCAGACAAATTGAAGATGGGAGCATTCAGAGC 464
Db      81 GlnValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 100
QY      465 CTAAAGCACCTCTCTAATTAATTTAGACAGAAACCCCATCCAGAGTTTATGCTGGGA 524
Db      101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
QY      525 GCGTTTTCGAGTATTCAGATTTCAGAGAGCTGTGCTGTGAGACAAATCTAGCATCT 584
Db      121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGluThrAsnLeuAlaSer 140
QY      585 CTAGAGAACTTCCCATTTGAGCATCTCAAAACTTTGAAAGACTTATGTGGCTCAAT 644
Db      141 LeuGluAsnPheProIleGlyHisLeuIleuIleuIleuIleuIleuIleuIleuIleu 160
QY      645 CTATTCCAATCTTCAATTAATTAAGCTGATTTTCTAATCTGACCAATCTAGACATTTG 704
Db      161 LeuIleGlnSerPheLeuSerProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu 180
QY      705 GACCTTTCAGACAAAGATTCAAAAGTATTATTATTCAGACAGACTTGGGGGTTCTACATCA 764
Db      181 AsnLeuSerSerAsnIleuIleGlnAsnIleTyrCysIleAspLeuGlnValLeuHisGln 200
QY      765 ATCCCTCTACTCATCTCTCTTATAGACCTGCTGACCTGACCTTGAACCTTATCCAGCA 824
Db      201 MetProLeuProAsnLeuSerLeuAspLeuSerLeuAsnProIleAsnProIleGlnPro 220
QY      825 GGTGATTAAAGAAATTAGGCTTTCATTAAGCTGATTTAGAGATCCATCGTTGGTTCTG 884
Db      221 GlyAlaPheLeuSerIleuIleArgLeuHisIleuLeuThrLeuArgSerAsnPheAspLeu 240
QY      885 AATGTATGAAAATTGTATTCAGAGTCTGGCTGTTTATAGATCCATCGTTGGTTCTG 944
Db      241 AsnValMetCysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 260
QY      945 GAGAAATTTAGAAATAGAGAACTTGGAAAGTTTGAACAAATCTGCTAGAGGGCTG 1004
Db      261 GlyLeuPheArgAsnGluArgAsnLeuGluLeuPheAspIleuGluGlyLeu 280
QY      1005 TGCATTTGACATTTAGAGAAATCCGATTAGCATTTAGACTTACCTGATGATATT 1064
Db      281 CysAsnLeuThrIleGluGluPheArgLeuThrTyrLeuAspIleuIleuAspAsnIle 300
QY      1065 ATTGACTTATTTAATTTGACAAATGTTTCTTCAATTTCCCTGAGTGAAGTACTATT 1124
Db      301 IleAspLeuPheAsnCysIleuAlaAsnAlaSerSerPheSerLeuValSerValAsnIle 320
QY      1125 GAAAGGTAATAAAGCTTTCTTATATTTTCGAGTGGCAATTTAGAAATTAAGTAACTGT 1184
Db      321 LysArgValGluAspPheSerTyrAsnPheArgTyrGlnHisIleuGluLeuValAsnCys 340
QY      1185 AATTTGACAGTTTCCACATTTGAACCTCAATCTCTCAAAAGGCTTACCTTCACTTCC 1244

```

```

Db      341 LysPheGluGlnPheProThrIleuGluLeuGlnIleuSerLeuIleuArgLeuThrPheThrAla 360
QY      1245 AACAAAGTGGGAATCTTTTTCAGAAAGTTGATCTACCAAGCTTGAGTTTCTAGATCTC 1304
Db      361 AsnIleGlyIleAsnAlaPheSerGluValAsnLeuProSerLeuGluPheLeuAspLeu 380
QY      1305 AGTAGAAATGCTTGAAGTTTCAAGGTTGCTGTCTCAAAAGTGAATTTTGGACACACAGC 1364
Db      381 SerArgAsnGlyLeuSerPheIleuGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
QY      1365 CTAAAGTATTTAGATCTTGAGCTTCAATGGTGTATTAACATGAGTTCAAACTTCTGGGC 1424
Db      401 LeuIleTyrLeuAspLeuSerPheAsnAspValIleThrMetGlySerAsnPheLeuGly 420
QY      1425 TTAGAAACAATGAAATCATGATCTGATTTCCAGCATTTCAAAATTTGAAGAGTGAATT 1484
Db      421 LeuGluGlnLeuGluHisIleuAspPheGlnHisSerAsnLeuIleGlnMetSerGlnPhe 440
QY      1485 TCAGATTTCTTATCTACTCAGAAACCTCATTTTACTTGAACATTTCTCATACTCACACCGA 1544
Db      441 SerValPheLeuSerIleuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThrThr 460
QY      1545 GTTGTCTTCAATGCAATCTTCAATGCTGTGTCCAGTCTGGAAGTCTTGAATGCTGGC 1604
Db      461 ValAlaPheAsnGlyIlePheAspGlyLeuLeuSerLeuIleuValLeuIleuIleuIleu 480
QY      1605 AATTTCTTCCAGGAAACCTTCTCCAGATTTCTTCAAGAGTGAAGAACTGACCTTC 1664
Db      481 AsnSerPheGlnIleuAsnPheLeuProAspIlePheThrAspLeuIleuAsnLeuThrPhe 500
QY      1665 CTGACCTCTCTCAGGTGTCACAGTGAAGCTGAGAGCTTGTCTCAACAGCATTTTACCTCTCC 1724
Db      501 LeuAspLeuSerGlnCysGlnLeuGlnIleuGlnLeuSerProThrAlaPheAspThrLeuAsn 520
QY      1725 AGTCTTCAAGTAAATTAATTAAGCCAAACAATCTTTTCAATGGAATGCTTCTTAT 1784
Db      521 LysLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspValPheProTyr 540
QY      1785 AAGTGTGAACCTCCCTCCAGGTTCTGATTTACGTTCAATCAATCAATTAATGACTTCCAA 1844
Db      541 LysCysLeuProSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetIleSerLys 560
QY      1845 AAAAGAGAACTACAGCATTTTCCAGATGCTTCAAGTCTTCTTCAATCTTCAAGATGAC 1904
Db      561 AsnGlnGluProGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY      1905 TTTGCTTGTACTTGTGAACAACAGATTTCTGCAATGGAATGGAACAGACAGCTC 1964
Db      581 PheAlaCysThrCysGlnIleGlnSerPheLeuGlnThrIleuIleAspGlnArgGlnLeu 600
QY      1965 TTGCTGGAAGTGAAGATGGAATGGAATGGAACCTTCAAGATGGAAGAGGCAAGCTGTC 2024
Db      601 LeuValGluAlaGluArgMetGluCysAlaThrProSerAspIleuGlnMetProVal 620
QY      2025 CTGAGTTGAATATCACTGTCAGATGAATTAAGACCATCATTTGCTGCTGCTGCTCAGT 2084
Db      621 LeuSerValAsnIleThrCysGlnMetAsnIleuIleIleGlyAlaSerValPheSer 640
QY      2085 GTGCTTGTAGTACTGTTGTAGACGTTCTGCTATTAAGTCTTATTTTCACTGATGCTT 2144
Db      641 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisIleuMetLeu 660
QY      2145 CTGCTGCTGTCATTAAGTATGGAAGTGAAGTGAACAACTATATATGCTTTGTTATCTAC 2204
Db      661 LeuAlaGlyCysIleIleTyrGlyArgGlyGluAsnIleTyrAspAlaPheValIleTyr 680
QY      2205 TCAAGCAGAGATGAGAGCTGCGGTGAGAGATGAGCTGTGAAGAAATTTAGAAAGAGGGT 2264
Db      681 SerSerGlnAspGluAspIlePheValArgAsnGluLeuValLysAsnLeuGluGlyVal 700
QY      2265 CCTCATTTCAAGTCTGCTTCACTACAGAGACTTTATTCGCGGTGAGCAATGCTGCTCC 2324
Db      701 ProProPheGlnLeuCysIleuHisTyrArgAspPheIleProGlyValAlaIleAlaAla 720

```

```

QY 2325 AACATCATCAGTAAGTTTCCATAAAGCCGAAAGTGATTTGTTGTTCCAGCAC 2384
Db 721 AaHilleHieHlGlnGlyPheHstSsArGlyValHleValValSerGlnHs 740
QY 2385 TTCATCCAGAGCGCGGTGTATCTTGAATATGAGATTGCTCAGACCTGAGTTCTG 2444
Db 741 PheHleGlnSerArGrTrpCyHlePheGlnuTrGlnHleGlnHrTrpGlnPheLeu 760
QY 2445 AGCAGTGTGCTGTATTCATTTTCATTTGCTTCGAGAGGTGAGAAAGCCCTGCTCAG 2504
Db 761 SerSerArGrAlGlyHlePheHleValHleGlnuTrGlnuTrHrLeuArG 780
QY 2505 CAGCAGGTGAGCTGATCCGCTTCACAGAGAACTTACTGAGTGGAGAGCACT 2564
Db 781 GlnGlnValGlnLeuTrArGrLeuLeuSerArGrArHrTruLeuGlnuTrpGlnuPSe 800
QY 2565 GTCTGTGGCGGCGCATCTTTCGAGAGCACTCAGAAAGCCCTGCTGAGTAAATCA 2624
Db 801 ValLeuGlnGlnHleHlePheHrArGrLeuArGrValAlaLeuLeuApGlyArGSe 820
QY 2625 TGGATTCAGAA 2636
Db 821 TrpApnProGln 824

RESULT 6
TIR4_HORSE STANDARD; PRT; 843 AA.
ID TIR4_HORSE STANDARD; PRT; 843 AA.
AC Q9MYW3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-1-like receptor 4 precursor.
GN Name=TIR4;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN (1)
RP SEQUENCE FROM N.A.
RA Vandenplas M.L., McNeill B.W., Barton M.H., Moore J.N.;
RT "Cloning and sequencing of equine Toll-1-like receptor 4 (TIR4).";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TIR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
CC their respective TIR domains (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Toll-1-like receptor family.
CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AY005808; AAF91076.1; -.
CC DR HSSP; Q15399; LFYV.
CC DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
CC DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
CC DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
CC DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
CC DR GO; GO:0016046; P:detection of fungi; ISS.
CC DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
CC DR GO; GO:0042116; P:macrophage activation; ISS.

```

```

DR GO; GO:0045576; P:macr cell activation; ISS.
DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR GO; GO:0045672; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR003591; LRR_TYP.
DR InterPro: IPR000157; TIR.
DR Pfam; PF00560; LRR; 13.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00369; LRR_TYP; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
DR Glycoprotein; Immune response; Inflammatory response;
KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
FT SIGNAL 1 23
FT CHAIN 24 843
FT DOMAIN 24 633
FT TRANSMEM 634 654
FT DOMAIN 655 843
FT REPEAT 53 76
FT REPEAT 77 100
FT REPEAT 101 124
FT REPEAT 128 149
FT REPEAT 150 173
FT REPEAT 174 197
FT REPEAT 203 225
FT REPEAT 227 300
FT REPEAT 311 334
FT REPEAT 351 373
FT REPEAT 374 399
FT REPEAT 401 422
FT REPEAT 423 446
FT REPEAT 447 470
FT REPEAT 471 495
FT REPEAT 496 519
FT REPEAT 521 544
FT REPEAT 545 566
FT REPEAT 569 593
FT DOMAIN 674 820
FT CARBOHYD 35
FT CARBOHYD 189
FT CARBOHYD 205
FT CARBOHYD 282
FT CARBOHYD 295
FT CARBOHYD 498
FT CARBOHYD 498
FT CARBOHYD 527
FT CARBOHYD 576
FT CARBOHYD 626
SQ SEQUENCE 843 AA; 96495 MW; B5976898AD6F7A69 CRC64;

Alignment Scores:
Pred. No.: 1,61e-241
Score: 3312.00
Percent Similarity: 83.18%
Best Local Similarity: 74.65%
Query Match: 49.26%
DB: 1 Gaps: 3

US-09-396-985B-3 (1-3811) x TIR4_HORSE (1-843)
QY 45 ATGATGTGCTGCGCGCTGCTGAGCTTGATCCAGCCATGCGCTTCTCTCTG 104
Db 1 MetMeProProThrArgLeuAlaGlyThrLeuHlePheAlaMetAlaPheLeuSerCys 20
QY 105 GTGAGACGAGAAAGCTGGAGCGCTGAGAGACTTGAGACTTGCGCCCTTAAACACAGAAAGAGC 164
Db 21 LeuArGrProGlnuSerTrpPSeProCysVal----- 30

```

QY 165 TGGATGAACCCAGAGCTTACAGACTCCGAGGCTCAGCCCTTACCCCGATTCAATG 224
Db 30 ----- 30
QY 225 CTCTTGTCTAAATGTCGCCGTTTATACGAGGTGGTCTTAATTAATTAATCAATGC 284
Db 31 ----- GlnValValProAbnThrThrTyrglnCys 40
QY 285 ATGAGCTGAATTTCTACAAATCCCGACAACTCCCTTCTTAACCAAGAACTTGAC 344
Db 41 MetAspLeuAsnLeuTyrlsileProGlnAsnIleProThrSerThrTyrglnLeuAsp 60
QY 345 CTGAGCTTAAATCCCTGAGGACATTTAGGAGCTTCTTCAAGTTTCCGAGACTG 404
Db 61 LeuSerPheAsnProLeuTyrglnLeuGlySerHisSerPheSerAsnPheProGlnLeu 80
QY 405 CAGGTGCTGATTTATTCAGGTGTGAATCCAGAACTGAGAAATGAGGAGCATTCAGAGC 464
Db 81 GlnValLeuAspLeuSerArgCysGlnIleGlnMetIleGlnAspArgAlaTyrglnGly 100
QY 465 CTGAGCCACTCTCTACCTTAATTAATTAACAGAAACCCCATCCAGACTTACCTGGGA 524
Db 101 LeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleArgSerLeuAlaLeuGly 120
QY 525 GCCCTTTCTGAGCTATCAAGTTTACAGAGGTGGTGGTGGAGCAAACTCAGACTC 584
Db 121 AlPheSerIleLeuSerSerLeuGlnThrLeuValAlaValGlnThrTyrlsleuSer 140
QY 585 CTGAGAACTTCCCATTTGAGACATCTCAAACTTTGAGAAACTTAATGTGCTCACAAT 644
Db 141 LeuGlnTyrlsPheProIleGlyHisLeuIleThrLeuTyrlsGlnLeuAsnValAlaHisAsn 160
QY 645 CTTAATCAATCTTCAATTAATTAATTAATTTTCTAATGACCAATCTCAGACTG 704
Db 161 LeuIleHisSerPheTyrlsLeuProGlnTyrlsPheSerTyrlsMetProAsnLeuGlnHisLeu 180
QY 705 GACCTTTCCAGAACAAAGATTCAAGATTATTTAGCACAGCTGGGGGTTTCAATCA 764
Db 181 AspLeuSerAsnAsnTyrlsIleGlnAsnIleSerHisGlnTyrlsLeuValGlnValHisGln 200
QY 765 ATGCCCTTACTCAATCTCTCTTTAGACCTGTCCCTGAAACCTTAATGAATTTATCAACA 824
Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuGlnPheIleGlnPro 220
QY 825 GGTGCTTAAAGAAATTAAGCTTCATTAAGCTGACCTTAAGAAATTAATTTGATGTTA 884
Db 221 AspAlaPheTyrlsGlnIleTyrlsLeuHisLeuIleThrLeuArgSerAsnPheAspSerIle 240
QY 885 AATGTAATGAACCTGTATTAAGGTCTGGCTGGTTTGAAGCCATCGTTGGTTCTG 944
Db 241 AspValMetTyrlsSerCysIleGlnGlyLeuAlaGlyLeuTyrlsValAsnArgLeuValLeu 260
QY 945 GGAGAAATTTGAATGAAGAACTTGAAGAAAGTTTGAACAAATCTGCTTGAAGGGCTG 1004
Db 261 GlyGlnPheTyrlsAsnGlnTyrlsGlyHisLeuArgPheAspThrSerAlaLeuAsnGlyLeu 280
QY 1005 TGCATTTGACATTTGAAGAAATTCGATTAACATTAATTAATTAATTAATTAATTAAT 1061
Db 281 HisAsnLeuThrIleGlnGlnPheArgLeuAlaTyrlsIleAspAsnTyrlsSerSerTyrlsAsp 300
QY 1062 AATTAATGCTTATTTAATTTGACAAATGTTTCTCATTTTCCCTGGAGGTGAGT 1121
Db 301 SerIleAspLeuAsnLeuAsnTyrlsValAlaAspIleSerTyrlsIleSerLeuValSerLeuAsp 320
QY 1122 ATGAAAGGCTAAAGACTTCTTAAATTTGATGAGTGAACATTTGAATTAATTAATTAAT 1181
Db 321 LeuGlyAsnLeuTyrlsAspPheProIleGlyPheGlyTyrlsGlnAspPheGlnLeuValAsn 340
QY 1182 TGTAAATTTGACAGCTTCCCACTTGAATGAATCAATCTCTCAAAAGCTTACTTCACT 1241
Db 341 CysArgIleGlnGlyPheProThrLeuGlnLeuThrSerLeuTyrlsArgLeuValPheThr 360

QY 1242 TCCAAAGAGGTGGAAATGCTTTTTCAGAGTTGATTCACAAAGCTTGAATTTAGAT 1301
Db 361 SerAsnTyrlsAspMetTyrlsSerPheAsnGlnValTyrlsLeuProSerLeuGlnPheLeuAsp 380
QY 1302 CTGAGTGAATTAAGCTTGAATTTCAAAAGTTCGTCTTCAAAAGTGAATTTGGACAC 1361
Db 381 LeuSerTyrlsAsnArgLeuSerPheTyrlsSerCysCysSerGlnAlaAspLeuTyrlsThr 400
QY 1362 AGCTTAAGTATTTAGATTCGAGCTTCATGAGGTATTAATTCATGAGTGAACCTTGTG 1421
Db 401 ArgLeuTyrlsHisLeuAspLeuSerPheAsnAspValIleSerMetSerSerAsnPheMet 420
QY 1422 GAGCTTAAGCAATTAAGACATCGAATTTCCACATTTCCAAATTTGAACAAATGAGTAG 1481
Db 421 GlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuTyrlsGlnAlaSerAsp 440
QY 1482 TTTTCAATTTCTTATCACTCAGAAACCTTCATTAATTTACCTTGAATTTCTCACTCAC 1541
Db 441 PheProValPheLeuSerLeuTyrlsAsnLeuArgTyrlsLeuAspIleSerTyrlsAsnThr 460
QY 1542 AGAGTTCCTTCAATGAGCTTCATGAGCTTCATGAGCTTCAGTCTCAGAGCTTGAAGAGCT 1601
Db 461 ArgValValPheHisGlyIlePheAspGlyLeuValSerLeuGlnValLeuTyrlsMetAla 480
QY 1602 GGCATTTCTTCCAGGAAACCTTCCCTCCAGATATCTTCCAGAGCTGAGAACTTGACC 1661
Db 481 GlyAsnSerPheTyrlsAspAsnPheLeuProAsnIlePheArgGlnMetThrAsnLeuThr 500
QY 1662 TTCCTGAGCTCTCTGAGTGTCACTGAGAGCTTGTCTCAACAGACTTAACTCACTC 1721
Db 501 ThrLeuAspLeuSerTyrlsCysAsnLeuGlnGlnValSerGlnGlnAlaPheCysLeuLeu 520
QY 1722 TCCAGTCTTCAAGTATTAATTAATGAGCCACAACTTCTTTCATTTGATTAATGATTCCT 1781
Db 521 ProArgLeuArgValLeuAsnMetSerHisAsnAsnLeuLeuPheLeuAspMetLeuPro 540
QY 1782 TATAGGTGTGAACCTCCCTCCAGGTCTTGAATTAAGCTTCATGACATCAATGACTTCC 1841
Db 541 TyrlsPheProLeuHisSerLeuGlnIleLeuAspCysSerPheAsnArgIleValAlaPhe 560
QY 1842 AAAAAACAGAACTACAGACTTTTCCAGATGCTTCAAGCTTCTTAATCTTACTCAGAA 1901
Db 561 TyrlsTyrlsGlnGlnLeuGlnHisPheProSerSerLeuHisSerLeuAsnLeuThrGlnAsn 580
QY 1902 GACTTGTCTTGAATCTTGTGAACCAAGACTTCTGCAATGATCAAGACCAAGAGCAG 1961
Db 581 AspPheAlaCysValCysGlnTyrlsGlnSerPheLeuGlnTyrlsAspGlnArgGln 600
QY 1962 CTCTGTGTGAAGTTGAAGAAATGAGATGGAACCTTCAGATTAAGCAGGGCATGCT 2021
Db 601 LeuLeuValGlnValGlnHisLeuValCysAlaAlaPheProLeuGlnMetArgGlyMetPro 620
QY 2022 GTGCTGAGTTGTTT--AATATCACTGTCAAGATGAATGAACATCATGCTGTGTCGCTC 2078
Db 621 ValLeuGlyPheAsnAsnAlaThrCysGlnIleSerTyrlsThrIleValGlyGlySerVal 640
QY 2079 CTGAGTGTCTTGAATGCTTGTGAACAGCTTCTGCTCAATGAATTTTCACTGACCTG 2138
Db 641 PheSerIleLeuMetValSerValIleAlaValLeuValTyrlsPheTyrlsPheHisLeu 660
QY 2139 ATGCTTCTTGTGCTGAGCAATGAATGATGAGAGGAGAAACATCATGATGCTTGTGTT 2198
Db 661 MetLeuLeuAlaGlyCysTyrlsTyrlsGlyArgGlyGlnSerIleTyrlsAspAlaPheVal 680
QY 2199 ATCTACTCAAGCCAGATGAGAGCTGGTGAAGAAAGAGCTAGTAAAGATTTGAAGAA 2258
Db 681 IleTyrlsSerSerGlnAspGlnAspTyrlsValArgAsnGlnLeuValTyrlsAsnLeuGlnGln 700
QY 2259 GGGGTGCTTCATTTCAAGCTCTGCTTCACTCAAGAGACTTTATCCCGGTGGCCAT 2318
Db 701 GlyValProProPheGlnLeuCysLeuHisTyrlsTyrlsAspPheIleProGlyValAlaIle 720
QY 2319 GCTGCAACATCATCATGAGGTTTCCATTAAGCGCAAGGATGTTGTTGTGTGCTC 2378

DR Db 721 AlaalaenillellelglngllyphnehslysseraglvsvallvalvaIvaSer 740

OY 2379 CAGCACTTCATCCAGAGCCGCGTGATCTTTGAATGATGATGTGCACAGCCTGGCAG 2438

Db 741 GlnhsphellelginserrargtTpcyslelnehgufurygluleahaglnthrTtpgln 760

OY 2439 TTTCTGACAGCTGCTGCTGTATCATCTTCATATTGCTGTGCAGAAGTGGAGAACCCCTG 2498

Db 761 PhelesserSerrarglaGlYlIellpheilleValleuhlslyseugluLyserrleu 780

OY 2499 CTCAGCGCAGCAGTGGACTGTAAccGCTTTCAGCGAGAACACTTACCCTGGATGGAG 2558

Db 781 leuaAggingInvalgluleutyrtgryleuenuSnAgaanThrTYrleugluTtpgln 800

OY 2559 GACAAGTCTCTGGGGCGGCACATCTTTCGAGAGACAGCTCAGAAAAAGCCTGCTGATGGT 2618

Db 801 ApservallleuglYarHIslelnehertprarghleuAglvSalaleuenuAsply 820

OY 2619 AAATCATGAATCCAGAAAGAACCA 2642

Db 821 LysPrtYpsrProAlaglYThr 828

RESULT 7

TUR4_BOVIN

ID TUR4 BOVIN STANDARD; PRF; 841 AA.

AC OQGL65;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Toll-like receptor 4 precursor.

GN Name=TLR4;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RA Guionaud C.T., Dubey C., Jung J.W.;

RT "Bovine Toll-like receptor 4 (TLR4)".

RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate immune response to bacterial lipopolysaccharide (LPS). Acts via MYD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response (By similarity).

CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor_a multi-protein complex containing at least CD14, LY96 and TLR4. Binds LY96 via the extracellular domain. Binds MYD88 and TRAP via their respective TIR domains (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -1- SIMILARITY: Belongs to the Toll-like receptor family.

CC -1- SIMILARITY: Contains 18 leucine-rich (LRR) repeats.

CC -1- SIMILARITY: Contains 1 TIR domain.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

CC CC

DR EMBL; AF310952; AACG2061.2; -.

DR HSBP; O60603; IFYX.

DR GO; GO:0046596; Cilipolylsaccharide receptor complex; ISS.

DR GO; GO:0001530; Filipolylsaccharide binding; ISS.

DR GO; GO:0004888; FIlipolylsaccharide receptor activity; ISS.

DR GO; GO:0007250; Pactivation of NF-kappa-inducing kinase; ISS.

DR GO; GO:0016046; P:detection of fungi; ISS.

DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.

DR GO; GO:0042116; P:mactrophage activation; ISS.

DR GO; GO:0045576; P:mact cell activation; ISS.

DR	GO:0045671; P:negative regulation of osteoclast different	ISS
DR <td>GO:0045367; P:positive regulation of interleukin-1 biosyn.</td> <td>ISS</td>	GO:0045367; P:positive regulation of interleukin-1 biosyn.	ISS
DR <td>GO:0045368; P:positive regulation of interleukin-12 biosyn.</td> <td>ISS</td>	GO:0045368; P:positive regulation of interleukin-12 biosyn.	ISS
DR <td>GO:0045369; P:positive regulation of interleukin-13 biosyn.</td> <td>ISS</td>	GO:0045369; P:positive regulation of interleukin-13 biosyn.	ISS
DR <td>GO:0045410; P:positive regulation of interleukin-6 biosyn.</td> <td>ISS</td>	GO:0045410; P:positive regulation of interleukin-6 biosyn.	ISS
DR <td>GO:0042088; P:T-helper 1 type immune response; ISS.</td> <td>ISS</td>	GO:0042088; P:T-helper 1 type immune response; ISS.	ISS
DR <td>InterPro; IPR01611; LRR.</td> <td></td>	InterPro; IPR01611; LRR.	
DR <td>InterPro; IPR00483; LRR_Cterm.</td> <td></td>	InterPro; IPR00483; LRR_Cterm.	
DR <td>InterPro; IPR003591; LRR_Typ.</td> <td></td>	InterPro; IPR003591; LRR_Typ.	
DR <td>InterPro; IPR00157; TIR.</td> <td></td>	InterPro; IPR00157; TIR.	
DR <td>Pfam; PF00560; LRR; 13.</td> <td></td>	Pfam; PF00560; LRR; 13.	
DR <td>Pfam; PF01463; LRRCT; 1.</td> <td></td>	Pfam; PF01463; LRRCT; 1.	
DR <td>Pfam; PF01582; TIR; 1.</td> <td></td>	Pfam; PF01582; TIR; 1.	
DR <td>PRINTS; PR0019; LEUICHRPT.</td> <td></td>	PRINTS; PR0019; LEUICHRPT.	
DR <td>SMART; SM00369; LRR_TYP; 1.</td> <td></td>	SMART; SM00369; LRR_TYP; 1.	
DR <td>SMART; SM00082; LRRCT; 1.</td> <td></td>	SMART; SM00082; LRRCT; 1.	
DR <td>SMART; SM00255; TIR; 1.</td> <td></td>	SMART; SM00255; TIR; 1.	
DR <td>PROSITE; PS50104; TIR; 1.</td> <td></td>	PROSITE; PS50104; TIR; 1.	
KM <td>Glycoprotein; Immune response; Inflammatory response;</td> <td></td>	Glycoprotein; Immune response; Inflammatory response;	
KW <td>Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.</td> <td></td>	Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.	
FT <td>SIGNAL</td> <td>1 23</td>	SIGNAL	1 23
FT <td>CHAIN</td> <td>24 841</td>	CHAIN	24 841
FT <td>DOMAIN</td> <td>24 632</td>	DOMAIN	24 632
FT <td>TRANSMEM</td> <td>633 653</td>	TRANSMEM	633 653
FT <td>DOMAIN</td> <td>654 841</td>	DOMAIN	654 841
FT <td>REPEAT</td> <td>53 76</td>	REPEAT	53 76
FT <td>REPEAT</td> <td>77 100</td>	REPEAT	77 100
FT <td>REPEAT</td> <td>102 124</td>	REPEAT	102 124
FT <td>REPEAT</td> <td>149 173</td>	REPEAT	149 173
FT <td>REPEAT</td> <td>174 197</td>	REPEAT	174 197
FT <td>REPEAT</td> <td>203 225</td>	REPEAT	203 225
FT <td>REPEAT</td> <td>277 300</td>	REPEAT	277 300
FT <td>REPEAT</td> <td>310 334</td>	REPEAT	310 334
FT <td>REPEAT</td> <td>350 372</td>	REPEAT	350 372
FT <td>REPEAT</td> <td>373 398</td>	REPEAT	373 398
FT <td>REPEAT</td> <td>400 421</td>	REPEAT	400 421
FT <td>REPEAT</td> <td>422 445</td>	REPEAT	422 445
FT <td>REPEAT</td> <td>446 469</td>	REPEAT	446 469
FT <td>REPEAT</td> <td>471 494</td>	REPEAT	471 494
FT <td>REPEAT</td> <td>495 518</td>	REPEAT	495 518
FT <td>REPEAT</td> <td>520 542</td>	REPEAT	520 542
FT <td>REPEAT</td> <td>544 566</td>	REPEAT	544 566
FT <td>REPEAT</td> <td>568 592</td>	REPEAT	568 592
FT <td>DOMAIN</td> <td>673 819</td>	DOMAIN	673 819
FT <td>CARBOHYD</td> <td>35 35</td>	CARBOHYD	35 35
FT <td>CARBOHYD</td> <td>73 73</td>	CARBOHYD	73 73
FT <td>CARBOHYD</td> <td>205 205</td>	CARBOHYD	205 205
FT <td>CARBOHYD</td> <td>228 228</td>	CARBOHYD	228 228
FT <td>CARBOHYD</td> <td>282 282</td>	CARBOHYD	282 282
FT <td>CARBOHYD</td> <td>309 309</td>	CARBOHYD	309 309
FT <td>CARBOHYD</td> <td>497 497</td>	CARBOHYD	497 497
FT <td>CARBOHYD</td> <td>526 526</td>	CARBOHYD	526 526
FT <td>CARBOHYD</td> <td>575 575</td>	CARBOHYD	575 575
FT <td>CARBOHYD</td> <td>625 625</td>	CARBOHYD	625 625
SQ <td>SEQUENCE</td> <td>841 AA; 96026 MW; CSEI7CB9C798CD16 CR64;</td>	SEQUENCE	841 AA; 96026 MW; CSEI7CB9C798CD16 CR64;
Alignment Scores:		
Pred. No.:	5, 71e-240	841
Score:	3291.50	Matches: 639
Percent Similarity:	82.488	Conservative: 86
Best Local Similarity:	72.704	Mismatches: 113
Query Match:	48.954	Indels: 41
DB:	1	Gaps: 2
US-09-396-985B-3 (1-3811) x TIR4_BOVIN (1-841)		
QY	45 ATGATGTCGCTCGGCGCTGCGTGGAGACTGATCCAGCCATGGCTTCTCTCTGC	104
DB	1 MetMetAlaArgAlaArgLeuAlaAlaAlaLeuIleProAlaThrAlaIleLeuSerCys	20
QY	105 GTGAGACCAAGAAAGCTGGAGCCCTCGCTGGAGACATTGGCCCTTAACACACAGAGAGC	164
DB	21 LeuArgThrGlnSerTyrPheProCysVal	30

QY 165 TGGCATGAAACCCAGAGCTTTCAGACTCCGAGCGCTCAGCCCTTCACCCGATTCATG 224
 Db 30 ----- 30
 QY 225 CTCTTGTCTAAATGCTGCCGTTTATATACGAGGTGGTTCCTTAATATTACTTCAATGC 284
 Db 31 ----- GlnValValProAsnIleSerTyrGlnCys 40
 QY 285 ATGAGAGTGAATTTCTACAAATATCCGACACCTCCCTTCACCAAGAACCTGGAC 344
 Db 41 MetGluLeuAsnLeuTyrLysIleProAspAsnIleProIleSerThrLysMetLeuAsp 60
 QY 345 CTGAGCTTTAATCCCTCAGAGCAATTTAGGAGCTATATAGCTTTCAGTTTCCGAGACTG 404
 Db 61 LeuSerPheAsnTyrLeuArgHisLeuGlySerHisAsnPheSerSerPheProGluLeu 80
 QY 405 CAGGTGCTGATTTATTCAGAGTGTGAATTCAGACAAATTGAAGTGGGCAATACAGAGC 464
 Db 81 GlnValLeuAspLeuSerArgCysGluIleLysIleIleGluAspArgThrPheGlnGly 100
 QY 465 CTAGAGCACTCTCTACCTTAATTTAGACAGAAACCCCATCCAGACTTATAGCCCTGGGA 524
 Db 101 LeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaTyrGly 120
 QY 525 GCCCTTTCTGACATCATCAAGTTTACAGAGCTGGTGGCTGGAGCAAAATCTAGCATCT 584
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuValSer 140
 QY 585 CTAGAGAACTTCCCATTTGACATCTGCAAACTTTGAAGAACTTAAATGTGGCTCACAAT 644
 Db 141 LeuAsnAspPheProIleGlyHisLeuLysAsnLeuLysGluLeuAsnValAlaHisAsn 160
 QY 645 CTATATCCAACTTTCAAAATTAACCTGAGATTTTCTAATCTGACCAATCTAGACACTTG 704
 Db 161 PheIleHisSerPheLysLeuProGluTyrPheSerAsnLeuProAsnLeuGluHisLeu 180
 QY 705 GACCTTTCCAGCAACAAGATTCAAAAGTATTTATTTGACAGACTGGCGGTTTCAATCAAA 764
 Db 181 AspLeuSerAsnAsnLysIleGlnAsnIleTyrTyrGluAspValLysValLeuHisGln 200
 QY 765 ATGCCCTTACTCAATCTCTTTAGACCTGTCCCTGAACCTTATGAACCTTATTCACAACA 824
 Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAspPheIleGluPro 220
 QY 825 GGTGCATTTTAAAGAAATTAAGCTTCATTAAGCTGACTTAAAGAAATATTTGATAGTTTA 884
 Db 221 GlyThrPheLysGluIleLysLeuAsnGlyLeuThrLeuArgSerAsnPheAsnSerSer 240
 QY 885 AATGTAATGAAAACTGTATTCAGAGTGGCTGGTTTGAAGCCATCGTTGGTCTCG 944
 Db 241 HisValMetLysThrCysIleGlnGlyLeuAlaGlyLeuLysThrAsnAlaGlyValLeu 260
 QY 945 GGAGAAATTTGAATGAAGAAACTTGAAGAAAGTTTGAACAATCTGCTTGAAGAGGCTG 1004
 Db 261 GlyGluPheLysAsnGluArgLysLeuGlnArgPheAspArgSerPheLeuGluGlyLeu 280
 QY 1005 TGCATTTTGAACATTTGAAGAAATTCGATTAAGCATTAAGCATTAAGCTCGATGATATT 1064
 Db 281 CysAsnLeuThrIleGlnGlnPheArgIleAlaTyrLeuAspLysPheSerGlyAspAsp 300
 QY 1065 ATGAGCTATTAATGTTTGAACAATGTTTCTTCATTTCCCGTGGAGATGAGCATATT 1124
 Db 301 ThrAspLeuPheAsnCysLeuAlaAsnValSerAlaIleSerLeuLeuSerIleSerLeu 320
 QY 1125 GAAAGGCTAAAGACTTTCTTATTAATTTGAGATGAGCAACATTTAGATTAAGTATCTG 1184
 Db 321 GlySerLeuGlnAlaLeuLeuLysAspPheArgTyrProIleHisLeuGluIleIleAsnCys 340
 QY 1185 AAATTGAGACATTTCCCAATTTGAACATCAATCTCTCAAAAGGCTTACTTTCATCTCC 1244
 Db 341 AspPheAspLysPheProAlaLeuLysLeuSerSerLeuLysLysPheValPheThrAsp 360

QY 1245 AACAAAGTGGAAATGCTTTTTCAGAGTTGATCTACAAAGCTTGATTTCTAGATCTC 1304
 Db 361 AsnLysAspIleSerThrPheThrGluPheGlnLeuProSerLeuGlnTyrLeuAspLeu 380
 QY 1305 AGTAGAAATGCGCTTGAGTTTTCAAAGGTGCTGTTCTCAAAAGTATTTTGGGACACACAGC 1364
 Db 381 LysArgAsnHisLeuSerPheLysGlyCysCysSerHisThrAspPheGlyThrThrAsn 400
 QY 1365 CTAAAGATTTTATGATCTGAGACTTCATAGGCTTGATTAACATAGTTTCAAACTTCTGGGC 1424
 Db 401 LeuLysHisLeuAspLeuSerPheAsnAspValIleThrLeuGlySerAsnPheMetGly 420
 QY 1425 TTGAAACAATAGACATCTGATTTTCAGACATTTCCAAATTTGAACAATAGAGAGATT 1484
 Db 421 LeuGlnGlnLeuGluHisLeuAspPheGlnHisSerThrLeuLysGlnIleAsnAlaPhe 440
 QY 1485 TCGATATCTTATCACTCAGAAAACCTCATTTACTTACCTTGACATTTCTCATCTACACAGA 1544
 Db 441 SerAlaPheLeuSerLeuArgAsnLeuArgTyrLeuAspIleSerTyrThrAsnIleArg 460
 QY 1545 GTTGCTTCAATGCGAATCTTTCATAGGCTTGCTCCAGCTCGAAGCTTGAAGAAATGGCTGGC 1604
 Db 461 IleValPheHisGlyLysIlePheThrGlyLeuValSerLeuGlnThrLeuLysMetAlaGly 480
 QY 1605 AATTCTTTCCAGAGAAACTTCTTCCAGATATCTTCAAGAGCTGAGAACTTGACCTTC 1664
 Db 481 AsnSerPheGlnAsnAsnLeuLeuProAspIlePheThrGluLeuThrAsnLeuThrVal 500
 QY 1665 CTGAGACCTCTCTCAGGTGTCACCTGAGACAGCTGTCTCCAAACAGCATTTAACTGATCTCC 1724
 Db 501 LeuAspLeuSerLysCysGlnLeuGlnGlnValAlaGlnThrAlaPheHisSerLeuSer 520
 QY 1725 AGTCTTCAAGGTATTAATATGACCAACAACAACTTCTTTCATTTGATAGTTTCCATT 1784
 Db 521 SerLeuGlnValLeuAsnMetSerHisAsnLysLeuLeuSerLeuAspThrPheLeuTyr 540
 QY 1785 AAGTGTGAACTCCCTCCAGGTTCTTGATTAAGTCAATGATCAATATGACTTCCAAA 1844
 Db 541 GluProLeuHisSerLeuAsnArgIleLeuAspCysSerPheAsnArgIleMetAlaSerLys 560
 QY 1845 AAACAGAACTTACAGCATTTTCCAAAGTATGCTTTCATTAATCTTACTCAGAAATGAC 1904
 Db 561 GlnGlnGlnLeuGlnAsnLeuProArgSerLeuThrTyrLeuAsnLeuThrGlnAsnAla 580
 QY 1905 TTTGCTTTGACTTGTGAACACAGAGTTTCCGATATGATCAAGACACGAGGACGCTC 1964
 Db 581 PheAlaCysValCysGlnHisGlnSerPheLeuGlnThrValLysAspGlnArgGlnLeu 600
 QY 1965 TTGCTGGAAGTTGAAGAAATGAATGTGCAACACTTTCAGATTAAGACAGGCGCATGCTGTG 2024
 Db 601 LeuValGlyAlaGluGlnMetMetCysAlaGluProLeuAspMetGluAspMetProVal 620
 QY 2025 CTGAGTTTG---AATATCACTGTCAAGATGAATGAACATCAATGCTGTGTCGCTC 2081
 Db 621 LeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrIleLeuSerValSerValVal 640
 QY 2082 AGTGTGCTGTAGTACTGTGTGAGCAAGTTCTGTGCTATTAAGTTTATTTTCACTGATG 2141
 Db 641 ThrValLeuLeuValSerValValGlyValLeuValTyrLysPheTyrPheHisLeuMet 660
 QY 2142 CTCTTGTGCTGCTGAATTAAGTATGAGTGAAGGAAACATCATGATGCTTGTGTTATC 2201
 Db 661 LeuLeuAlaGlyCysLysLysTyrGlyArgGlyLeuSerIleTyrAspAlaPheValIle 680
 QY 2202 TACTCAAGCCAGGATGAGGACTGGGTAAAGATGAAGATGATGAATTAAGAAAGG 2261
 Db 681 TyrSerSerGlnAspGluAspTyrValArgAsnGluLeuValLysAsnLeuGluGly 700
 QY 2262 GTGCCCTCATTTAGCTGTGCTTCACTACAGAGACTTTATTTCCGCGTGGGCACTTGTCT 2321
 Db 701 ValProProPheGlnLeuCysLeuHisTyrTyrArgAspPheIleProGlyValAlaIleVal 720
 QY 2322 GCCAATCATCATGAAAGTTTCCATTAAGCCGAAAGGTGATTTGTGTGCTGCCAG 2381

Qy	1005	GCAATTGACATTCAGTAAGAAATCCGATTACATCTACCTAGCTACCTGATGAACTTT	1064
Db	281	CysasnleuhtirilegluGlnpheargIlealaTytleuabpIyspheserclYAspasp	300
Qy	1065	ATTGACTTATTTAAATTGTTTGACAAATGTTTCTTCATTTTCCGTGGAGTGATTAATT	1124
Db	301	ThraspleuPheaucYsleualasbnValserValIleSerlleuSerlleuSerlleu	320
Qy	1125	GAAGAAGGTAAGAAGCTTTTCTTAATAATTCCGATGGGCAACATTTAAGATTAGTAACTGT	1184
Db	321	GlyserleuGlnIalaleuLeuIysasphneargItrpGlnIhIleuGlnIleIleasnYs	340
Qy	1185	AAATTTGGACAGTTTCCACATTTGGAAATCCAAATCTCCAAAGAGCTTACCTTCACTTC	1244
Db	341	AsphneapIysPheProIalaleuIyIeuserSerleuIyIysPheValPhehtrasp	360
Qy	1245	AACAAAGGTGGAAATGCTTTTTCAGAGTTGATTTACCAAGCTTGAGTTCTAGATTC	1304
Db	361	AsnIysapIleSerThrPhehtrclIubheGlnleuProserleuGlnTytleuabpIeu	380
Qy	1305	AGTGAATAATGCTTGAGTTTCAAAGAGTGCCTGTTCTCAAAGATTTTGGACAAACAGC	1364
Db	381	LysargasnIhIleuserPheIybelYcyCysserIhIsthrapPheclYThrIthrasn	400
Qy	1365	CTAAAGATTAGATCTGAGCTTCAATGATGTATTATACATGACTTCAAACCTTCTGGGC	1424
Db	401	LeuIyshiIleleuapIeuserPheasnIapValIleThrleuGlySerAsnPhemeclY	420
Qy	1425	TTTAAGAACATCTAGAACATCTGATTTCCAGACATTTCCAAATTTGAAACAAATGATGACTT	1484
Db	421	leuGlnGlnleuGlnIhIleuabpPheGlnIhIserThrIleuIyGlnIleasnIalhe	440
Qy	1485	TCAGTATTCCTATACATCTCAGAAACCTCATTTTACCTTGACATTTCTCATCTACACACGA	1544
Db	441	SerIalpheuserSerleuargIasnleuargIytleuabpIleSerTyThrAsnIlearg	460
Qy	1545	GTTGCTTTCAAATGCGATTTTCAAATGGCTTGTTCAGCTCTGCAGAGTCTGAAATGGCTGGC	1604
Db	461	IleValPhehIsgIyIlePhehtrclYleuValIserleuGlnThrIleuIyIeueclIy	480
Qy	1605	AAATCTTTCCAGGAAAACTTCCTTCCAAATTCCTTCCAGAGCTGAGAACTTGACCTTC	1664
Db	481	AsnserPheGlnAsnasnleuIeuProaspIlePhehtrclYleuThrIhAsnleuIhVal	500
Qy	1665	CTGACACTCTCTCAGGTGCAACTGAGAGAGTGTCTCCAAAGCATTTTAACTCACTCTCC	1724
Db	501	leuaspIeuserIyIyCysGlnleuGlnIValIalGlnThrIalPhehIleSerleuser	520
Qy	1725	AGTCTTACGGTACTTAATATATGAGCCAAACAACTTCTTTCAATGGATAGCTTCTTAT	1784
Db	521	SerleuGlnIValIleuasnIeuserIhIasnIyIseuIeuserIeudaspIthPheIeuIyI	540
Qy	1785	AAGTGTGGAATCCCTCCAGGTTCTTGATTACAGTCTCAATTCACATATGACTTCCAA	1844
Db	541	GluProleuhtIserSerleuargIleleuabpCysSerPheasnargIleMetIalaserIys	560
Qy	1845	AAACAGCACTACAGACATTTTCCAAATGTCTAGCTTCTTAAATCTTACTCAGATGAC	1904
Db	561	GlnGlnGlnIleuGlnIasnleuProargSerleuThrItrPleuasnleuThrGlnIasnIa	580
Qy	1905	TTTGCTGTACTTGGAACACAGAGTTTCCGCAATGAGATCAGAGACAGAGGAGCTC	1964
Db	581	PhealacYsValIySGlnIhIserPheIeuGlnItrValIyAspGlnIhrgIleu	600
Qy	1965	TTGTGTGAAGTTGAACGATGGAATGTGCAACACTTCAGATTAAGCAGGAGATGCTGTG	2024
Db	601	leuValIglYalIagIuGlnIeMetIeCysIalGlnIProleuaspMetGluaspMetProVal	620
Qy	2025	CTGAGTTG---AATATCACTGTTCAGATGAATAGAACATCATGATGGTGTGGTCTCTC	2081
Db	621	leuSerPheargAsnIalathIrcYsGlnIeuserIyIsthrIleIleSerValIserValI	640

QY	2082	AGTGTGGTCTGTAAGTATCTGTTGGTAAGCAAGTTCTGGTCTGTAATGAGTCTTATTTGACCTGATG	21441
Db	641	ThrlValLeuValSerValSerValGlyValLeuValTyrIleSerPheTyrPheHisLeuMet	660
QY	2142	CTTCTGCTGGCTGCATTAAGTATGGTGAAGGTGAACACATCTATGATGCGCTTGTGTATC	2201
Db	661	LeuLeuValLeuValCysIleValTyrGlyValGlyGlnSerIleTyrPheAlaPheValIle	680
QY	2202	TACTCAAGCCAGGATGAGGACTGGGTGAAGGATGACCTAGTAAAGATTGAGAGAGGG	2261
Db	681	TySerSerGlnSerGlnAspGlnAspGlnValArgAsnGlnLeuValIleAsnLeuGlnGlnGly	700
QY	2262	GTCGCTCCATTTGACGCTCTGCGCTTCACTACAGAGAGCTTATTCGCGGTGGGCAATTCCT	2321
Db	701	ValProProPheGlnLeuValCysLeuHisValTyrValAspPheIleProGlyValAlaIleAla	720
QY	2322	GCCAACTCATCTCAGTGAAGGTTCCATTAAGGCGGAAGGTGATGTTGTTGGTGTCCAG	2381
Db	721	AlaAsnIleIleGlnGlnGlnGlyPheHisIleSerHisGlyValIleValValValSerGln	740
QY	2382	CATTTCATCCAGAGCGCGCTGTGTATCTTGGAAATATGATGATGCTCTAGACCTGGCAGTTT	2441
Db	741	HisPheIleGlnSerArgTyrCysIlePheGlnTyrGlnIleValGlnIleThrTyrGlnPhe	760
QY	2442	CTGAGCAGTGTGTGTGTATCATCTTCATTCATTCCTGTCGAGAGAGGTGAGAGAGCCGTCCTC	2501
Db	761	LeuSerSerArgAlaGlyIleIleIlePheIleValLeuGlnIleValLeuGlnIleValSerLeuLeu	780
QY	2502	AGGACAGAGGTGAGAGTGTATCGCGCTCTTCAGACAGGAAACCTTACCTGAGTGGAGAGAC	2561
Db	781	ArgGlnGlnValGlnLeuTyrValGlyLeuLeuSerHisArgHisThrTyrLeuGlnIleTyrGlnAsp	800
QY	2562	AGTGTCTGTGGCGCGGACATCTTCTGTGAGACGACTCAGAAAGCCCTGTGATGGTAA	2621
Db	801	SerValLeuGlyArgHisValPheTyrPArgValLeuArgValAlaLeuValAlaGlyLeu	820
QY	2622	TCATGAAATCCAGAGGAAACAGTGGGTAACAGATGCATTTGGCAGGAGAGGAAACATCT	2678
Db	821	ProGlnIleSerProGlnGlyThrAlaAspAlaGlnIleThrAsnProGlnGlnIleAlaThrThr	839
RESULT 9			
Q6WCDS	PRELIMINARY;	PRT;	841 AA.
Q6WCDS	Q6WCDS;		
AC	05-JUL-2004 (TREMBlrel. 27, Created)		
DT	05-JUL-2004 (TREMBlrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBlrel. 27, Last annotation update)		
DE	Toll-like receptor 4.		
GN	Name=TLR4;		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
CC	Bovine; Bos;		
CK	NCBI_TaxID=9913;		
KN	[1]		
RP	SEQUENCE FROM N.A.		
FX	MEDLINE=2283971; PubMed=12915733; DOI=10.1073/pnas.1333957100;		
RA	White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.E.;		
RT	"Haplotype variation in bovine Toll-like receptor 4 and computational		
RT	prediction of a positively selected ligand-binding domain.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).		
DR	EMBL; AY297040; AAQ62700.1; -		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0004888; P:transmembrane receptor activity; IEA.		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR000483; LRR_Cterm.		
DR	InterPro; IPR003885; LRR_cyst.		
DR	InterPro; IPR003591; LRR_Typ.		
DR	InterPro; IPR000157; TIR.		
DR	Pfam; PF01463; LRRCT; 1.		
DR	Pfam; PF00560; LRR_1; 12.		
DR	Pfam; PF01582; TIR; 1.		
DR	PRINTS; PR00019; LEURICHRPT.		

DR SMART; SM00082; IRECT; 1.
DR SMART; SM00365; IRR_SD2P; 6.
DR SMART; SM00369; IRR_TYP; 13.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PSS0104; TIR; 1.
KW Receptor.
SQ SEQUENCE 841 AA; 96014 MW; 603936A17E834735 CRC64;

Alignment Scores:

Pred. No.:	1.36e-239	Length:	841
Score:	3286.50	Matches:	638
Percent Similarity:	82.37%	Conservative:	86
Best Local Similarity:	72.58%	Mismatches:	114
Query Match:	48.88%	Indels:	41
DB:	2	Gaps:	2

US-09-396-985b-3 (1-3811) x Q6WCDS (1-841)

```
QY 45 ATGATGCTGCGCTCGCGCTGCTGGAGACTGTGATCCAGCCAGTGGCCCTTCCTCCGTC 104
   |||||:::|||||
Db 1 MetMetAlaArgAlaArgLeuAlaAlaLeuIleProAlaThrAlaIleLeuSerCys 20
QY 105 GTGAGACCAAGAAAGCTGGAGCCCTGCTGAGAACTTGCCCTAAACACAGAAAGAC 164
   ::|||
Db 21 LeuArgThrGluSerThrAspProCysVal----- 30
QY 165 TGGCATGAAGAACCAAGAGCTTCAGACTCCGAGCCCTCAGCCCTCAGCCGATTCATTG 224
   30 ----- 30
QY 225 CTTCCTGCTAAATGCTGCGCTGCTTTATCAAGAGGTGCTCTAATATTCTTAATGAC 284
   |||||:::|||||
Db 31 -----GlnValValProAsnIleSerTyrGlnCys 40
QY 285 ATGAGAGCTGAATTTCTACAAATATCCCGACACACCTCCCTTCTACACAAAGAACTGGAC 344
   |||||:::|||||
Db 41 MetGluLeuAsnLeuTyrIleProAspAsnIleProIleSerThrIlysmetLeuAsp 60
QY 345 CTGAGCTTAAATCCCTGAGAGCACTTTAGAGCACTATAGCTTCTTCAGTTTCCAGAAATG 404
   |||||
Db 61 LeuSerPheAsnTyrLeuArgIleGluGlySerHisAsnPheSerPheProGluLeu 80
QY 405 CAGGTGCTGATTTATTCAGAGTGTGAATTCAGACAAATGAGAGATGAGCATATCAGAGC 464
   |||||
Db 81 GlnValLeuAsnLeuSerArgCysGluIleIleValIleLeuAspThrPheGlnGly 100
QY 465 CTAGGCCACTCTCTACCTTAATATTGACAGAAACCCCATCCAGAGTTTATGCTGGGAA 524
   |||||
Db 101 LeuAsnHisLeuSerThrIleuIleLeuThrGlyAsnProIleGlnSerIleuAlaTprGly 120
QY 525 GCGTTTTCTGAGCTATGATTAAGATTGACAGAGCTGCTGCTGGAGCAATCTAGACATCT 584
   |||||
Db 121 AlaPheSerGlyLeuSerSerIleGlnIleValAlaValGluThrAsnLeuValSer 140
QY 585 CTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAAAGACTTAATGTGCTCAAT 644
   ::|||
Db 141 LeuAsnAspPheProIleGlyHisLeuIleValAsnLeuValAlaHisAsn 160
QY 645 CTATTCATCTTTCAATTAATCTGAGTATTTTCTAATGTGACCAATCTTAGAGCACTTG 704
   |||||
Db 161 PheIleHisSerPheIleuProGluTyrPheSerAsnLeuProAsnLeuGluHisLeu 180
QY 705 GACCTTTCCAGCAAGAAAGATTCAAGATTATTTGACAGACTTGGGGTTCTACATCA 764
   |||||
Db 181 AsnLeuSerAsnAsnIleGlnAsnIleTyrGluAspValIleValHisGln 200
QY 765 ATGCCCTACTCATCTCTCTTAGAGCTGCTCCCTGAGACCTTAGAACTTATTCACAGCA 824
   |||||
Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAspPheIleGluPro 220
QY 825 GTGCACTTAAAGAAATTAGGCTTCATAGCTGACTTAAAGAAATAATTTGATAGTTTA 884
   |||||
Db 221 GlyThrPheIleGluIleIleValAsnGlyLeuThrIleuArgSerAsnPheAsnSerSer 240
```

```
QY 885 AATGTAATGAAACTTTGATTCAGAGTCTGCGGTTTAGAATGTCATGTTTGGTTCTG 944
   ::|||
Db 241 HisValMetCysThrCysIleGlnGlyLeuAlaGlyLeuIleValAsnArgLeuValIle 260
QY 945 GGAAGATTTAGAAATGAGAAAGAACTTGAAGAAATTGACAAATGTGCTCTAGAGGCTG 1004
   |||||
Db 261 GlyGluPheIleAsnGluArgIleGlyLeuGlnArgPheAspArgSerPheLeuGluGlyLeu 280
QY 1005 TGCATTTTACCACTTGAAGAAATTCGATTTAGCATTTACTTACTACTCTCGATGATATT 1064
   |||||
Db 281 CysAsnLeuThrIleGluIlePheArgIleAlaTyrLeuAspArgIlePheSerGlyAspArg 300
QY 1065 ATTTGACTTATTAATTTGTCAGAAATGTTTCTCAATTTTCCCTGGTGGAGTGAATTATT 1124
   |||||
Db 301 ThrAspLeuPheAsnIleValAsnValSerValIleSerLeuLeuSerIleSerLeu 320
QY 1125 GAAAGGTAAGAAAGACTTTTCTAATATTTCGAGTGGACAACTTTAGAAATTAGATCTG 1184
   ::|||
Db 321 GlySerLeuGlnAlaLeuLeuIleAspPheArgTprGlnHisLeuGluIleIleAsnCys 340
QY 1185 AAATTTGACAGTTTCCCATTTGAATTCGAAATCTCTGAAAGCTTACTTCACTTCC 1244
   |||||
Db 341 AspPheAspArgIlePheProAlaLeuIleLeuSerSerLeuIleValPheThrAsp 360
QY 1245 AACAAAGTGGGAAATGCTTTTCTAAGATTTGATCTACCAAGCTTGAAGTTTCTAGATCTC 1304
   |||||
Db 361 AsnIleAspArgIleSerThrPheThrGluPheGlnLeuProSerLeuGlnTyrLeuAspLeu 380
QY 1305 AGTAGAAATGCTTGAATTTCAAGGTTGCTGTCTCAAGATGATTTTGGACAAACAGC 1364
   |||||
Db 381 LysArgAsnHisLeuSerPheIleGlyCysCysSerHisThrAspPheGlyThrThrAsn 400
QY 1365 CTAAAGTATTTAGATTTGAGCTTCAATGAGTGTATTAACATGAGTTCAAACTTTGGGC 1424
   |||||
Db 401 LeuIleValLeuAspLeuSerPheAsnAspValIleThrLeuGlySerAsnPheMetGly 420
QY 1425 TTAGAAACAATGACATCTGATTTCCAGACTTCCAACTTTGAAACAAATGAGTGGATT 1484
   |||||
Db 421 LeuGluGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuIleGlnIleAsnAlaPhe 440
QY 1485 TCAGATTTCTACTACTCAGAAACCTCATTTAATCTTGAATTTCTCATCTACACAGAA 1544
   |||||
Db 441 SerAlaPheLeuSerIleuArgAsnLeuArgTyrLeuAspArgIleSerTyrThrAsnIleArg 460
QY 1545 GTTGCTTTTGAAGGCACTTTCAATGAGCTTGTCCAGTCTGAAAGTCTTGAAGATGCTGGC 1604
   ::|||
Db 461 IleValPheHisGlyIlePheThrGlyLeuValSerLeuGlnThrIleuIleMetAlaGly 480
QY 1605 AATCTTTCCAGAAAGAACTTCCCTGAGATTCCTTCAAGAGCTGAGAAAGTTCAGCTTC 1664
   |||||
Db 481 AsnSerPheGlnAsnAsnLeuLeuProAspArgIlePheThrGluLeuThrAsnLeuThrVal 500
QY 1665 CTGAGACTCTCTCAGTGTCACTGAGAGAGTGTCTCAACAGACATTTAATCACTCTCC 1724
   |||||
Db 501 LeuAspLeuSerIleCysGlnGlnGlnValAlaGlnThrAlaPheHisSerLeuSer 520
QY 1725 AGTCTTCAAGTACTTAATATGAGCCACAACTTTTTCATGAGATACGTTTCTTAT 1784
   |||||
Db 521 SerLeuGlnValLeuAsnMetSerHisAsnIleValLeuLeuSerLeuAspThrPheLeuTyr 540
QY 1785 AAGTGTCAAGCTCCCTGAGGTTCTTGATTCAGTCTCAATCAACATTAATGACTTCCAA 1844
   ::|||
Db 541 GluProLeuHisSerIleuArgIleLeuAspArgSerPheAsnArgIleMetAlaSerIleVal 560
QY 1845 AAACAGAACTACAGCAATTTTCCAGATAGCTTAGCTTTCTTAATCTTACAGAAATGAC 1904
   ::|||
Db 561 GlnGlnGlnIleuGlnHisAsnLeuProArgSerLeuThrTyrLeuAsnLeuThrGlnAsnAla 580
QY 1905 TTGCTTGTACTTGTGAACAACAAGATTCTCTGCAATGGAATGAGACAGACAGGACGCTC 1964
   |||||
Db 581 PheAlaCysValaCysGluHisGlnSerPheLeuGlnTyrValIleAspArgIleArgGlnLeu 600
```

Oy		1965	TTGGGGAAGATTGAACCAATGGAAATGTCTCAACAACCTTCAGATTAAGCAGGCAGTCTGTG	2024
Db		601	LeuValIGlyalagluGlnMetMeCCysAlaGluProLeuabpMecGIaspMecProVal	620
Oy		2025	CTGAGTTTG---AATATCACCTGTTCAGATGATAAGAACCATCATTTGTGTGTGGTCTCTC	2081
Db		621	LeuSerPheakxgAsnAlatThrCyedInleuSerIyrStrIIeIseValSerValVal	640
Oy		2082	AGTGTGCTTGAAGATCTGTGTGTAGACAGTTCTGTGCTTAAGTCTATTTTCACTGTATG	2141
Db		641	ThrValLeuLeuValSerValValIGlyValLeuValTYrLysPheTYrPheHisIeuMet	660
Oy		2142	CTTCTGTGCGCTGCATTAAGATGATGGTAGAGTGTAAGAAAACPTATNGATGCCCTTGTATTC	2201
Db		661	LeuLeuAlaGLYcysLysLysTyreLYrAgelYgluSerThrTYrAspAlaPheValIle	680
Oy		2202	TACTCAAGCCAGATGAGACCTGGGTAAAGATGAGAGCTAGTATTAAGAATTATTAAGAAAGG	2261
Db		681	TyreSerSerGIaspIleapTrpValArgasnGluLeuValLybAsnIeuGluGlu	700
Oy		2262	GTCGCTCCATTTCAGCTCTGCCTTCATCAAGAGACTTATTCGCCGTGTGGCCATTGCT	2321
Db		701	ValProPheGlnIeuCYLeuHIEtyrArgasPheIleProGlyValAlaIlela	720
Oy		2322	GCCAACATCATCCATGAAGGTTTCCATTAAGACCGAAGAGTGATTTGTGTGTCTCCAG	2381
Db		721	AlaasnIleIlegIngluGlyPheHisLysSerArgLysValIleValValSerGIasp	740
Oy		2382	CAC TTCATCCAGAGCCGCTGGGTATCTTTTAATATGATGATGTCAGACCTGGCAGTTT	2441
Db		741	HispheIleGlnSerArgITryPCyalIephelIuTYrGluIlealaglnIthrTrpGlnPhe	760
Oy		2442	CTGAGCAGTCGTCTGTATCATCTTCATTGTCTCTGAGAGAGTGAGAGAACCCCTGTCTC	2501
Db		761	LeuSerSerArgIaGLYLleIlePheIleValIeuGlnLysIeuGlnLysSerIeuLeu	780
Oy		2502	AGGAGAGAGGTGGAGCTGTACCCTTCTTCAGCAGAGAACATTATTCCTGAGATGGGAAGAC	2561
Db		781	ArgIngluInValIGluLeuTYrArgLeuLeuSerArganThrTYrLeuGluTrpGIasp	800
Oy		2562	AGTGTCCCTGGGGCGGCACATCTTCCTGGAGAGAGCATCGAAAAAGCCCTGTGATGTATA	2621
Db		801	SerValIleugLYarghIsvalaPheTrpArgArgLeuargLysAlaLeuLeuAlaGlyLys	820
Oy		2622	TCATGATGCAGAGAAAGAAAGTGGGTACACAGATGATCATTCGGAGAGAGCAACATCT	2678
Db		821	ProGlnSerProGlnGluTYrThralaSpIaGluIthrAsnProGlnGluIalaIethrThr	839

RESULT 10
 TLR4_FELCA STANDARD; PRT; 833 AA.

```

ID      TLR4_FELCA          STANDARD;          PRT;          833 AA.
AC       P58727;
DT       28-FEB-2003 (Rel. 41, Created)
DT       28-FEB-2003 (Rel. 41, Last sequence update)
DT       05-JUL-2004 (Rel. 44, Last annotation update)
DE       Toll-like receptor 4 precursor.
GN       Name=TLR4;
OS       Felis silvestris catus (Cat).
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX       NCBI_TaxId=9685;
RN       [1]
RP       SEQUENCE FROM N.A.
RA       Yoshida N., Kano R.;
RL       Submitted (APR-2001) to the EMBL/Genbank/DDBJ databases.
CC       -1- FUNCTION: Cooperates with Ly6e and CD14 to mediate the innate
CC       immune response to bacterial lipopolysaccharide (LPS). Acts via
CC       MYD88, TRAF6 and IRAK4, leading to NF-kappa-B activation, cytokine
CC       secretion and the inflammatory response (By similarity).
CC       -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC       multi-protein complex containing at least CD14, LY6E and TLR4.
CC       Binds Ly6e via the extracellular domain. Binds MYD88 and TRAF6 via
    
```

CC		the respective TIR domains (By similarity).
CC	-1	SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	-1	SIMILARITY: Belongs to the Toll-like receptor family.
CC	-1	SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC	-1	SIMILARITY: Contains 1 TIR domain.
CC		-----
CC		This SWISS-PROT entry is copyright. It is produced through a collaboration
CC		between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC		the European Bioinformatics Institute. There are no restrictions on its
CC		use by non-profit institutions as long as its content is in no way used
CC		modified and this statement is not removed. Usage by and for commercial
CC		entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC		or send an email to license@isb-sib.ch).
CC		-----
DR	EMBL; AB060687; BAB3947.1; .	
DR	HSSP; O60603; LEYX.	
DR	GO; GO:0046696; C.i.lipopolysaccharide receptor complex; ISS.	
DR	GO; GO:0001550; F.lipopolysaccharide binding; ISS.	
DR	GO; GO:0004888; P.transmembrane receptor activity; ISS.	
DR	GO; GO:0007250; P.activation of NF-kappaB-inducing kinase; ISS.	
DR	GO; GO:0016046; P.detection of fungi; ISS.	
DR	GO; GO:0009598; P.detection of pathogenic bacteria; ISS.	
DR	GO; GO:0042116; P.macrophage activation; ISS.	
DR	GO; GO:0045576; P.mast cell activation; ISS.	
DR	GO; GO:0045671; P.negative regulation of osteoclast different. . . ; ISS.	
DR	GO; GO:0045362; P.positive regulation of interleukin-1 biosyn. . . ; ISS.	
DR	GO; GO:0045084; P.positive regulation of interleukin-12 biosy. . . ; ISS.	
DR	GO; GO:0045368; P.positive regulation of interleukin-13 biosy. . . ; ISS.	
DR	GO; GO:0045410; P.positive regulation of interleukin-6 biosyn. . . ; ISS.	
DR	GO; GO:0042088; P.T-helper 1 type immune response; ISS.	
DR	InterPro; IPRO01611; LRR.	
DR	InterPro; IPRO00483; LRR_Cterm.	
DR	InterPro; IPRO03591; LRR_Typ.	
DR	InterPro; IPRO00157; TIR.	
DR	Pfam; PF00560; LRR: 12.	
DR	Pfam; PF01463; LRRCt: 1.	
DR	Pfam; PF01582; TIR: 1.	
DR	PRINTS; PR00019; LEURICHRPT.	
DR	SMART; SM00369; LRR_TYP; 1.	
DR	SMART; SM00082; LRRCt; 1.	
DR	SMART; SM00255; TIR: 1.	
DR	PROSITE; PSS0104; TIR: 1.	
KW	Glycoprotein; Immune response; Inflammatory response;	
KW	Leucine-rich repeat; Receptor; Signal; Transmembrane.	
FT	SIGNAL	1 23 Potential.
FT	CHAIN	24 833 Toll-like receptor 4.
FT	DOMAIN	24 632 Extracellular (Potential).
FT	TRANSNEM	633 653 Potential.
FT	DOMAIN	654 833 Cytoplasmic (Potential).
FT	REPEAT	53 76 LRR 1.
FT	REPEAT	77 100 LRR 2.
FT	REPEAT	101 124 LRR 3.
FT	REPEAT	128 149 LRR 4.
FT	REPEAT	150 173 LRR 5.
FT	REPEAT	174 197 LRR 6.
FT	REPEAT	203 225 LRR 7.
FT	REPEAT	228 252 LRR 8.
FT	REPEAT	310 334 LRR 9.
FT	REPEAT	350 372 LRR 10.
FT	REPEAT	373 398 LRR 11.
FT	REPEAT	399 421 LRR 12.
FT	REPEAT	422 445 LRR 13.
FT	REPEAT	447 469 LRR 14.
FT	REPEAT	470 494 LRR 15.
FT	REPEAT	495 518 LRR 16.
FT	REPEAT	520 542 LRR 17.
FT	REPEAT	544 566 LRR 18.
FT	REPEAT	568 592 LRR 19.
FT	TIR	.
FT	CARBOHYD	35 35 N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	173 173 N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	205 205 N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	238 238 N-linked (GlcNAc. . .) (Potential).

FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 570 570 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 625 625 N-linked (GlcNAc . . .) (Potential) .
 SQ SEQUENCE 833 AA; 95592 MW; 3E3A84F2BB8A55EA CRC64;

Alignment Scores:
 Pred. No.: 2,29e-239 Length: 833
 Score: 3283.50 Matches: 637
 Percent Similarity: 83.49% Conservative: 86
 Best Local Similarity: 73.56% Mismatches: 102
 Query Match: 48.83% Indels: 41
 DB: 1 Gaps: 2

US-09-396-985B-3 (1-3811) x TLR4_FELCA (1-833)

```

QY 45 ATGATGTCGCGCGCGGCGTGGAGCTGTGATCCAGACCATGGCCTTCTCTGCG 104
   ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MetMetProProthrlArgLeuAlaGlyThrLeuIleProHlaMetAlaPheLeuSerCys 20

QY 105 GTGAGACCAAGAACTGGAGAGCCCTGCGTGGAGACTTGGCCCTTAAACACAGAGAGAC 164
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 21 LeuArgProGluSerThrAspProCysVal-----

QY 165 TGGCATGAACCCAGAGCTTTCAGACTCGGAGACCTCAGCCCTTACCCCGATTCCATTG 224
   30 -----

QY 225 CTTCCTGTAATAGTCGCGGTTTATTCACGAGAGTGATTCCTAATATTAATTATCAATG 284
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 -----GluValAlaProAsnIleThrIleArgCys 40

QY 285 ATGAGACTGAATTTCTACAAATCCCGACACCTCCCTTCTCAACCAAGAACTGGAC 344
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 41 MetAspLeuAsnLeuHisIleProAspAsnIleProSerSerThrIleAspLeu 60

QY 345 CTGAGCTTAATCCCTGAGAGCACTTAAAGCACTAATAGCTTCTTCAAGTTTCCAGAACTG 404
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 MetSerPheAsnProLeuArgLeuGlySerHisSerPheSerAsnPheProGluLeu 80

QY 405 CAGGCTGCTGATTTATTCAGAGTGTGAATCCAGACAACTTGAAGTGGGCAATTCAGAGC 464
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 81 GluValLeuAspLeuSerArgCysGluIleGlnIleIleGluAspAlaIleArgIleGly 100

QY 465 CTAAAGCACCTCTCTACTTAATATTGACAGAAACCCCATCCAGAGTTTGAAGCTGGAGA 524
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 101 LeuAsnHisLeuSerIleLeuIleLeuThrGlyAsnProIleGlnArgLeuPheProGly 120

QY 525 GCGTTTTCGAGTATTCAGATTTCAGAGCTGTGCTGTGGAGACAAATCTAGCATCT 584
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 AlaPheSerGlyLeuSerSerIleuGlnThrLeuValAlaValIleThrAsnIleAlaSer 140

QY 585 CTAGAGAACTTCCCACTTGACATCTCAAAACTTTGAAAGACTTAAATGAGCTCAAT 644
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 141 LeuGlnAspPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 160

QY 645 CTATCCCAATCTTCAATTAATCTAGATATTTTCTAATCTGACCAATCTAGAGACTGG 704
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 161 LeuIleHisSerPheLeuSerProGluIlePheSerAsnMetSerAsnLeuGluIleu 180

QY 705 GACCTTTCAGACCAAGATTCAGAAATTAATTTATTCAGACATCTGGGGTTTCAATCA 764
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 181 AspLeuSerAsnAsnLysIleGlnAsnIleIleIleLysAspLeuGlnValLeuHisGln 200

QY 765 ATCCCTTACTCATCTCTCTTAGACCTGTCCCTGAACCTTAACCTTATTCACACA 824
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 201 LysProLeuLeuAsnLeuSerIleAspLeuSerIleuAsnProLeuAspPheIleGlnPro 220

QY 825 GGTGCAATTTAAGAAATTAAGCTTCATAGCTGACTTAAAGAAATAATTTGATAGTTTA 884
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 221 GlyAlaPheLysGluValLysLeuArgGluLeuThrLeuArgSerAsnPheAsnSerThr 240
  
```

```

QY 885 AATGTAATGAAAACTTGATTTCAAGATCGCTGGGTTTGAAGTCCATGTTGGTTCTG 944
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 AspValMetLysAlaSerIleGlnIleLysLeuAlaGlyLeuGlnIleHisGlnLeuValLeu 260

QY 945 GGAGAAATTTAGAAATGAAGAAACTTGGAAAACTTGGACAATCTGCTTGAAGGGCTTG 1004
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 261 GlyGluPheLysAsnGluLysGlnLeuGlyArgPheAspLysSerIleLeuGluGlyLeu 280

QY 1005 TGGCAATTTGACCATTTGAAGAAATTCGAGTATAGATCTTAGACTACTGATGATATT 1064
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 281 CysAsnLeuIleIleGluLysPheArgIleAlaIleIleAlaIlePheAspLysPheSerGluAspAla 300

QY 1065 ATTTGACTTAATTAATTTGTTGACAAATGTTTCTTCAATTTTCCCTGGTGAATGACTATT 1124
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 IleAspSerPheAsnCysLeuAlaAsnValaSerThrIleSerLeuValHisLeuIleuIleu 320

QY 1125 GAAAGGGTAAAGACTTTTCTTAATAATTTGCGATGGCAACATTTGAATTAAGTTAACTGT 1184
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 321 LysGlyLeuLysGlnLeuProLysAsnLeuGlyIleArgIleArgGlnLeuValaAsnCys 340

QY 1185 AATTTTGGACAGTTTCCCATTTGAAGCTCAATCTCTCAAAAGCTTCACTTCACTTCC 1244
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 341 GluPheGluGlnPheProThrIlePheLysLeuAspProLeuLysGluLeuValaPheSerAla 360

QY 1245 AACAAAGGTGGGAATGCTTTTCAAGAGTTGATCTACAAAGCTTGAAGTTTCTAGATCTC 1304
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 361 AsnGluValaArgAsnAlaPheThrGlnValLysLeuGlnSerLeuGluLeuLeuAspLeu 380

QY 1305 AGTAGAATGCGTTGAGTTTCAAGGTTGCTGTTTCAAGAGATTTTGGACACACACAC 1364
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 381 SerArgAsnAspPheSerLeuLysSerCysSerGluLysArgAspLeuGlyThrIleArg 400

QY 1365 CTAAAGTATTTAGATTCGAGCTTCAATGCGTATTAACATAGACTTCAAACTTCTGGGG 1424
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 401 LeuLysHisLeuAspLeuSerPheAsnAsnIleIleThrIleSerSerAsnPheLeuGly 420

QY 1425 TTAGAACACTGAACATCTGATTTCCAGACTTCCAGACTTCCAAATTTGAAACAAATGAAGTGA 1484
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 421 LeuGluGlnLeuGluIleuIleuAspPheGlnHisSerSerLeuLysGlnValaSerAspPhe 440

QY 1485 TCAGATTCCTATCTACTCAGAAACCTCAATTAATCTTGAATTTCTCATCTCACACACAGA 1544
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 441 SerValaPheLeuProLeuLysAsnLeuArgIleLeuAspIleSerIleThrHisIleGln 460

QY 1545 GTTGCTTTCAATGAGCATCTTCAATGCGCTGTCCAGTCTGGAAGCTCTTGAAGAAAGCGTGC 1604
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 461 ValAlaPheHisIleGlyIlePheAsnGlyLeuIleSerLeuGlnIleLeuLysMetAlaGly 480

QY 1605 AATTTTCCAGGAAAACTTCTTCCAGATATCTTCAAGAGCTGAGAAACTTGAACCTTTC 1664
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 481 AsnSerPheGlnAspAsnPheLeuProAsnIlePheMetGlnLeuThrAsnLeuThrIle 500

QY 1665 CTGAGACCTCTCTCAGTGTCAACTGAGACAGTGTCTTCAACAGACTTTAACTCACTCTCC 1724
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 501 LeuAspLeuSerAspCysGlnLeuGlnValaIleValaIlePheAsnSerLeuPro 520

QY 1725 AGCTTTCAGGTACTAATATGAGCCCAACAACTTCTTTCATTTGATGATACGTTCCATT 1784
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 521 LysLeuGlnLeuLeuAsnMetSerHisAsnHisLeuLeuSerLeuAspThrLeuProIle 540

QY 1785 AAGTGTGAACTCCCTCCAGGTTTCTTGATTAACAGTCTCAACATCAATCAATGACTTCAAA 1844
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 541 GluProLeuHisSerLeuGlnThrLeuAspCysSerPheAsnArgIleValaIleSerLys 560

QY 1845 AAAACAGAACTACAGCAATTTTCCAGATGCTTAGCTTTCTTAATCTTACTCAAGATGAC 1904
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 561 GluGlnGluLeuLysArgHisPheProSerAsnLeuSerSerLeuAsnLeuThrArgAsnAsp 580

QY 1905 TTGGCTTGACTTGTTGAACACCAAGATTTCTTCGATATGATCAAGACCAAGGACGCTC 1964
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 581 PheAlaCysValCysGluHisGlnSerPheLeuGlnIleThrValLysAspGlnArgGlnLeu 600
  
```

QY 1965 TTGGTGAAGTTGAACGATGAGATGTGCACACCTTCAGATAGACGGGCGATCGCTGTG 2024
 Db 601 LeuValGluValGluGlnMetValCysAlaIysProLeuAspMetGlnGlyMetProMet 620
 QY 2025 CTGAGTTTG--AAATACACCTGTGCAGATGAATAAGCCATCATTTGGTGTGGTCTC 2081
 Db 621 LeuAspMetArgAspMetArgCysGlnValArgLysThrIleThrGlySerValPhe 640
 QY 2082 AGTGTCTGTGATGATCTGTGTAGACGATCTGTGTATTAAGTTCTATTTTCACTGATG 2141
 Db 641 ThrValLeuLeuValPheLeuValValValLeuValTyrLysPheTyrPheHisLeuMet 660
 QY 2142 CTTCCTGTGGCTGCATTAAGTATGTAGAGGTGAAGAACTATGATGCTTGTATTC 2201
 Db 661 LeuLeuAlaGlyCysLysLysTyrSerArgGlyGluSerThrTyrAspAlaPheValIle 680
 QY 2202 TACTCAAGCCAGATGAGACTGGGTAGAGATGAGCTAGTATTAAGATTTAGAAAGAGG 2261
 Db 681 TyrSerSerGlnAspGlnAspTyrValArgAsnGluLeuValLysAsnLeuGlnGly 700
 QY 2262 GTGCTTCATTTAGCTGTGCTCTTCACTACAGAGACTTTATCCCGGTGCGCATTCGT 2321
 Db 701 ValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 720
 QY 2322 GCCACATCATCCATGAGGTTTCCATTAAGCCGAAAGGTGATGTTGTGTGTCCTCAG 2381
 Db 721 AlaAsnIleIleGlnGlnGlyPheHisLysSerArgLysValIleValValSerGln 740
 QY 2382 CATTTCATCCAGAGCCGCTGTGTATCTTGAATATGAGATTGCTCAGACCTGCGAGTTT 2441
 Db 741 HisPheIleGlnSerArgTyrCysIlePheGlnTyrGlyIleAlaGlnThrTyrGlnPhe 760
 QY 2442 CTGAGAGTGTGCTGTATCATCTTCATTTGCTGTGAGAGAGGTTGAGAGACCTGCTC 2501
 Db 761 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeuGlyLysSerLeuLeu 780
 QY 2502 AGGACAGAGGTGAGCTGTATCCGCTTCTCAGCAGAGAACCTTACTGAGTGGAGAGAC 2561
 Db 781 ArgGlnGlnValGlnLeuTyrArgLeuLeuAsnArgAsnThrTyrLeuGlnTyrGlnAsp 800
 QY 2562 AGTGTCTGTGGGGCGGACATCTTCTGAGAGACCTCAGAAAGCCCTGTGATGTAA 2621
 Db 801 SerValLeuGlnTyrArgHisIlePheTyrArgArgLeuArgLysAlaLeuLeuAspGlyLys 820
 QY 2622 TCATGGAATCCAGAGGA 2639
 Db 821 ProArgCysProGlnGly 826

RESULT 11
 Q6MCD4 PRELIMINARY; PRT; 841 AA.
 AC Q6MCD4; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Toll-1-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.1333957100;
 RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.E.;
 RT "Haplotype variation in bovine Toll-1-like receptor 4 and computational
 prediction of a positively selected ligand-binding domain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
 DR EMBL; AY297043; AA062701.1; -
 DR EMBL; AY297041; AA062701.1; JOINED.
 DR EMBL; AY297042; AA062701.1; JOINED.
 DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003885; LRR_cyst.
 DR InterPro; IPR003591; LRR_tyrp.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF00560; LRR_1; 12.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO0019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00365; LRR_TYP; 1.
 DR SMART; SM00369; LRR_S022; 6.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KW Receptor.
 SQ SEQUENCE 841 AA; 95954 MW; ADSD06ACEF4CC91 CRC64;

Alignment Scores:
 Pred. No.: 6,54e-239 Length: 841
 Score: 3277.50 Matches: 637
 Percent Similarity: 82.25% Conservative: 86
 Best Local Similarity: 72.47% Mismatches: 115
 Query Match: 48.74% Indels: 41
 DB: 2 Gaps: 2

US-09-396-985b-3 (1-3811) x Q6MCD4 (1-841)

QY 45 ATGATGTCTGCTCGCGCTGTGCTGAGACTGTGATCCAGACCTGCTCTCTCTGC 104
 Db 1 MetMetAlaArgAlaArgLeuAlaAlaAlaLeuIleProAlaThrAlaIleLeuSerCys 20
 QY 105 GTGAGACCAAGAAAGCTGGGAGCCCTGCTGGAGACTTGCGCCCTAAACACAGAAAGAGC 164
 Db 21 LeuArgThrGluSerTyrAspProCysVal----- 30
 QY 165 TGCGATGAACAACCGAGACTTTCAGACTCGGAGCCTCAGCCTTCACCCGATTCATTG 224
 Db 30 ----- 30
 QY 225 CTTCCTGTAATATGCTGCCGCTTTTATCAGGAGGTGGTTCCTAATATTAATCAATGC 284
 Db 31 -----GlnValValProAsnIleSerTyrGlnCys 40
 QY 285 ATGAGACTGAATTTCTACAAAATCCCGCAACACTCCCTTCCACCAAGAACTGGAGC 344
 Db 41 MetGlnLeuAsnLeuTyrLysIleProAspAsnIleProIleSerThrLysMetLeuAsp 60
 QY 345 CTGAGCTTAATCCCTGAGAGCATTTAGAGCATATAGCTTCTTCAGTTTCCAGAACTG 404
 Db 61 LeuSerPheAsnTyrLeuArgHisIleGlnLysSerHisAsnPheSerSerPheProGlnLeu 80
 QY 405 CAGGTCTGATTTATTCAGGTGTGAATTCAGACAAATTGAAGATGGGCGATTCAGAGC 464
 Db 81 GlnValLeuAspLeuSerArgCysGlnIleLysIleIleGlnLysAspThrPheGlnGly 100
 QY 465 CTAAAGCACTCTCTTCACTTAATATGACAGAGAAACCCATCCAGAGTTTAAAGCCCTGGGA 524
 Db 101 LeuAsnHisLeuSerThrLeuLeuThrGlnLysAspProIleGlnSerLeuAlaIleAsn 120
 QY 525 GCCTTTTCTGACTATCAAGTTTACAGAGCTGGTGGTGGAGCAAAATCTAGACATCT 584
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuValSer 140
 QY 585 CTAGAGACTTCCCATTTGAGACTTCAAAATCTTGAAGAACTTAATATGAGCTCAAT 644
 Db 141 LeuAsnAspPheProIleGlnHisLeuLysAsnLeuLysGlnLeuAsnValAlaHisAsn 160
 QY 645 CTATTCATCATCTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGAGCACTTG 704
 Db 161 PheIleHisSerPheLysLeuPro****PheSerAsnLeuProAsnLeuGlnLysLeu 180
 QY 705 GACCTTTCAGACAACAAGATTCAAGTATTATTCACAGACTTGGGGTTCATCAATCA 764

Db 181 AspleSerAshbnshlylleglnAenllEtyrTyrGluAspValylsValleuHlsgln 200
Qy 765 ATGCCCTACTCAATCTCTTTAGACCTGTCCCTGAACCTTAGAACCTTTATCCAAACA 824
Db 201 MetProleuAenShSerleuAerleuSerleuAenProleuAenPheHlleglupro 220
Qy 825 GGTGCAATTAAGAAATTTAGGCTTCATAGCTGATTTAGAAATATTTGATAGTTA 884
Db 221 GlyThrPheylseGluileuylsleuAenGlyLeuThrleuAerSerAenPheAenSer 240
Qy 885 AATGATATGAAAATTTGATTTCAAGGCTGGCTGTTGAGAGTCAATGCTTGTCTG 944
Db 241 HisValMetCysThrCysHlleglnGlyleuAglGlyleuYsThrAsnAglleuValleu 260
Qy 945 GGAATATTAGAAATGAGAAATTTGAAAAGTTGACAATCTGCTTAGAGGGCTG 1004
Db 261 GlyGluPheylsAenGluAglGlyleuGlnAArgPheAspAerSerPheleuGluGlyLeu 280
Qy 1005 TGCAATTTGACCATGAGAAATCCGATTTAGCATTTAGCATTAACCTCGATGATAT 1064
Db 281 CysAsnleuThrHlleglnPheAglleuAlyleuAspYsPheSerGlyAspAer 300
Qy 1065 ATTAGCTATTTATTTGTTGACAAATGTTCTTCAATTTCCCTGGAGTGGTACTAT 1124
Db 301 ThrAspLeuPheAenCysleuAlyAenValSerValHlSerleuAenSerHlSerleu 320
Qy 1125 GAAAGGTTAAAGACTTTCTTATTAATTTGCAATGCGACATTTAGATTAAGTTAACTG 1184
Db 321 GlySerleuGlnHlaleuLeuYsAspPheAglTrpGlnHlAenGluHlleAenCys 340
Qy 1185 AATTTGAGACGTTCCCATTTGAAATGCAATCTCTCAAGGCTTACTTCACTGCC 1244
Db 341 AspPheAspYsPheProAlaleuYsleuSerSerleuYsYsPheValPheThrAsp 360
Qy 1245 AACAAAGTGGAGATCTTTTTCAGAAATGATCTACCAAGCCTTGAGTTCTAGATTC 1304
Db 361 AsnYsAspHlSerThrPheThrGlnPheGlnleuProSerleuGlnYrleuAerleu 380
Qy 1305 AGTAGAAATGCTTGAATTCAAAGGTTGCTGTTCTCAAGTATTTGGACACACGAC 1364
Db 381 LysAArgAenHlAenleuSerPheYsGlyCysCysSerHlAerAspPheGlyThrThrAsn 400
Qy 1365 CTAAAGATTTAGATCGAGCTTCATGAGTGTATTTACATGAGTTGAAAATCTTGAGG 1424
Db 401 LeuYsHlAenleuAenleuSerPheAenAspValHlThrleuGlySerAenPheMetGly 420
Qy 1425 TTAGAACAACTAGAACATCTGATTTCCAGATTTCCAAATTTGAAAACAAATGAGTGA 1484
Db 421 LeuGlnleuGlnHlAenleuAerPheGlnHlSerThrleuYsGlnHlAenAlAerPhe 440
Qy 1485 TCGATATTTCTATGACTGACGAAACCTGATTTACCTTGACATTTCTCATCTCACACAGA 1544
Db 441 SerAlAerleuSerleuAArgAenleuAglGlyrleuAspHlSerleuYrThrAsnHlAerG 460
Qy 1545 GTTGCTTCAATGAGCATCTTCAATGAGTGTGCGAGTCCAGTCCGAAGCTTGAATGGCTGC 1604
Db 461 HlValAerPheHlsglyHlPheThrGlyleuValSerleuGlnHlThrleuYsMetAlAglY 480
Qy 1605 AATTTCTTCCAGGAAATCTTCCATGATATTTCCAGAGCTGAGAAATTTGACCTTC 1664
Db 481 AsnSerPheGlnAenAenleuAenleuProAerHlPheThrGlyleuThrAenleuThrVal 500
Qy 1665 CTGACCTCTCTCAAGTCAACTGAGACAGTGTCTCCAAACAGCATTTAACTCATCTCC 1724
Db 501 LeuAerleuSerYsCysGlnleuGlnGlnValAlAglHlThrAlAerHlAerSerleuSer 520
Qy 1725 AGCTTTAGAGTAAATTAAGACCAACAACATTTCTTTGATGATAGCTTCTTAT 1784
Db 521 SerleuHlValleuAenMetSerHlAenYsleuAenleuSerleuAerThrPheleuYr 540
Qy 1785 AAGTGTGAACTCCCTCCAGGTTCTTGAATTAAGTCTCATGACATTAATGACTCCAAA 1844
::: |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||

Db 541 GluProleuHlSerleuAglleuAerPheCysSerPheAenAglleuAerAlAerYs 560
Qy 1845 AAAACGAACTACAGATTTTCCAGTAGTCTAGCTTCTTTAACTTACCTGACGATGAC 1904
Db 561 GlnGlnleuGlnAenleuProAerSerleuThrTrpLeuAenleuThrGlnAenAlA 580
Qy 1905 TTTGCTTGTACTTGTGACACACAGATTTCTCGCAATGATGATCAAGACACAGACCTC 1964
Db 581 PheAlAerYsValCysGlnHlsglnSerPheleuGlnTrpValYsAerPglAerGlnleu 600
Qy 1965 TTGTGGAAGTTGAAACGAAATGGAATGTCACACCTTCAATAGACAGGACCTGCTG 2024
Db 601 LeuValGlyAlAglGlnMetMetCysAlAgluproleuAerMetCylAspMetProAl 620
Qy 2025 CTGAGTTTG---AATTCACCTGTGACATGAATTAAGACCATGATTTGGTGGCTGC 2081
Db 621 LeuSerPheAArgAenAlAerCysGlnleuSerYsThrHlleSerValSerValVal 640
Qy 2082 AGTGTCTGTAGTATCTGTTGATGACGATTTGCTGCTATAGTTCTATTTTCACTGATG 2141
Db 641 ThrValleuAerValSerValGlyValleuValTyrlYsPheThrPheHlAerMet 660
Qy 2142 CTTTGTGCTGCTGCTAATAAGTAGTAGGTAAGTGAACATCTATGATGCTTTGTTATC 2201
Db 661 LeuAenAlAglCysYsYsYsYrGlyAArgGlyGlnSerHlTyrlAspAlAerValHl 680
Qy 2202 TACTCAAGCAGATGACGAGCTGGGTAAGATGAGTGTAGTAAGAAATTTAGAAAGAG 2261
Db 681 TyrSerSerGlnAspHlAspTrpValAArgAenGlnleuValYsAenleuGlnGlnY 700
Qy 2262 GTGCTCTCATTTCAAGCTGCTGCTTCACTACAGACATTTATTTCCGCTGGCCATGCT 2321
Db 701 ValProProPheGlnleuYsleuHlAerYrAArgAerPheHlAerGlyAlAerAlA 720
Qy 2322 GCCACATCATTCATGAAGCTTCCATTAAGCCGAAAGTGATTTGTGTGCTCCAG 2381
Db 721 AlAenHlHlleglnGlnGlnPheHlAerYsSerAArgYsValHlValValAerGln 740
Qy 2382 CACTGATCCAGACCGCGGTGATCTTGAATAGAGTGTCTGACAGCTGCGAGTTT 2441
Db 741 HisPheHlleglnSerAglTrpCysHlPheGlnTyrlleAglHlHlThrGlnPhe 760
Qy 2442 CTGAGACGTGTGCTGCTGATTCATCTTCAATGCTCTGACAGAGTGAGAAAGCTGCTC 2501
Db 761 LeuSerSerAArgAlAglYrleHlPheHlValleuGlnYsleuGlnYsSerleuAer 780
Qy 2502 AGCAGCAGGTGAGCTGTACCGCTTCTCAGCAGAAACATTAACCTGAGTGGAGGAC 2561
Db 781 ArgGlnGlnValGlnleuYrAArgleuAerSerAArgAenThrYrleuGlnTrpGlnAer 800
Qy 2562 AGTGTCTGGGGGCGGACATCTTCTGAGAGCAGCTGAGAAAGCCTGCGTGAATGGTAA 2621
Db 801 SerValleuGlyAArgHlValPheTrpAArgleuAerYsAlAerleuAlAglYs 820
Qy 2622 TCATGATCCAGAAAGAAACAGTGGGTACAGATGCAATTTGGACAGAAAGCAATCT 2678
Db 821 ProGlnSerProGlnGlyThrAlAerAlAgluThrAsnProGlnGlnAlAerThr 839
RESULT 12
TLR4_PIG ID TLR4_PIG STANDARD; PRT; 841 AA.
AC 068Y56;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE T011-like receptor 4 precursor.
GN Name=TLR4;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sui.
OX NCBI_TaxID=9823;
RN [1]
SEQUENCE FROM N.A.

RC TISSUE=Alveolus;
 RA Shinkai H.; Uenishi H.;
 RT "The function of porcine TLR4 gene."
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 1 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; AB188301; BAD36843.1; -.
 DR PROSITE; PS50104; TLR1.1.
 KW Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 841
 FT DOMAIN 24 632
 FT TRANSMEM 633 653
 FT DOMAIN 654 841
 FT REPEAT 53 76
 FT REPEAT 77 100
 FT REPEAT 102 124
 FT REPEAT 149 173
 FT REPEAT 174 197
 FT REPEAT 203 225
 FT REPEAT 277 300
 FT REPEAT 310 334
 FT REPEAT 350 372
 FT REPEAT 373 398
 FT REPEAT 400 421
 FT REPEAT 442 445
 FT REPEAT 446 469
 FT REPEAT 471 494
 FT REPEAT 495 518
 FT REPEAT 520 542
 FT REPEAT 544 566
 FT REPEAT 568 592
 FT DOMAIN 673 819
 FT CARBOHYD 35 35
 FT CARBOHYD 205 205
 FT CARBOHYD 238 238
 FT CARBOHYD 282 282
 FT CARBOHYD 309 309
 FT CARBOHYD 526 526
 FT CARBOHYD 575 575
 FT CARBOHYD 625 625
 SQ SEQUENCE 841 AA; 96308 MW; C52B2622D1C0E253 CRC64;

Alignment Scores:

Pred. No.: 1.37e-230
 Score: 3167.50
 Percent Similarity: 80.20%
 Best Local Similarity: 69.74%
 Query Match: 47.11%
 DB: 1
 Gaps: 2

US-09-396-985b-3 (1-3811) x TLR4_PIG (1-841)

QY 45 ATGATGTCGCTCGCGCTGGCTGGAGCTGTGATCCAGACCATGAGCTTCCTCTGCTG 104
 Db 1 MetiletrroalrgtleagtleuAlaValAlathrilletrroalmetAlaPheLeuSerCys 20
 QY 105 GTGAGACCAAGAAAGCTGGAGCCCTGGCTGGAGACTTGGCCCTTAACACAGAGAAAGC 164
 Db 21 LeuArgSerGluSerThrPaeProCysVal----- 30
 QY 165 TGGATGAAACCCAGACCTTCAGACTCCGAGGCTCAGGCCCTTACCCGATTCATTG 224
 Db 30 ----- 30
 QY 225 CTCTTGCTTAATGCTGCGCTTTATGACGAGGTGGCTCTATATTACTTAACTTAACTG 284
 Db 31 -----GlnValAlaProenilleSerTyrGlnCys 40
 QY 285 ATGAGCTGAATTTCACAAATCCCGACAACTCCCTTTCACACCAAGACCTGGAC 344
 Db 41 MetGluLeuAsnPhenTyrIleProAspAsnIleProThrSerValIleLeuAsp 60
 QY 345 CTGAGCTTAAATCCCGAGGCACTTGAAGCTATAGCTTTCAGTTCCCGAGACTG 404
 Db 61 LeuSerPheAsnTyrLeuSerThrIleAspSerAsnSerPheSerSerPheProGluLeu 80
 QY 405 CAGGTGCTGATTTATCCAGGTGGAATCCAGACATCCAGACATTAAGATGGGATATCAGAGC 464
 Db 81 GlnValLeuAsnPhenSerArgCysGlnIleGlnThrIleAspPheAsnAlaTyrGlnGly 100
 QY 465 CTAGCCACCTCTCTTAACTTAATATGACAGAAACCCATCCAGACTTAAAGCCCTGGGA 524
 Db 101 LeuAsnTyrLeuSerThrIleuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
 QY 525 GCGTTTTCGACTATCAATTTAAGAACTGGCTGGCTGGAGACAAATTCAGACTCT 584
 Db 121 AlaPheSerGlyLeuProSerIleGluValAlaValGlnThrAsnLeuAlaSer 140
 QY 585 CTAGAGACTTCCCATTTGAGACATCTCAAACTTTGAAGAACTTAATGTGCTCACAAT 644
 Db 141 LeuGluAspPheProIleGlyIleLeuIleThrLeuAsnGluLeuAsnValAlaHisAsn 160
 QY 645 CTATTCATCTTCAATTAATTAATCTGATATTTTCTTAATGTGACCAATTCAGACACTTG 704
 Db 161 HisIleHisSerPheIleuProGluTyrPheSerAsnLeuProAsnIleuGluHisIleu 180
 QY 705 GACCTTTCAGCAACAGATTCAAAGTATTATTTGACACAGACTTGGCGGTTTCATCAAA 764
 Db 181 AspLeuSerIleAsnIleGluAsnIleTyrHisGlnIleAsnGlnValIleuHisGln 200
 QY 765 ATGCCCTACTCAATCTCTTAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 824
 Db 201 ValProLeuHisAsnLeuSerIleuAspLeuSerIleuAsnProLeuAsnProIleGluPro 220
 QY 825 GGTGCAATTAAGAAATTAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 884
 Db 221 GlyAlaPheAsnIleuIleuGluAsnGlyLeuThrIleuArgSerPheAsnSer 240
 QY 885 AATGTAATGAAGAACTTGTATTCAGAGCTGCTGCTGCTTGAAGTCCATCGTTGGTCTG 944
 Db 241 AsnValMetCysThrCysIleGlnIleGlyLeuAlaGlySerValAsnGlnLeuValLeu 260
 QY 945 GAGGAATTTTGAAGTAAGAGAACTTGAAGAACTTGAAGAACTTGAAGAACTTGAAGAGGCTG 1004
 Db 261 GlyLeuPheLeuAsnGlnIleuGluAsnLeuGluSerPheAsnIleuGluGluLeu 280
 QY 1005 TGCATTTTGAAGTAAGAAATTCGATTAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGTAT 1064
 Db 281 CysAsnIleThrIleuGluGlnPheArgIleAlaHisPheIleuGluPheProAspArgVal 300
 QY 1065 ATTAGCTTATTTATTTGTTGACAAATGTTTCTTCAATTTTCCCTGGAGTGGACATAT 1124
 Db 301 SerAspLeuPheAsnIleuAlaAsnAlaSerValIleSerIleuLeuSerIleuAsnLeu 320
 QY 1125 GAAAGGTAAGAAAGCTTTCTTAATTAATTCGATGAGCAATTTAGAAATTAAGTAACTGT 1184


```

Db      321  HisGlyLeuGlu1aLeuProAsnAspPheArgTrpGlnHisLeuGluValaValaAsnCys 340
      1185  AAATTTGGACAGTTTCCACATTTGAACSTCAATCTCTCAAAAGGCTTACTTCACTTCC 1244
      341  LysLeuGlnGlnPheProAlaLeuLysPheAsnSerLeuLysPheValPheLysAsp 360
      1245  AACAAAGTGGAGATGCTTTTTCAGAGTGAATGATCTACCAAGCCCTGAGTTTCTAGATCTC 1304
      361  AsnLysHisMetHisThrPheThrGlnGlnLeuAsnLeuProAsnLeuGlnPheLeuAspLeu 380
      1305  AGTGAAGATGGCTTGAATTTCAAAAGTGTCTTCAAAAGTGAATTTTGGACACACAGC 1364
      381  SerGlyAsnHisLeuSerPheLysGlyCysCysSerHisAsnGlnPheGlyThrThrLys 400
      1365  CTAAAGATTTTGAATGCTGAGCTTCAATGAGTGTATTTATTCAGATGTTTCAAACTTGGGC 1424
      401  LeuLysHisLeuAspLeuSerPheAsnGlnGlnLeuThrMetLysSerAsnPheMetGly 420
      1425  TTAGAACAACSTAGAACATCTGATTTTCCAGCATTTCCATTTGAAACAAATAGTGAATT 1484
      421  LeuGlnGlnLeuGlnLysLeuAspPheGlnHisSerSerLeuLysGlnAlaAsnAspPhe 440
      1485  TCAATATTTCTATCTACATCAAGAACCTGATTTTACCTTGAATTTCTCACTACTACACCA 1544
      441  SerLeuPheLeuSerLeuArgAsnLeuHisThrLeuAspLysLeuSerTyThrAsnHis 460
      1545  GTTGCTTTCAATGGACATTTCAATGAGTGTCTCCAGCTGTCGAGTCAAAAGTGGCTGGC 1604
      461  ValValaPheArgGlyLeuPheAlaGlyLeuValaSerLeuGlnThrLeuLysMetAlaGly 480
      1605  AATTTCTTCCAGGAAACTTCTTCCAGATATTTTCAAGAGCTGAGAGCTTGAACCTTCC 1664
      481  AsnSerPheGlnAsnAsnLeuLeuProAspValPheThrAspLeuThrAsnLeuLeu 500
      1665  CTGAGACTCTCTCAGTGTCAACCTGAGAGCTGTCTCCAAACAGATTTAACTCACTTCC 1724
      501  LeuAspSerLeuLysCysGlnLeuGlnGlnValaSerGlnArgAlaPheHisSerLeuPro 520
      1725  AGCTTTCAGGTACCAATATATGAGCAGACAACTTCTTTCATTTGATGATGTTTCCCTAT 1784
      521  ArgLeuGlnValaLeuAsnMetSerHisAsnArgLeuLeuPheLeuAspThrLeuProTy 540
      1785  AAGTGTGTAACCTCCACAGTCTTGAATTTTACATGATCAATGATCAATGATGTTCCAA 1844
      541  LysProLeuHisSerLeuAlaGlyLeuAspCysSerTyThrAsnLeuLeuAlaSerLys 560
      1845  AAACAGGAACTACAGCATTTTCCAAAGTGTCTTGAATTTTAACTTACTCAGAAATGAC 1904
      561  GlnGlnGlnLeuGlnHisLeuProArgSerLeuAlaPheLeuAsnLeuThrLysAsnAsp 580
      1905  TTTGCTTGTACTTGTGAACACCAAGTCTTCTGAAATGATCAAGACCAAGGACACTC 1964
      581  PheSerCysAlaCysGlnHisGlnThrPheLeuGlnThrValLysAspGlnLysGlnLeu 600
      1965  TTGGTGAAGTGAACCAATGATGTGCAACACTTCAATGAAGAGGAGGAGTCTGTG 2024
      601  LeuValGlyAlaGlnGlnMetValCysThrGlnPheLeuGlnMetGlnAspLeuProVal 620
      2025  CTGAGATTG--AATATCACCTGTGAGATGAATGAACATCATTTGTTGTGTGGTCTC 2081
      621  LeuSerPheArgAsnAlaThrCysGlnHisSerGlnAlaValHisSerAlaSerValLeu 640
      2082  AGTGTGTTGATGATCTGTTTGTAGACAGTCTGTCTATTAAGTTCTATTTTCACTGATG 2141
      641  ThrPheLeuLeuValSerValAlaGlyLeuValLysPheTyThrPheHisLeuLeu 660
      2142  CTCTCTGCTGCTGCTCAATAAGTATGTAGAGTGAAGAAACATCTTATGCTTGTATGTC 2201
      661  LeuPheValGlyCysLysLysTyGlyArgGlyLysSerThrTyThrAlaPheValIle 680
      2202  TACTCAAGCAGAGATGAGACTGGGTAAAGAAATGAGCTAAGAAATTTAGAAAGAGG 2261

```

```

Db      681  TyrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGly 700
      2262  GTCCTTCATTTCAAGCTGTGCTTCACTCACTACAGAGACTTATTTCCCGTGTGGCATTTGCT 2321
      701  ValProProPheHisLeuCysLeuHisThrArgAspPheIleProGlyValAlaIleAla 720
      2322  GCCAATCATATCCATGAAGGTTTCCATTAAGCCGAAAGGTGATTTGTGTGCTCCAG 2381
      721  AlaAsnIleIleGlnGlnGlyPheHisLysSerArgLysValIleValValaValSerGln 740
      2382  CACTTATTCAGAGCCGCTGTGTATCTTGTGAATATGAATTTCTGACACCTGGCAGTTT 2441
      741  HisPheIleGlnSerArgTrpCysIlePheGlyTyGlnIleAlaGlnThrTrpGlnPhe 760
      2442  CTGACAGCTGCTGTATCATCTTCAATGCTTCTCAGAGGTGAGAGAGACCTGTCTC 2501
      761  LeuArgSerHisAlaGlyIleIlePheIleValLeuGlnLysLeuGlnLysSerLeuLeu 780
      2502  AGGACAGGTGAGCTGTACCGCTTCTCAGACAGAACATTTACTGAGTGGAGAGAC 2561
      781  ArgGlnGlnValGlnLeuTyThrArgLeuLeuSerArgAsnThrTyThrLeuGlnTrpGlnAsp 800
      2562  AGTGTCTGTGGCGGCGACATCTTCTGAGACACACTCAAGAAAGCCCTGTGATGTTAA 2621
      801  SerValLeuGlyArgHisIlePheTrpArgArgLeuLysAlaLeuLeuAspGlyLys 820
      2622  TCATGGAATCCAGAAAGAACAGTGGGTACAGATGCAATTTGGACGAGAACACATCT 2678
      821  ProTrpSerProGlnGlyThrGlnAspSerGlnSerGlnHisAspThrThrAla 839

RESULT 13
ID      08MI02      PRELIMINARY;      PRT;      839 AA.
AC      08MI02;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      TOLL-like receptor 4.
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Kajikawa O., Frevort C.W., Goodman R.B., Wong V.A., Martin T.R.;
RL      Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AI101394; AA050060.1; -.
DR      HSSP; O60603; 1077.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR000483; LRR_Cterm.
DR      InterPro; IPR003591; LRR_Cyp.
DR      Pfam; PF00560; LRR_1; 11.
DR      Pfam; PF01582; TIR; 1.
DR      PRINTS; PR00019; LEURICHRPT.
DR      SMART; SM00082; LRCT; 1.
DR      SMART; SM00369; LRR_TYP; 1.
DR      SMART; SM00255; TIR; 1.
DR      PROSITE; PS50104; TIR; 1.
KW      Receptor.
SQ      SHQUNCE 839 AA; 96338 MW; 09F7D401EC14B6A CRC64;

Alignment Scores:
Pred. No.:      2,09e-223
Score:          3072.50
Percent Similarity: 78.89%
Best Local Similarity: 69.35%
Query Match:    45.69%
DB:             2
Gaps:           4

```

US-09-396-985b-3 (1-3811) x Q8MI02 (1-839)


```

Db 678 IletySerSerGlnAspGluAspTrpValArgAsnGluLeuValLysAsnLeuGluGlu 697
Qy 2259 GGGGTGCTTCATTCATTCAGCTCTGCTTCATTCAGAGACTTTATCCCGGTGGCCATT 2318
Db 698 GLYVALProProPheArgLeuCySLeuHISLYArgAspPheIleProGlyValAlaIle 717
Qy 2319 GCTGCCAAGCATCATCCATGAAGGTTTCCATAAAGCCGAAGGATGTGTGGTGTC 2378
Db 718 AlaAlaAsnIleIleGlnGlnGlyPheHISLeuSerArgLysValIleValValSer 737
Qy 2379 CAGACATTCATCCAGAGCCGCTGGTGTATTTGAATATAGATTGCTGACCTGGCAG 2438
Db 738 GlnHISpHeIleGlnSerArgTrpCySLeuPheLurGluIleAlaGlnTrpGln 757
Qy 2439 TTTCTGAGCAGTGTGCTGTATCATTTTCATTTCTCTGAGAGAGGTGGAGAACCTG 2498
Db 758 PheLeuSerSerHISAlaGlyIleIlePheIleValLeuGlnLysValGlnLysSerLeu 777
Qy 2499 CTCAGGAGAGAGGTGGAGCTGTACCGCTTCAGAGAGAACTTACCTGAGTGGAG 2558
Db 778 LeuArgGlnArgValGluLeuTrpArgLeuLeuSerArgAsnTrpLysGluTrpGlu 797
Qy 2559 GACAGTGTCTGGGGCGGACATCTTCTGAGAGAGACTCAGAAAGCCCTGTGATGT 2618
Db 798 AspPheValLeuGlyArgHISLeuPheTrpArgArgLeuArgLysAlaLeuLeuAspGly 817
Qy 2619 AAATCATGATCATCAGAGAGAAAGAGTGGGTACAGAGATGATTCGCGAGAGCACTCT 2678
Db 818 LysThrLeuSerProGlnGluMetAlaArgAlaGluAsnGlnGlnAlaMetThr 837
Qy 2679 ATC 2681
Db 838 Leu 838

RESULT 14
TLR4_CRIGR STANDARD; PRT; 838 AA.
ID TLR4_CRIGR
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Cricetus griseus (Chinese hamster).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_Taxid=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RX MEDLINE=2014868; PubMed=10683379;
RA Lien B., Means T.K., Heine H., Yoshimura A., Kusumoto S., Fukase K.,
RA Penton M.J., Oikawa M., Qureshi N., Monks B., Finberg R.W.,
RA Ingalls S.R., Golenbock D.T.;
RT "Toll-like receptor 4 imparts ligand-specific recognition of bacterial
RT lipopolysaccharide."
RL J. Clin. Invest. 105:497-504(2000).
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
CC their respective TIR domains.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- TISSUE SPECIFICITY: Detected in macrophages and the Chinese
CC hamster ovary fibroblast cell line.
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.

```

```

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AF153676; AAD41891.1; -.
DR HSSP; Q15399; IPTV.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01562; TIR; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00369; LRR_TYP; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KW Glycoprotein; Immune response; Inflammatory response;
KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 838
FT DOMAIN 26 629
FT TRANSMEM 630 650
FT DOMAIN 651 838
FT REPEAT 31 52
FT REPEAT 53 75
FT REPEAT 76 99
FT REPEAT 100 123
FT REPEAT 127 148
FT REPEAT 149 172
FT REPEAT 173 196
FT REPEAT 200 224
FT REPEAT 227 251
FT REPEAT 305 330
FT REPEAT 351 370
FT REPEAT 371 393
FT REPEAT 396 419
FT REPEAT 420 443
FT REPEAT 468 492
FT REPEAT 494 516
FT REPEAT 517 538
FT REPEAT 541 563
FT REPEAT 565 589
FT REPEAT 670 816
FT DOMAIN 34 816
FT CARBOHYD 34 34
FT CARBOHYD 115 115
FT CARBOHYD 172 172
FT CARBOHYD 204 204
FT CARBOHYD 237 237
FT CARBOHYD 307 307
FT CARBOHYD 492 492
FT CARBOHYD 495 495
FT CARBOHYD 524 524
FT CARBOHYD 524 524
FT CARBOHYD 572 572
FT CARBOHYD 622 622
SQ SEQUENCE 838 AA; 96277 MW; 129B33596B908B48 CRC64;

Alignment Scores:
Pred. No.: 6.13e-217
Score: 2987.00
Percent Similarity: 78.84%
Best Local Similarity: 66.10%
Query Match: 44.42%
DB: 1 Gaps: 5

US-09-396-985b-3 (1-3811) x TLR4_CRIGR (1-838)
Qy 45 ATGATGTCCTGCTGGGCTGCTGAGACTGATCCAGCAGTGGCTTCCTCTCTGCTG 104

```

```

Db      1 MetMetProSerPheCysLeuAlaGlyThrLeuMetAlaLeu---PheLeuSerSer 19
      105 GTGAGACCAAGAGGAGGAGCCGTGGGTGAGACTTGCCCTTAACACACAGAGAAGC 164
      20 LeuArgProGluSerLeuAspProCysVal----- 29
      165 TGGCATGAAACCCAGAGCTTTCAGACTCCGAGGCTCAGCCCTTACCCCGATTTCATTG 224
      29 ----- 29
      225 CTTCTTGCTAATGCTGCCGTTTATACGAGAGGTGTTCTTAATATTACTTATCATGC 284
      30 -----GluValAspSerAsnThrSerTyGlnCys 39
      285 ATGAGCTGAATTTCTCAAAATCCCGACAACTCCCTCTGCAACCAAGAACTGAC 344
      40 MetAspArgAsnLeuAsnLysIleProAspAsnIleProSerSerValLysHisLeuAsp 59
      345 CTGAGCTTTAATCCCTGAGGCAATTGAGCAGTATAGCTTCTTCAAGTTTCCAGAACTG 404
      60 LeuSerPheAsnProLeuLysThrLeuGlySerHisSerPheAsnPheProGluLeu 79
      405 CAGGTGCTGATTTATCCAGGTGGAATTCAGACAATTGAAGATGGGCAATATCAGAC 464
      80 LysLeuLeuAspLeuSerArgCysGluIleGluThrIleGluAspLysAlaTyGlnGly 99
      465 CTAGACCACTCTCTACTTAAATATATGACAGAAACCCCATCCAGAGTTTACCCCTGGA 524
      100 LeuHisGlnLeuThrIleThrLeuIleLeuThrIleGluAsnProIleGlnAsnLeuSerLysGly 119
      525 GCTTTTCTGAGACTATCAAGTTTACAGAAAGCTGGGCTGGAGACAAATCTAGACTCT 584
      120 ThrPheSerGlyLeuAlaAsnLeuGlnAsnLeuValAlaValGluIleLysLeuAlaSer 139
      585 CTAGACCACTTCCCATTTGACATCTCAAACTTTGAAGAAGCTTAATGTGGCTCACAAT 644
      140 LeuAspSerLeuProIleGlyHisLeuValThrLeuLysLysLeuAsnValAlaHisAsn 159
      645 CTTATCCAACTTTCAAAATTAACCTGAGATTTTCTAATCTGACCAATCTAGACACTTG 704
      160 LeuIleHisSerPheLysLeuProGluLysPheSerAsnLeuThrAsnLeuGlnHisLeu 179
      705 GACCTTTCAGACCAAGATTCAGAGTATTATATGACAGACTGGCGGTTCTCATCA 764
      180 AspLeuSerAsnAsnIleGlnThrIleGlyTyThrAspLeuGlnThrLeuArgGlu 199
      765 ATGCCCTACTCAATCTCTCTTTAGACCTGTCCCTGAACCTTGAACCTTATCAACA 824
      200 AsnProGlnLeuAsnLeuSerLeuGlnLeuSerLeuAsnProIleAspPheIleGlnPro 219
      825 GGTGCTATTAAAGAAATTAAGCTTCAAGCTGACCTTAAGAAATTAATTTGATAGTTTA 884
      220 GlyAlaPheGlnGlyIleArgLeuHisGlnLeuThrLeuArgSerAsnPheAsnSerThr 239
      885 AATGTAATGAAGAACTTGATTAACAAGTCTGCTGTTTGAAGTCAATCGTTGGTCTG 944
      240 AsnValIleCysIleHisAsnLeuAspGlyLeuGlnValHisAspGluIleLeu 259
      945 GAGAAATTTGAATGAAGAACTTGAAGAAAGTTTGAACAATGTGCTTAGAGGCTG 1004
      260 GlyGluPheLysAsnGluArgAsnValGluArgPheAspArgLysValIleGluGlyLeu 279
      1005 TGCATTTGACATTTGAAGAAATTCGATAGCATATTGAACATACTACCTCGATGATATT 1064
      280 CysLysValThrIleGluGluPheArgPheThrTyAlaAsnGluPheSerGlnAspIle 299
      1065 ATTACTTAATTAATGTTTGAACAATGTTTCTCATTTCCCGGAGAGTGCATATT 1124
      300 ThrAsp--PheAspCysLeuAlaAsnValSerAlaMetSerLeuAlaAsnValTyLeu 318
      1125 GAAAGGTAAAGACTTTTCTTATATTTGCGATGCGAACATTTAGATTAGTACTGT 1184
      :::::

```

```

Db      319 LysArgLeuGluAspIleProLysTyPheLysTrpGlnThrLeuAlaValIleArgCys 338
      1185 AATTTGACAGTTTCCCAATTGAACCTCAAAATCTGCAAAAGGCTTACTTCACTCC 1244
      339 GluLeuLysGlnPheProProLeuGluLeuProPheLeuLysAspGluIlePheIleThr 358
      1245 AACAAAGGTGGAATGCTTTTTCAGAAATTGATCTCAACAGCTTGAGTTTCTAGATCTC 1304
      359 AsnLysGlyAlaThrSerPheProGluValAsnLeuProSerLeuThrPheLeuAspLeu 378
      1305 AGTGAATATGCTTGAAGTTTCAAAAGTGTCTGTTCTCAAAAGTATTTTGGGACACACAGC 1364
      379 SerGlyAsnGlyMetSerPheArgGlyCysCysSerTyThrAspLeuGlyAlaArgSer 398
      1365 CTAAAGTATTTAGATCGAGCTTCAATGAGTTTATCAATGATTCAAATCTTGAGGC 1424
      399 LeuLysHisLeuAspLeuSerPheAsnGlyValIleSerMetSerGluAsnPheMetGly 418
      1425 TTAGAACACTAGAACATCTGATTTCCAGACTTCCAAATTTGAACAATGAGTACTTT 1484
      419 LeuGluGlnLeuGluLysThrLeuAspPheGlnHisSerThrLeuLysLysAlaThrGluPhe 438
      1485 TCAATATTTCTATCACTCAAGAAACCTGATTTACTTCAATTTCTCATCTACACACAGA 1544
      439 SerMetPheLeuProLeuGluGlyLysLeuLeuTyThrLeuAspIleSerTyThrAsnThrLys 458
      1545 GTTCTTTCAATGAGCACTTTCATGCTGTGCTTCCAGTGTCCAGAGCTTGAAGTGAAGTGGCGC 1604
      459 IleAspPheAsnGlyIlePhePheGlyLeuThrSerLeuAsnThrLeuLysMetAlaGly 478
      1605 AATCTTTCAGACAAATCTCTCCAGATATCTTCAAGAGCTGAGAACTTGACCTTC 1664
      479 AsnSerPheLysAspAsnIleLeuSerAsnValPheThrAsnThrAsnLeuThrPhe 498
      1665 CTGACCTCTCTCAAGTCACTGAGACAGTGTCTCCAAACAGATTAACTCATCTCC 1724
      499 LeuAspIleSerLysCysGlnLeuGlnGlnValSerTrpGlyValPheAspThrLeuHis 518
      1725 AGCTTCAGGTACTAAATATAGAGCCCAACAACCTTCTTCAATGATAGTTCCTTAT 1784
      519 ArgLeuGlnIleLeuAsnMetSerHisAsnAsnLeuLeuLeuAspLeuPheHisTy 538
      1785 AAGTGTGTAACCTCCCTCCAGGTTCTTGATTTAAGCTTCATGACATAGATGATCCAAA 1844
      539 LysGlnLeuHisSerLeuLysThrLeuAspCysSerPheAsnHisIleGluThrSer--- 557
      1845 AAACAGGAACCTACAGCAATTTTCAAGTAGTCTAGCTTTCTTAATCTTACTCAGAAATGAC 1904
      558 LysGlyLysLeuGlnHisPheProLysSerLeuAlaPheLeuAsnLeuThrAsnAsnPro 577
      1905 TTTGCTTGATCTTGTAACACCAAGATTTCTGCAATGATCAAGACCAAGGACAGCTC 1964
      578 PheAlaCysIleCysGlnHisGlnAsnPheLeuGlnThrValLysAspGlnArgLeuPhe 597
      1965 TTGCTGGAATTTGAAGAAATGAATGCAACCTTCAATGAAGCAAGGAGGATCCCTGTG 2024
      598 LeuValLysThrGluGlnMetThrCysAlaThrProValGluMetLysAspSerLeuVal 617
      2025 CTGAGTTT---AATATCACTGTTCAGATGATGAATGAACATGATGCTGTGCTGCTC 2081
      618 LeuAspPheArgAsnAlaThrCysTyValGlnLysThrIleIleSerValSerValIle 637
      2082 AGTGTGCTTGATGATCTGTGTGAGCAATTCGCTGTATAGTTTCAATTTTCACTGATG 2141
      638 SerValLeuValAlaSerThrIleAlaPheLeuValTyTrpAspPheTyPheHisLeuIle 657
      2142 CTTCTTGGCTGCTGCAATAAGTATGAGTGAAGGAAACCTATGATGCTTGTGATC 2201
      658 LeuIleAlaGlyCysLysTySerArgGlyGlnSerIleTyTrpAlaPheValIle 677
      2202 TACTCAAGCCAGATGAGCACTGGTGAAGAAATGAGCTAGTGAATTAAGATTAAGAGAGG 2261
      678 TyrSerSerGlnAspGluAspTrpValArgAsnGluLeuValLysAsnLeuGluGlnGly 697

```


QY 225 CTTCTGCTAAATGCTGCGCTTTTATGACGAGGTGGTTCCTAATATTATTAATGATGC 284
 DB 30 -----GluValLeuProAsnIleThrTyrGlnCys 39
 QY 285 ATGAGAGCTGAATTTCTACAAAATCCCGACAACTCCCTTCTGACCAAGAACCTTGAC 344
 DB 40 MetAspGlnAsnLeuSerLysIleProIleAspIleProTyrSerThrLysAsnLeuAsp 59
 QY 345 CTGAGCTTTAATCCCGTGGAGCATTTAGGACGCTTATAGCTTTCAGTTCCCGAAATCG 404
 DB 60 LeuSerPheAsnProLeuLysIleLeuArgSerTyrSerPheThrAsnPheSerGlnLeu 79
 QY 405 CAGGTGCTGATTTATCCAGGTGTGAATCCAGACAAATTGAAGATGGGACATATCAGAGC 464
 DB 80 GlnThrLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspLysValaThrPheGly 99
 QY 465 CTAGAGCACTCTCTACCTTAATATATGACAGAAACCCCATCCAGAGTTTAGCCCTGGGA 524
 DB 100 LeuAsnGlnLeuSerThrLeuValIleuThrGlyAsnProIleLysSerPheSerProGly 119
 QY 525 GCGCTTTCTGACATATCAAGTTTACAGAGCTGGTGGTGGAGCAAACTTGACATCT 584
 DB 120 SerPheSerGlyLeuThrAsnLeuGlnAsnLeuValAlaValGlnThrLysMetThrSer 139
 QY 585 CTAGAGAACTTCCCGCATCTGACATCTCAAACTTTGAAAGAACTTAATGGCTGACAAAT 644
 DB 140 LeuGlnIlePheAsnIleGlyGlnLeuIleSerLeuLysValAsnValAlaIleAsn 159
 QY 645 CTATTCGAATCTTTCAAAATTAACCTGAGTATTTTCTAATGACCAATCTAGACACTTG 704
 DB 160 LeuIleIleSerPheLysLeuProGlnTyrPheSerAsnLeuThrAsnLeuGlnIleVal 179
 QY 705 GACCTTTCCAGCAACAAGATTCAGATTTTATTTGACACAGCTTCCGGGTTCTACATCA 764
 DB 180 AspLeuSerTyrAsnTyrIleGlnThrIleSerValLysAspLeuGlnPheLeuArgGln 199
 QY 765 ATGCGCCCTACATCTCTCTTTAGACCTGCGCCCTGAAACCTTAGAATTTATCAACA 824
 DB 200 AsnProGlnValAsnLeuSerLeuAspLeuSerLeuAsnProIleAspSerIleGlnAla 219
 QY 825 GGTCGATTTAAAGAAATTAAGCTTCATAGCTGACCTTAAGAAATTAATTTGATAGTTTA 884
 DB 220 GlnIlePheGlnGlyIleArgLeuIleGlnLeuThrIleuArgSerAsnPheAsnSerSer 239
 QY 885 AATGATATGAAAATCTGTATTCAAGGTCTGCTGGTTAGAGTCCATCGTTGGTTCTG 944
 DB 240 AsnValLeuLysMetCysLeuGlnAsnMetThrGlyLeuIleValIleAspLeuIleLeu 259
 QY 945 GAGAAATTTGAATGAAGAACTTGAAAGAAATTTGAACAATTTGCTCTAGAGGGCTG 1004
 DB 260 GlyGlnPheLysAsnGlnArgAsnLeuGlnSerPheAspArgSerValMetGlnGlyLeu 279
 QY 1005 TGCAAATTTGACATGGAAGATTCGATAGCATATGACATGACATCTCTGATGATATT 1064
 DB 280 CysAsnValSerIleAspGlnPheArgLeuThrTyrIleAsnIlePheSerAspAspIle 299
 QY 1065 ATTGACTTATTTAATTTGTTGACAAATGTTTCTTATTTCCCTGGAGTGTGACATATT 1124
 DB 300 TyrAsnLeu--AsnCysLeuAlaAsnIleSerAlaMetSerPheThrGlyValAlaIle 318
 QY 1125 GAAAGGTAAGAACTTTTCTTAATTTGCGATGGAACAATTGAAATTAAGTTAGTAACGT 1184
 DB 319 LysIleIleAlaAspValProArgIlePheLysThrGlnSerLeuSerIleIleArgCys 338
 QY 1185 AAATTTGACAGTTTCCACATTTGAAATCTCAAAATCTGCAAAAGCTTACTTTGACATCC 1244
 DB 339 HisLeuLysProPheProLysLeuSerLeuProPheLysSerTrpIleuThrThr 358
 QY 1245 AACAAAGGTGGGAATGCTTTTTCAGAAATGATGATCCAGAGCTTTGAGTTCTAGATCTC 1304
 DB 359 AsnArgGlnAspIleSerPheGlyGlnLeuAlaLeuProSerLeuArgTyrLeuAspLeu 378

QY 1305 AGTAAAGATGCTGAGATTTCAAAAGTTCGTGTTCTCAAGATGATTTGGGACACAGC 1364
 DB 379 SerArgAsnAlaMetSerPheArgGlyCysCysSerTyrSerAspPheGlyThrAsnAsn 398
 QY 1365 CTAAAGTATTTAATGCTGACCTTCATAGTGTTATTTACATGAGTTCAAACTTTGGGC 1424
 DB 399 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleLeuMetSerAlaAsnPheMetGly 418
 QY 1425 TTGAAACAATGACATGACATGATTTCCAGATTTCCAAATTTGAAACAAATGAGAGATT 1484
 DB 419 LeuGlnIleuGlnTyrLeuAspPheGlnIleSerThrLeuLysValIleGlnPhe 438
 QY 1485 TCAGTATTTCTATCACTACAGAAACCTCATTTTACCTTGACATTTCTCTACTACACAGA 1544
 DB 439 SerValPheLeuSerLeuGlnLysValLeuLysThrLeuAspIleSerTyrThrAsnThrLys 458
 QY 1545 GTTGCTTTCAATGGCATCTTCAATGGCTTGTCCAGTCTGCAAGTCTTGAATGGCTGGC 1604
 DB 459 IleAspPheAspGlyIlePheLeuGlyLeuIleSerLeuAsnThrLeuLysMetAlaGly 478
 QY 1605 AATTTCTTCCAGAAAATTCCTTCCAGATATCTTCCAGAGCTGAGGAGAACTTGACCTTC 1664
 DB 479 AsnSerPheLysAspAsnThrLeuSerAsnValPheThrAsnThrThrAsnLeuThrPhe 498
 QY 1665 CTGAGACCTCTCTCAGTGTCAACTGAGACAGTGTCTTCCACAGCATTTAATCTACTCTCC 1724
 DB 499 LeuAspLeuSerTyrCysGlnLeuGlnIleIleSerArgGlyValPheAspThrLeuTyr 518
 QY 1725 AGTCTTCAAGTAAATATATGAGCCACACAACTCTTTTCAATGATGATAGCTTCTTAT 1784
 DB 519 ArgLeuGlnIleuLeuAsnMetSerThrAsnAsnLeuLeuPheLeuAspProSerHisTyr 538
 QY 1785 AAGTGTCTGAATCCCTCCAGCTTCTGATTTAAGTCTGTACATGACATGAATGATCCAA 1844
 DB 539 LysGlnLeuLysTyrLeuLeuArgThrLeuAspCysSerPheAsnArgIleGlnThrSer-- 557
 QY 1845 AAACAGGAATCTACAGCATTTTCCAAAGTGTCTAGCTTTCTTAATCTTACTACAGATGAC 1904
 DB 558 LysGlyLysIleuGlnIlePheProLysSerLeuAlaValPheAsnLeuThrAsnAsnSer 577
 QY 1905 TTGCTTGTATCTGTGAACACAGAGTTCCTGCAATGATGATCAAGACACAGGACACTC 1964
 DB 578 ValAlaCysIleCysGlnTyrGlnAsnPheLeuGlnThrValLysAspGlnLysMetPhe 597
 QY 1965 TTGCTGAATGTGAACAAATGGAATGGAACAACCTTCAATGATGACAGGGCATCTGTC 2024
 DB 598 LeuValAsnValGlnGlnMetLysCysAlaSerProIleAspMetLysAlaSerLeuVal 617
 QY 2025 CTGAGTTTG--AATATCACTGTGACAGATGAATGAAGCATCATTTGGTGTGCTGCTC 2081
 DB 618 LeuAspPheThrAsnSerThrCysTyrIleTyrLysThrIleIleSerValSerValVal 637
 QY 2082 AGTGTGCTTGTAGTATCTGTGTAGACAGTTCTGCTGTATAGTTCTAATTTTCACTGATG 2141
 DB 638 SerValLeuValValAlaThrValAlaPheLeuIleTyrHisPheTyrPheHisLeuIle 657
 QY 2142 CTTCTGTGCTGCTGCAATGAATGATGATGAGAGGAAACATGATGATGCTTGTATGCT 2201
 DB 658 LeuIleAlaGlyCysLysLysTyrSerArgGlyGlnSerIleTyrAspAlaPheValIle 677
 QY 2202 TACTCAAGCAGAGATGAGACTGGGTGAAGAAAGAGCTAGTAAAGAAATTTGAAGAAAGG 2261
 DB 678 TyrSerSerGlnAsnGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlnGly 697
 QY 2262 GTGCTTCATTTCACTGTGCTCTTCACTACAGACATTTATTTCCGGTGTGCGCATTTGCT 2321
 DB 698 ValProArgPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 717
 QY 2322 GCCAATCATCATGAAAGTTTCCATTAAGCGGAAAGGATGATGTTGTGTGGTGTGCCAG 2381
 DB 718 AlaAsnIleIleGlnGlnGlyPheHisLysSerArgLysValIleValValIleSerArg 737
 QY 2382 CACTTATCCAGAGCGCTGTGATCTTTGAATATGATGATGCTCAGACCTGCGACGTTT 2441

Db	738	H	i	s	t	p	e	l	e	g	i	n	s	e	r	a	r	g	t	r	p	c	a	l	e	p	e	g	u	r	g	u	i	e	a	g	i	n	t	r	p	g	i	n	p	e		757			
Qy	2442	C	T	G	A	C	A	C	T	C	G	T	G	T	A	T	A	T	T	C	T	T	C	C	T	G	A	G	A	G	T	G	A	A	A	C	C	T	G	T	C		2501								
Db	758	L	e	u	s	e	r	S	e	r	G	e	r	G	Y	I	e	l	e	h	e	l	e	v	a	l	e	u	g	u	y	S	e	r	G	u	y	S	e	r	L	e	u	e	n		777				
Qy	2502	A	G	G	C	A	G	A	G	T	G	A	C	T	T	A	C	C	G	C	T	T	T	C	A	G	A	G	A	A	C	A	C	T	T	A	C	T	G	A	G	T	G	A	G	A	C		2561		
Db	778	A	r	g	i	n	g	i	n	a	l	G	l	u	e	u	r	A	r	g	p	e	u	S	e	r	A	r	g	a	n	t	r	T	Y	L	e	u	G	i	n	T	r	p	g	i	a	s	p		797
Qy	2562	A	G	T	G	C	T	G	G	G	C	G	C	A	C	A	T	C	T	T	C	T	G	A	G	A	G	A	A	A	A	C	C	T	G	T	G	A	T	G	T	A	A		2621						
Db	798	A	s	n	a	l	a	u	e	u	G	Y	A	r	g	H	i	e	p	h	e	r	T	r	p	r	g	r	g	u	e	u	S	Y	S	a	l	a	u	e	u	L	e	a	S	p	G	Y	S		817
Qy	2622	T	C	A	T	G	A	T	C	C	A	G	A	G	A	A	C	A	G	T	G	G	T	C	A	G	A	T	G	C	A	A	T	T	G	C	A	G	A	A	A	C	A	T	A	T	C		2681		
Db	818	A	l	a	l	e	u	a	n	a	n	P	r	o	A	S	-----	G	l	u	T	S	e	r	G	l	u	g	i	n	g	u	g	i	n	g	u	a	l	a	t	H	-----	834							

Search completed: March 29, 2005, 17:28:15
Job time : 280.959 secs


```

XX DR WPI; 2003-040607/03.
XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1439; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and
XX polynucleotides are particularly useful for treating or preventing
XX myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX lymphoma or leukemia. These are also useful for screening agents for
XX treating the above mentioned diseases. This sequence represents an
XX expressed protein tag (EPT) isolated from human tissue for translational
XX profiling. Note: This sequence does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 839 AA:
XX
XX Alignment Scores:
XX Pred. No.: 2,7e-303 Length: 839
XX Score: 2792.00 Matches: 557
XX Percent Similarity: 79.35% Conservative: 100
XX Best Local Similarity: 67.27% Mismatches: 166
XX Query Match: 53.93% Indels: 6
XX DB: Gaps: 4
XX
US-09-396-985b-46 (1-2951) x ABU04773 (1-839)
XX
XX 208 ATGATGCTCCCTGCTCTGCTAGAGACTGTGATGACATG--TTCTTCTCTGTC 264
XX 1 MetMetSerAlaSerAlaGluAlaGlyThrIleuIleProAlaMetAlaPheLeuSerCys 20
XX
XX 265 CTGACACAGAGACTTGAAATCCCTGATAGAGTACTTCTTATATATACCTACATGC 324
XX 21 ValArgProGluSerTrpGluProCysValGluValAlaProAsnIleThrTyrGlnCys 40
XX
XX 325 ATGATGACGAAACTCAGCAAAAGTCCCTGATGACATTCCTTCTGCAACCAAGACATAGAT 384
XX 41 MetGluLeuAsnProPheTyrIleProAspAsnLeuProPheSerThrIlyAsnLeuAsp 60
XX
XX 385 CTGAGCTTCAACCCCTTGAGAGATTTTAAAAAGCTTAGCTTCTCCAAATTTTCAGAATT 444
XX 61 LeuSerPheAsnProLeuArgGlnIleGlnGlySerTyrSerPhePheSerPheProGluLeu 80
XX
XX 445 CAGGCGGTGATTTATCCAGGTGTAATGAAATTGAAACATTTGAAAGCAAGGATGGCATGGC 504
XX 81 GlnValIleuAspLeuSerArgCysGlnIleGlnThrIleGlnIleAspGlyAlaTyrGlnSer 100
XX
XX 505 TTACACCACTCTCAAACTTGATATGACAGAAACCTTATCCAGAGTTTTCCTCCAGGA 564
XX 101 LeuSerIleLeuSerThrIleuIleLeuThrGlyAsnProIleGlnIleuAlaLeuGly 120
XX
XX 565 AGTTTCTCTGAGTCAACAGTTTGAACAATCTGGTGGCTGTGAGACAAAATTTGGCTCT 624
XX 121 AlaPheSerGlyLeuSerSerLeuGlnIleuValAlaValGluThrAsnLeuAlaSer 140
XX
XX 625 CTAAAGAGCTTCCCTATATGACAGCTTATATACCTTAAAGAAACCTCAATGGGCTCAAT 684
XX 141 LeuIleuAsnProIleGlnIleGlnIleuIleuIleuIleuIleuIleuIleuIleuIleu 160
XX
XX 685 TTATACATTCCTGTAGTTACTGCATATTTTCAATCTGACGAACCTTAGTACATGTG 744

```

```

DB 161 LeuIleGlnSerPheLeuSerProGluTyrPheSerAsnLeuThrAsnLeuGlnIleu 180
XX
XX 745 GATCTTCTTATATACCTATATTTCAACTATATCTGATCAAGACTTACAGTTTACAGTGA 804
XX 181 AspLeuSerSerAsnIleGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 200
XX
XX 805 AATCCACAAGTCATCTCTTATAGACATGTCTTGAACCCCAATGACTTCAATCCAGAC 864
XX 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetCAsnIleGlnPro 220
XX
XX 865 CAAGCTTTCAGGAAATTAAGTCCATGACACTTGAAGGATATTTAATAGCTCA 924
XX 221 GlyAlaPheGlyGluIleArgLeuIleuIleuIleuIleuIleuIleuIleuIleuIleu 240
XX
XX 925 AATATATGAAACTTCCCTTCAAAACCTGGCTGTTTACAGTCCATGGTGTGATCTTG 984
XX 241 AsnValMetIleThrCysIleGlnIleuAlaGlyLeuGlnValIleIleuValIleu 260
XX
XX 985 GGAGATTTAAAGATGAAGAAATCTGAAATTTTGAACCCCTATCATGAGAGACTA 1044
XX 261 GlyIleuPheArgAsnIleuIleuAsnLeuGluIlyPheAspIlySerAlaLeuGlnIlyLeu 280
XX
XX 1045 TGTGATGTGACCATTTGATAGTTCAGCTTAAACATATACAAATGATTTTCAATGATATT 1104
XX 281 CysAsnLeuThrIleGlnIleuPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 300
XX
XX 1105 GTTTAAG--TTCCATGCTTGGGAAATGTTTCTGCAATGCTCTGACAGGTGATATTA 1161
XX 301 IleAspLeuPheAsnIlyLeuThrAsnValIleSerPheSerLeuValIleValIleThr 320
XX
XX 1162 AATATCTGAAAGATGTTCTTAAACATTTCAATGAGCAATCTTATCAATCATTTAGATGT 1221
XX 321 GluArgValIlyAspPheSerTyrAsnPheGlyTrpGlnIleuGlnIleuValIleCys 340
XX
XX 1222 CAACATAAG-CAGTTTCAACCTGATGATACCTTTCTTAAAGTTTGAACCTTAACTATG 1280
XX 341 LysPheGlyGlnPheProThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 360
XX
XX 1281 AACAAAGGCTCTATGATTTTAAAAAGGCGCTTACCAAGTCTCAGCTATCTAGATCTT 1340
XX 361 AsnIlyGlyIlyAsnAlaPheSerGlyValAlaPheProSerLeuIleuIleuAspLeu 380
XX
XX 1341 AGTAAAGAAATGACATGAGCTTTAGTGGCTGTGTTTATTTGATTTGGGAAACAAACAGC 1400
XX 381 SerArgAsnIlyLeuSerPheIlyCysCysSerGlnSerAspPheGlyThrTrsSer 400
XX
XX 1401 CTGAGACACTTACCTCAGCTTCAATGGTGCATCATTAATAGTACCAATTCATGGT 1460
XX 401 LeuIlyTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
XX
XX 1461 CTGAGAGCTGACAGACCTGATTTTTCAGACCTTACTTAAAGAGGTACACAATTT 1520
XX 421 LeuGlnIleuIleuIleuIleuAsp-PheGlnIleSerAsnLeuIlyGlnMetSerIleuP 440
XX
XX 1521 CTCAGGTTCTTATCCCTTGAAGACTACTTATCTTGAACATCTTATATCAACCA 1580
XX 440 eSerValIleuLeuSerLeuIlyAsnLeuIleTyrLeuAspIleSerHisThrHisThr 460
XX
XX 1581 AATTACTTGATGTATATTTCTGGCTTGAACAGCTTCAACATTAATAAAATGGCTGG 1640
XX 460 GValAlaPheAsnGlyIlePheAsnIlyLeuSerSerLeuGlnValIleuIleuMetAlaG 480
XX
XX 1641 CAATTTCTTCAAGACAAACCTTCAATGCTTTCGAAACCAACAACAACTTGACATT 1700
XX 480 yAsnSerPheGlnIleuAsnPheProAspIlePheThrGlnLeuArgAsnLeuThrP 500
XX
XX 1701 CCTGATCCCTCTTAATGTCAATTTGGAACAATATCTGGGGGATTTGACACCTTCA 1760
XX 500 eLeuAspLeuSerGlnCysGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 520
XX
XX 1761 TAGACTTCAATTAATAATATGAGTCAACAACATCTATTGTTTGGATTCATCCATTA 1820
XX

```



```

Db      520 rSerLeuGlnValLeuSenMetSerHisAsnAsnPhenPheSerLeuAspThrPheProTy 540
Qy      1821 TAACCAGCTGATTCCTCCAGACACTTGTGATGAGTTCAATGGCATAGAGATCT-- 1878
Db      540 rLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 560
Qy      1879 -AAGGAATACATGCAACATTTTCCAAAGAGCTTCAGCTTCTTCAATCTTCAACATTC 1937
Db      560 sLysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAs 580
Qy      1938 TGTTCCTGTATATATGTAACATCAAGAAATTCCTCAGTGGGTCAAGAAACAGAACAGTT 1997
Db      580 pPheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysPheGlnArgGlnLe 600
Qy      1998 CTTGGTGAATGTGAACAATGACATGTGCACACCTGTAGACATGAAATACCTCTTAGT 2057
Db      600 uLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProVa 620
Qy      2058 GTTGGAATTTAATATCTACCTGTATATGTATACAAACATCATCAGTGTGTCAGTGT 2117
Db      620 lLeuSerLeu--AsnIleThrCysGlnMetCAsnLysThrIleIleGlyValSerValle 639
Qy      2118 CAGTGTGATTTGTGATTCACCTGATGCAATTTCTGATATACACTTCAATTTTCACTGAT 2177
Db      639 uSerValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMe 659
Qy      2178 ACTTATTTGCTGGCTGTAAAAAGTACAGACAGAGGAAAGCATCTATGATGATTTGGAT 2237
Db      659 tLeuLeuAlaGlyCysIleLysTyrGlyArgGlyGlnAsnIleLysPheAlaPheValIle 679
Qy      2238 CTACTCGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2297
Db      679 eLysSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGly 699
Qy      2298 AGTCCCGCTTTTCACTGCTGCTTCACTACAGACACTTATTCCTGCTGAGCCATTC 2357
Db      699 yValProProheGlnLeuGlnCysLeuHisTyrArgAspPheIleProGlyValAlaIleAl 719
Qy      2358 TGCACACATCATCCAGAGAGAGCTTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2417
Db      719 aAlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValValSerGI 739
Qy      2418 ACACCTTATTCAGAGCGGTGGTGTGATCTTGAATATGAGATGAGTGGTCAACATGGCAGTT 2477
Db      739 nHisPheIleGlnSerArgTrpCysIlePheGlnTrpIleAlaGlnThrTrpGlnPh 759
Qy      2478 TCTGAGACAGCCGCTCTGGCATCATCTTCAATGCTCTTGAAGAGGTGAGAGTCCCTGCT 2537
Db      759 eLeuSerSerArgLagIleIleIlePheIleValLeuGlnHisValGlnLysThrLeuLe 779
Qy      2538 GAGGACAGAGGTGAATTTGATCGCTTCTTACAGAGAAACCTTACCTGGAATGGAGAGA 2597
Db      779 uArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTrpGlnAs 799
Qy      2598 CAATCTCTGGGGAGGAGCATCTTCTGAGAGAACTTAAATAATGCCATTTGATGGAGAA 2657
Db      799 pSerValLeuGlyArgHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlyLys 819
Qy      2658 AGCCTCGAATCTGAGCAACACA 2679
Db      819 sSerTrpAsnProGlnGlyThr 826

```

```

RESULT 2
ABU04774
ID      ABU04774 standard; protein, 839 AA.
AC      ABU04774;
XX      29-JAN-2003 (first entry)
XX      Human expressed protein tag (EPT) #1440.
DE      Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW

```

```

KW      protease; protease inhibitor; transporter; cytoskeletal protein;
KW      receptor; transcription factor; cancer; MHC;
KW      major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW      adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
OS      Homo sapiens.
PN      WO200278524-A2.
PD      10-OCT-2002.
PF      28-MAR-2002; 2002WO-US009671.
PR      28-MAR-2001; 2001US-0279495P.
PR      21-MAY-2001; 2001US-0292544P.
PR      08-AUG-2001; 2001US-0310801P.
PR      01-OCT-2001; 2001US-0326370P.
PR      04-DEC-2001; 2001US-0336780P.
PR      20-FEB-2002; 2002US-0358985P.
PA      (ZYCO-) ZYCO INC.
PI      Chicx RM, Tomlinson AJ, Urban RG;
PI      WPI; 2003-040607/03.
PT      New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT      cytoskeletal proteins, receptors or transcription factors), useful for
PT      treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT      leukemia.
PS      Example 2; SEQ ID NO 1440; 134p; English.
XX      CC      The invention describes a purified polypeptide, which comprises a
XX      CC      fragment of a kinase, phosphatase, protease, protease inhibitor,
XX      CC      transporter, cytoskeletal protein, receptor or transcription factor. The
XX      CC      polypeptide is useful as an immunogenic composition for eliciting in a
XX      CC      mammal an immunogenic response directed against any of the purified
XX      CC      polypeptide. The purified polypeptide, or the antibody that binds to this
XX      CC      polypeptide, is useful for treating cancer. The polypeptide is also
XX      CC      useful for identifying compounds that binds to a naturally processed
XX      CC      class I or class II MHC-binding polypeptide. The polypeptides and
XX      CC      polynucleotides are particularly useful for treating or preventing
XX      CC      myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX      CC      lymphoma or leukaemia. These are also useful for screening agents for
XX      CC      treating the above mentioned diseases. This sequence represents an
XX      CC      expressed protein tag (EPT) isolated from human tissue for translational
XX      CC      profiling. Note: This sequence does not appear in the printed
XX      CC      specification but was obtained in electronic format directly from WIPO at
XX      CC      ftp.wipo.int/pub/published_pct_sequences
XX      SQ      Sequence 839 AA:
XX
XX      Alignment Scores:
XX      Pred. No.:      2,7e-303      Length:      839
XX      Score:          2792.00      Matches:      557
XX      Percent Similarity: 79.35%      Conservative: 100
XX      Best Local Similarity: 67.27%      Mismatches: 166
XX      Query Match:      53.93%      Indels:      6
XX      DB:              6      Gaps:      4
XX
XX      US-09-396-985b-46 (1-2951) x ABU04774 (1-839)
Qy      208 ATGATGCTCTCCGCTGCTGCTGAGATCTGTATGACATGCACTG---TTCTTCTCTGC 264
Db      1 MetMetSerAlaSerArgLagIleIleIlePheIleProAlaMetAlaPheLeuSerCys 20
Qy      265 CTGACACAGAGAGCTTGAATCCCTGATGAGAGTGTCTCTATATATTACCTCAATGC 324
Db      21 ValArgProGlnSerTrpGlnProCysValGlnValValProAsnIleThrTyrGlnCys 40
Qy      325 ATGATCAGAAACTCAGCAAGAGCTCCGATGACATTCCTTCAACCAAGAACTATGAT 384

```

Db 41 MetGluLeuAsnPhetyrLyLeProAsnLeuProPheSerThrLyAsnLeuAsp 60
 Qy 385 CTGAGCTTCAACCCCTTGAAGATCTTAAAGATGATATGCTTCCATATTTTTCAGAACTT 444
 Db 61 LeuSerPheAsnProLeuAsnGlnLeuGlySerTySerPheSerPheProGlnLeu 80
 Qy 445 CAGTGGCTGATTTATTCAGGTGTGAATGAAACAAATTGAAAGCAAGGACATGGCATGCG 504
 Db 81 GlnValLeuAsnLeuSerArgCysGluLileGlnThrLileGlnAspGlyAlaTyArgLins 100
 Qy 505 TTACACACCTCTCAAACTGATATCTGACAGAAACCCCTATCCGAGTCTTCCCGACGA 564
 Db 101 LeuSerThrLeuSerThrLeuLileLeuThrLyAsnProLileGlnInsLeuAlaLeuGly 120
 Qy 565 AGTTCTCTGGACTCAACAGTTTAGACATCTGGTGGCTGTGAGACAAAATTGGCTCT 624
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnLeuValAlaValGlnThrAsnLeuAlaSer 140
 Qy 625 CTAGAAAGCTTCCCTATTTGACACGCTTATACCTTAAAGAACTCAATGTGGCTCACAT 684
 Db 141 LeuGlnAsnPherProLileGlyLileLeuLysThrLeuLysGluLeuAsnValAlaLileAsn 160
 Qy 685 TTTTATACATTCCTTAAAGTTACCTGCAATTTTTCATCTGACGAACTTATGATGTC 744
 Db 161 LeuLileGlnSerPheLyLeuProGlyTyPheSerAsnLeuThrAsnLeuGlnLileLeu 180
 Qy 745 GATCTTCTTATATCTATATCAATCAATATTAAGTCTGACACGACTTACAGTTTCTACGTTAA 804
 Db 181 AspLeuSerSerAsnLyLileGlnSerLileTyCysThrAsnLeuAlaValLileAsnGln 200
 Qy 805 AATCACAAGTCAATCTCTCTTTTAAAGATGCTTTTGAACCCCATGGAATTCATTCAGAAC 864
 Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheLileGlnPro 220
 Qy 865 CAACCTTTTACGGAATTAAGCTCCATGAACTGATCTCTTAAAGGTAATTTTAAATAGTCA 924
 Db 221 GlyAlaPheLyGlnLileArgLileLileLyLeuThrLeuArgAsnAsnPheAspSerLeu 240
 Qy 925 AATTAATTAAGAACTGTGCTTCAAACTGGCTGTTTACACGTCACATCGGTTGATCTTG 984
 Db 241 AsnValLeuLySerCysLileGlnGlyLeuAlaGlyLeuGlnValAlaLileAspLeuValLeu 260
 Qy 985 GGAGAATTTTAAAGTGAAGAAAGATCTGAAATTTTGAACCCCTATCATGGAAGACTA 1044
 Db 261 GlyGlnPheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 280
 Qy 1045 TGTGATGTGACCATTTGATGAGTTCAAGTTTAAACATATACAAATGATTTTTCAGATGATTT 1104
 Db 281 CysAsnLeuThrLileGlnGlnPheArgLeuAlaTyLeuAspTyTyTyLeuAspAspLile 300
 Qy 1105 GTTAAAG--TTCCATGTGGTGGCAAGTTTCTGCAATGTCTCGGACAGGTATCTATA 1161
 Db 301 LileAsnLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrLile 320
 Qy 1162 AAATATCTAGAAGATGTTCTTCAACATTTCAATGCGCAATCTTATCAATCATAGATGAT 1221
 Db 321 GlnTyArgValLysAsnPheserTyArgAsnPheGlyTyArgLinsLileGlnLileValAlaAsnCys 340
 Qy 1222 CAATTAAG-CAGTTTCCACTCTGATCTACCTTTCTTAAAGTTTGAAGTTTAACTATG 1280
 Db 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuLysPheThrSer 360
 Qy 1281 AAGAAAGGCTATACAGTTTAAAGAGTGGCCCTCAACAGTCTCAGATCATCTGATCTT 1340
 Db 361 AsnLySerGlyLysAsnAlaPheSerGlnValAsnLeuProSerLeuGlnPheLeuAsnLeu 380
 Qy 1341 AGTAAATGCACTGAGCTTATGAGTGGCTGTTCTTATTTGATTTGGAACAAAGAC 1400
 Db 381 SerTyArgAsnGlyLeuSerPheLyGlyCysCysSerGlnSerAsnPheserGlyThrThrSer 400
 Qy 1401 CTGAGACACTTAAAGCTTCAAGTGGTCCATCATTTAGAGTCCCAATTTTATGGGT 1460
 Db 401 LeuTySerTyLeuAsnLeuSerPheAsnGlyValLileThrMetSerSerAsnPheserGly 420

Qy 1461 CTAGAAAGCTGAGACGCTGATTTTTCAGACATCTTATTAAGAGGTCAAGAAAT 1520
 Db 421 LeuGlnGlnLeuGlnLileLeuAsnProPheGlnLileSerAsnLeuLysGlnMetSerGlyLub 440
 Qy 1521 CTCAGCGTTCTTATCCCTTGAAGACTTATTAACCTTGAACATCTCTTATTAACACCA 1580
 Db 440 SerValPheLeuSerLeuAlaArgAsnLeuLileTyLeuAspLileSerThrLileThrArg 460
 Qy 1581 AATTGACTTCGATGATGATATTTCTTGGCTTGAACAGTCTCAACATTAATAAAGTCTG 1640
 Db 460 GValAlaPheAsnGlyLilePheAsnGlyLeuSerSerLeuGlnValLeuLysMetValArg 480
 Qy 1641 CAATCTTCAAGACACACACCTTCAATGTCTTTGCAACACACAACTTGAACAT 1700
 Db 480 TyAsnSerPheGlnGlnAsnPheLeuProAspLilePheThrGlnLeuAlaArgAsnLeuThr 500
 Qy 1701 CTTGATCTCTTAAATGTCAATTGGAACAAATATTTGGGGGGTATTTGACACCTTCCA 1760
 Db 500 LeuAsnLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSer 520
 Qy 1761 TAGACTTCAATTAATTAATGATGACAAACATCATTTGTTTGGATTCATCCCATTA 1820
 Db 520 rSerLeuGlnValLeuAsnMetSerThrAsnAsnPhePheSerLeuAspThrPheProTy 540
 Db 540 rTySerCysLeuAsnSerLeuGlnValLeuAspTySerLeuAsnLileLileMetThrSerLy 560
 Qy 1879 -AAGAAATATCTCAACATTTTCAAGAGTCTAGCTCTTCAATCTTATTAACATTC 1937
 Db 560 sTySerGlnGlnLeuGlnLilePheProSerSerLeuAlaPheLeuAsnLeuThrGlnLinsAs 580
 Qy 1938 TGTGCTTGAATATGGAACATCAGAAATTCGCAAGTGGTCAAGAAACAGAAAGACTT 1997
 Db 580 PheAlaCysThrCysGlnLileGlnSerPheLeuGlnThrLileLyAsnGlnArgGlnLe 600
 Qy 1998 CTGAGTGAATGTGGAACAAATGACATGTGCAACACCTGTGATGAATTAACCTCTTAA 2057
 Db 600 uLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLyGlnGlyMetProTy 620
 Qy 2058 GTTGAATTTTAATATCTTACCTGTTATATGTAACAACATCATCATGATGTCACTGAT 2117
 Db 620 LileSerLeu--AsnLileThrCysGlnMetAsnLyThrLileLileGlyValSerValLile 639
 Qy 2118 CAGTGTGATTTGGTATCCAGCTGATCTTGTGATTCATTCACCTGAT 2177
 Db 639 uSerValLeuValSerValAlaValLeuValTyTyLeuPheTyPheThrLileLeu 659
 Qy 2178 ACTTATGTGCTGCTGTAAGAAAGTACAGACAGAGAAAGACATCTATGATGATTTGTGAT 2237
 Db 659 tLeuLeuAlaGlyCysLileTySerGlyTyArgGlyLysAsnLileTyAsnAlaPheValLile 679
 Qy 2238 CTACTGAGTCAAGATGAGACTGTGGTGAAGAAATGCTGTGTAAGAAATTTAGAGAGG 2297
 Db 679 eTySerSerGlnAspGlnAspTyArgValAlaArgAsnGlnLeuValLysAsnLeuGlnGln 699
 Qy 2298 AGTGGCCCGCTTCACTCGCTTCACTACAGACGCTTATTCCTGCTGATGACCTTGC 2357
 Db 699 yValProProPheGlnLeuCysLeuLileTyArgAsnPheLileProGlyValAlaLileAl 719
 Qy 2358 TGGCAACATCATCAGAGAGGCTTCCACAAAGACCGGAAGGTTATTTGGTATGCTGAT 2417
 Db 719 AlaAlaAsnLileLileGlnGlyLysPheThrLysSerArgLyValLileValValSerG 739
 Qy 2418 ACACTTTATTCAGAGCGGTGTGATCTTTGAATATGAGATTTGCAACATGCGCAT 2477
 Db 739 nHisPheLileGlnSerArgTyPheCysLilePheGlyTyGlnLileAlaGlnThrTyArgLins 759
 Qy 2478 TCTGAGACAGCGCTCTGAGATCATCTTCAATGTCTTGAAGACTTGAAGTCCCTGCT 2537
 Db 759 eLeuSerSerArgAlaGlyLileLilePheLileValLeuGlnLysValGlnLysThrLeu 779

QY 2538 GAGGACAGAGTGAATGTATGCTCTTGTAGAGAAACCTTACCTGGAAATGGAGGA 2597
 |||||
 Db uArgGInGInValGInLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGInTrrpGInAs 799

QY 2598 CAATCTCTGGGAGGACATCTTGTGAGAAAGCTTAAAGCCCTATTGGATGAAA 2657
 |||||
 Db pSerValLeuGInYArgHisIlePheTrpArgLeuArgLysAlaLeuLeuAspGly 819

QY 2658 AGCCTGCAATCTGAGCAACA 2679
 |||||
 Db sSerTrpAsnProGInGlyThr 826

RESULT 3
 ABU04775
 ID ABU04775 standard; protein: 839 AA.
 AC ABU04775;
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1441.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN MO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOs INC.
 XX
 PI Chicz RM, Tomlinson AJ, Urban RG;
 PT MPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1441; 134bp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIP0 at
 CC ftp.wipo.int/pub/published_pct_sequences

XX
 SQ Sequence 839 AA:
 Alignment Scores:
 Pred. No.: 2.7e-303 Length: 839
 Score: 2792.00 Matches: 557
 Percent Similarity: 79.35% Conservative: 100
 Best Local Similarity: 67.27% Mismatches: 166
 Query Match: 53.93% Indels: 6
 DB: 6 Gaps: 4

US-09-396-985b-46 (1-2951) x ABU04775 (1-839)

QY 208 ATGATGCTCCCTCGGCTCCGAGTAGACTGATGAGCACTG--TTCTTCCTCGC 264
 |||||
 Db 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20

QY 265 CTGACACAGAGAGCTTGAATCCCTGCATAGAGAGTTCCTAATAATTACCTCAATGC 324
 |||||
 Db 21 ValArgProGInSerTrpGInProCysValGInValProAsnIleThrTyrGInCys 40

QY 325 ATGATCAGAAACTCGCAAAAGTCCCTGATGACATTCCTTCAACCAAGACATAGAT 384
 |||||
 Db 41 MetGInLeuAsnPheTyrIleProAspAsnLeuProPheSerThrIleAsnLeuAsp 60

QY 385 CTGAGCTCAACCCCTTGAAGATCTTAAAGCTATAGCTTCCCAATTTTTCAGAACTT 444
 |||||
 Db 61 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPheSerPheProGInLeu 80

QY 445 CAGTGCCTGATTTATTCAGAGTGTGAATGAAATGAAACATGAAACAGAGCATGCGC 504
 |||||
 Db 81 GInValLeuAspLeuSerArgCysGInIleGInThrIleGInLeuAspGlyAlaTyrGInSer 100

QY 505 TTACACCACTCTCAAACTTGATCTGACAGAAACCTTATCCAGAGTTTCCCAAGA 564
 |||||
 Db 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGInSerLeuAlaLeuGly 120

QY 565 AGTTTCTGGAATACTAAGATTAGACAATCTGCTGCTGTGGAGCAAAATTGGCCTCT 624
 |||||
 Db 121 AlaPheSerTyrLeuSerSerLeuGInLysLeuValAlaValGInThrAsnLeuAlaSer 140

QY 625 CTAGAAAGCTCCCTATTGGACAGCTTATTAACCTTAAAGAACTCAATGTGCTCAAT 684
 |||||
 Db 141 LeuGInAsnPheProIleGlyHisLeuLysThrLeuLysGInLeuAsnValAlaHisAsn 160

QY 685 TTTATACATTCCTGTAGATTACTGCAATTTTTCATGTGACGAACCTAGTATGTG 744
 |||||
 Db 161 LeuIleGInSerPheLysLeuProGInTyrPheSerAsnLeuThrAsnLeuGInHisLeu 180

QY 745 GATCTTTCTTATACATATATTAACATTTATTCGTACAGACTTACAGTTTTCACGGA 804
 |||||
 Db 181 AspLeuSerSerAsnLysIleGInSerIleTyrCysThrAspLeuArgValHisGln 200

QY 805 AATCCACAAGTCAATCTCTTATAGACATGCTTTGAACCAATGACTTACATTCAGAAC 864
 |||||
 Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGInPro 220

QY 865 CAAGCTTTCAAGGAATTAAGTTCATGAGTACTTAAAGAGTATTTAAATAGCTCA 924
 |||||
 Db 221 GlyAlaPheLysGInLeuArgLeuHisLysLeuThrLeuArgAsnPheAspSerLeu 240

QY 925 AATATATGAAAACTTGCCCTTCAAAACCTGCTGCTTTACAGCTCCATGCTGATCTTG 984
 |||||
 Db 241 AsnValMetLysThrCysIleGInGlyLeuAlaGlyLeuGInValHisArgLeuValLeu 260

QY 985 GGAGATTTAAAGATGAAGAGATCTGAAATTTTGAACCCCTATTCATGGAAGAGCTA 1044
 |||||
 Db 261 GlyGInPheArgAsnGInLysAsnLeuGInLysPheAspLysSerAlaLeuGInGlyLeu 280

QY 1045 TGTGATGTGACATTGATGAGTTCAGGTTTAACTATTAACAATGATTTTTCAGATGAT 1104
 |||||
 Db 281 CysAsnLeuThrIleGInGInPheArgLeuAlaTyrLeuAspLysTyrLeuAspAspIle 300

OY		1105	GTTAAG---TTC	CATTGGCCGCAATCTTCTGC	AAGTGTCTCGCAGGCTGTA	TATA	1161
Db		301	:::	:::	:::	:::	
OY		1162	AAATATCTAGA	GAAGTGTTCTTAAACATTTTCAAATCGCAATCCTTATCATATCATTAAGATGT			1221
Db		321	GIATAGVal	LysAspPheSerPheSerThrAsn	PheGlyTrpGlnHisLeuGluLeuAla	AsnCys	340
OY		1222	CAACTAAG-CAG	TTTTCCAATCTTGAGTTACCCCTTTCTTAAAAGTTTGACTTTAACAATAG			1280
Db		341	LysPhe	GlyGlnPheProThrLeuLysSerLeuLysArgLeuThrPhe	ThrSer		360
OY		1281	AACAAAGG	STCATAGTTTAAAAAABATGGCCCTCAACAATCTCAGTACTATCATGATCTT			1340
Db		361	AsnLys	GlyGlyAlaMetPheSerIleValAspLeuProSerLeuGluPheLeuAspLeu			380
OY		1341	AGTAGAAATG	CACCTAGCTTAAAGTGGTGGCTGTCTTATTTCTGAATTTGGCAACAAACAGC			1400
Db		381	SerArg	AnngLysLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrThrSer			400
OY		1401	CTGAGACA	CTTAGACCTTCAGCTTCAGTGGCCATCATTAATGAGTGCATATTCAGGT			1460
Db		401	LeuLys	TrpLeuAspLeuSerPheAnngLysIleThrMetSerAspPheLeuGly			420
OY		1461	CTAGAAGAG	CTGCAGCACCTGGAATTTTTCACACCTCTTAAAAAAGGTCACAGAAAT			1520
Db		421	LeuGln	GlnLeuGlnHisLeuAsp-PheGlnHisSerAsnLeuLysGlnMetSerGluPh			440
OY		1521	CTCAGCGT	CTTATCCCTTGAAGAGCTTTCACCTTACACATCTCTTATCTAACACCA			1580
Db		440	eSerValPhe	LeuSerLeuArgAsnLeuIleTyrlLeuAspIleSerHisThrHisThrXr			460
OY		1581	AATTGACTT	CGATGTATATTTCTTGGCTTGAACAGTCAACACATTTAAAATGGCTGG			1640
Db		460	GValAlaPhe	AnngLysIlePheAnngLysSerSerLeuGluValLeuLysMetAlaGl			480
OY		1641	CAATCTCTT	CAAAAGCACACCCTTTCAAATGTCTTTGCCAAACACACAAACTTGACATT			1700
Db		480	YasnSerPhe	GlnGlnAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPh			500
OY		1701	CTGGATCCTT	CTAATATGCATTTGGACAATATCTTGGGGGGATTTGACACCCCTCA			1760
Db		500	eLeuAspLeu	SerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSe			520
OY		1761	TAGACTTCA	ATTTAAATATGAGTCACACAACATCTATGTGTTTGGATTCATCCCATTA			1820
Db		520	rSerLeu	GlnValLeuAsnMetSerHisAsnAspPheSerLeuAspThrProtyl			540
OY		1821	TAAACAGT	GTATTCCTCAGACACTCTTGATTTGACGTTCAATGCGATAGACATCT--			1878
Db		540	rLysCys	LeuAsnSerLeuGlnValLeuAspLysSerLeuAsnHisIleMetThrSerLys			560
OY		1879	-AAAGGAAT	CTGCACAATTTCCAAAGCTACCCCTTTCATCTTACTAACAATTC			1937
Db		560	sLysGln	GluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAs			580
OY		1938	TGTTGCTGT	ATATGATGAACATCAGAAATTCCTGCAGTGGGTCAAGAACAGAAAGACTT			1997
Db		580	pPheAlaCys	ThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLe			600
OY		1998	CTTGCTGA	ATGTGAACAAATGACATGTGGCAACACTGTAAAGATGAATACCTCCTTAGT			2057
Db		600	uLeuValGlu	ValGluArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProva			620
OY		2058	GTTGGA	TTTTAATAATCTACCTGTATATGACAAGACATTCATCAGTGTGACAGGT			2117
Db		620	IleuSerLeu--	AsnIleThrCysGlnMetAsnLysThrIleIleGlyAlaSerValLe			639
OY		2118	CAGTGTGA	TGTGTGATTCACCTGTAGACTTTCTTGAATACACACTTCTATTTACCTGAT			2177
Db		639	uSerAlaLeu	ValAlaSerValAlaAlaValLeuValTyrlLysPheTyrlPheHisLeuMe			659
OY		2178	ACTTATTC	TGCTGGCTGTAAAAAGTACAGCAGAGGAGAAAAGCATCTATGATGCAATTTGAT			2237

Db	659	CTLEUENLAAGLYGYSLEIYSTRYGGLYAGGGLYGLAASMLETYRASPAAAPHEVALII	679
QY	2238	CTACTCGAGTCAGATAGGACTGGGTGAGAAATGAGCTGTAAAGATTAGAAAGG	2297
Db	679	ETYSERBERGLINAPRLINAPRTIPVALAAGANGILUENVALLYSASNENUGLUGL	699
QY	2298	AGTGCCCCGGCTTCACTCTGCTCTCACTACAGAGACTTATTCCTGGGTAGCCATTGC	2357
Db	699	YVALPRPBROBHEGLINLEUCYSLEUHSISTYRARGASPPHEILEPROGLYVALAIALEAI	719
QY	2358	TGCCAATATCATCCAGGAAGGCTCCCAAGAGCCGGAAGTTATGTGGTAGTGTAG	2417
Db	719	AALASMLEILEIIEGLUGLIPHEKISLYSSEARGLYVALILEVALVALSERGI	739
QY	2418	ACACTTTATTCAGAGCCGTTGGTGTATCTTTGAATATGAGATTGCTCAACATGGCAGTT	2477
Db	739	NHISPHLEILEGLINSEIRGRITRPSYSLIEPHEGLIUTRYGLIUILEAGLINHTRIPGLNPH	759
QY	2478	TCTGAGAGCCCGCTCTGGCATCATCTTCATTGTCCTTGAGAGGTTGAGAAGTCCCTGCT	2537
Db	759	ELEUSERSERARGALAGILYILEIIEPHEILEVALLEUGLNLVAGLIULYSTRHLEULE	779
QY	2538	GAGGACACAGGTGGAAATTGTATGCGCTTTAGAGAAAACCTACCTGGAAATGGAGGA	2597
Db	779	UARGGLINGLINALGLINLEUTYRARGLEULSEARGASPTHTRYENGLUTRIPGLVAS	799
QY	2598	CAATCTCTGGGGAGGACATCTTCTTGAGAGAGCTTAAATAGCCCTATTGGATGGAAA	2657
Db	799	PSERVALLEUGLYARGHSISLIEPHEITRPARAGLEUARGLYALALEUENUGLGLY	819
QY	2658	AGCCTCGAATCTTGAGCAACA	2679
Db	819	SSERTPRASNPRLUGLTYTHR	826
RESULT 4			
ADCT8785.			
ID	ADCT8785	standard; protein; 839 AA.	
AC	ADCT8785;		
XX			
DT	01-JAN-2004	(first entry)	
XX			
DE	Human PRO protein #7.		
XX			
KW	human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;		
XX	Crohn's disease.		
OS	Homo sapiens.		
XX			
PN	WO2003034984-A2.		
XX			
PD	01-MAY-2003.		
XX			
PF	15-OCT-2002; 2002WO-US033070.		
XX			
PR	19-OCT-2001; 2001US-0340083P.		
XX			
PA	(GETH) GENENTECH INC.		
XX			
PI	Goddard A, Gurney AL;		
XX			
DR	WPI; 2003-481990/45.		
XX			
DR	N-PSDB; ADCT8784.		
XX			
PT	New PRO polynucleotide and polypeptide, useful for the manufacture of a		
PT	medicament for diagnosing or treating cancer or inflammatory bowel		
PT	disorder e.g., ulcerative colitis or Crohn's disease.		
XX			
PS	Claim 12; SEQ ID NO 14; 327p; English.		
XX			
CC	The invention comprises the amino acid and coding sequences of human PRO		
CC	proteins. The DNA and protein sequences of the invention are useful for		

CC the diagnosis and treatment of cancer and inflammatory bowel disease
 CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
 CC sequence represents a human PRO protein of the invention.

SO Sequence 839 AA:

Alignment Scores:

Pred. No.:	2,76-303	Length:	839
Score:	2792.00	Matches:	557
Percent Similarity:	79.35%	Conservative:	100
Best Local Similarity:	67.27%	Mismatches:	166
Query Match:	53.93%	Indels:	6
		Gaps:	4

US-09-396-985B-46 (1-2951) x ADC78785 (1-839)

```

QY 208 ATATGCTCCCTGGCTCTGCTGAGACTGATCATGACATG---TTCTTCTCTGC 264
DB 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 265 CTGACACGAGAACTGGAATCCCTGCATAGAGGAGTCTCTATATTACTTACCTACATGC 324
DB 21 ValArgProGluSerThrGluProCysValGluValAlaProAsnIleThrTyrGlnCys 40
QY 325 ATGATCAGAAACTCAGCAAGTCCCTGATGACATTCCTTCTTCAACCAAGAAATGAT 384
DB 41 MetIleuLeuAsnPheTyrIleProAsnLeuProPheSerThrIlyAsnLeuAsp 60
QY 385 CTGAGCTTCAACCCCTTGAAAGATTTTAAAGCTTATAGCTTCTCCAAATTTTCAAACTT 444
DB 61 LeuSerPheAsnProLeuArgHISLeuGlySerTyrSerPhePheSerPheProGluLeu 80
QY 445 CAGTGGCTGATTTATCCAGGTGGAATGAAATGAAACAATTGAAAGCAAGCATGGCATGGC 504
DB 81 GluAlaIleuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 100
QY 505 TTACACCACTCTCAAACTTGATATCTGACAGAAACCTTATCCAGATTTTCCCAAGA 564
DB 101 LeuSerHISLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
QY 565 AGTTTCTGAGCTTACAAAGTTTGAACAATCTGGTGGCTGAGAACAAATGGCCCTT 624
DB 121 AlaPheSerGlyLeuSerSerLeuGlnIlyLeuValAlaValIleGluThrAsnLeuAlaSer 140
QY 625 CTAAAGACTCCCTATATGACAGCTTATACCTTAAAGAAACCTCAATGGTGGCTCAAT 684
DB 141 LeuIleAsnPheProIleGlyHISLeuIlySerThrLeuIlyGluLeuAsnValAlaHISAsn 160
QY 685 TTATACATTCCTGTAAGTTACTGTCATATTTTCCAACTGACGAACTAGTACATGTG 744
DB 161 LeuIleGlnSerPheIlySerLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHISLeu 180
QY 745 GATCTTTCTTAACTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 804
DB 181 AspLeuSerSerAsnIlyIleGlnSerIleTyrCysThrAspLeuArgValLeuHISGln 200
QY 805 AATTCACAAGTCATCTCTTCTTGAACATGCTTGAACCCCAATGATGATCTTCAAGAC 864
DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
QY 865 CAACCTTTTCAAGAAATTAAGCTCATGACTGATTAAGAGATTAATTTAATTAAGTCA 924
DB 221 GlyAlaPheIlySerGluIleArgLeuHISIlySerLeuThrLeuArgAsnAsnPheAspSerLeu 240
QY 925 AATATTAATGAATCTTGCTTCAAAACCTGGCTGGTTTACAGTCCATCGGTTGATCTTG 984
DB 241 AsnValMetIlySerThrCysIleGlnIlyLeuAlaGlyLeuGluValHISArgLeuValLeu 260
QY 985 GGAGAATTTAAGATGAAGAAATCTGGAATTTTGAACCTCTATCATGGAAGAGCTA 1044
DB 261 GlyIleuPheArgGlnGlyIlyAsnLeuGluIlySerPheAspIlySerAlaLeuGluGlyLeu 280
QY 1045 TGTGATGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1104

```

```

DB 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspIlyTyrTyrLeuAspAspIle 300
QY 1105 GTTAAG---TTCAATGCTTGGGGAATGTTTTCGACATGCTCTGGCAGAGTATCATTA 1161
DB 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerAlaIleIle 320
QY 1162 AATATCTAGAAATGATGTTCTTAAACATTTCAAAATGCAATCTTATCATCATTAAGATGT 1221
DB 321 GluArgValIlyAspPheSerTyrAsnPheGlyTyrGlnHISLeuGluLeuValAsnCys 340
QY 1222 CAACTAAG-CAGTTTCAATCTGATCTTACCTTTCTTAAAGTTTGAATTAACATG 1280
DB 341 IlyAspGlyGlnPheProThrLeuIlySerLeuIlySerLeuIlyArgLeuThrPheThrSer 360
QY 1281 AACAAAGGCTTATCAATTTTAAAAAGTGGCCCTCAAGTCTCAAGCTTATAGATCTT 1340
DB 361 AsnIlyGlyGlyIlyAsnAlaPheSerGluValAspLeuProSerLeuGluIleAspLeu 380
QY 1341 AGTAGAAATCAGCTGAGCTTATGAGTGGCTGCTTATTTCTGATTTGGAGCAACAGC 1400
DB 381 SerArgAsnIlyLeuSerPheIlySerGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
QY 1401 CTGAGACCTTAACTGACCTTCAATGATGTCATCATTAATGAGTCCAAATTTCAATGGT 1460
DB 401 LeuIlyTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1461 CTGAAAGAGCTGACAGACCTTGAATTTTTCAGACCTCTACTTTAAAGGTCACAGATT 1520
DB 421 LeuGlnIleuGlnHISLeuAsp-PheGlnHISAsnLeuIlySerGlnIleSerGluPhe 440
QY 1521 CTGAGGCTTATACCTTGAAGAAAGCTATTTTCAATCTTGAATCTTATATCAACCA 1580
DB 440 eSerValPheLeuSerLeuArgAsnLeuIleTyrIleuAspIleSerHISThrThrArg 460
QY 1581 AATGACTTGATGATGATATTTCTTGCTTGAACAGTCTCAACATTAATAATGGCTGG 1640
DB 460 GValAlaPheAsnGlyIlyPheAsnGlyLeuSerSerLeuGluValLeuIlyMetAlaGly 480
QY 1641 CAATCTTTTCAAAAGACACACCTTTCAAATGCTTTCGAAACAAACAAACAACTTGACAT 1700
DB 480 YAsnSerPheGlnGluAsnLeuPheProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
QY 1701 CTGAGATCTTCAATATGATCAATTTGGAACAAATATCTTGGGGGATTTTGAACCCCTCA 1760
DB 500 eLeuAspLeuSerGlnCysGlnIleuGlnIleuGlnIleuSerProThrAlaPheAsnSerLeu 520
QY 1761 TAGACTTCAATTAATTAATTAATGAGTCAACAAATCTATTGTTTGATTCATCCATTA 1820
DB 520 rSerLeuGlnValLeuAsnMetSerHISAsnAsnPhePheSerLeuAspThrPheProTy 540
QY 1821 TAAACAGCTGATTTCCCTCAGCACTCTGATTTGACGTTTCAATCGCATTAAGCATCT 1878
DB 540 IlyIlyCysLeuAsnSerLeuGlnValLeuAspIlySerLeuAsnHISIleMetThrSerIly 560
QY 1879 -AAAGAAATCTGCAACATTTTCAAAAGAGTCTTCTTCAATCTTCTTCAATCTTCAATTC 1937
DB 560 IlyIlyGlnIlyLeuGlnHISpheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAs 580
QY 1938 TGTGCTTGTATATGTAACATCAGAAATTTCTGCAATGGGCTCAAGACAGAAAGATT 1997
DB 580 PheAlaCysThrCysGlnIleGlnSerPheLeuGlnIleIlyAspGlnArgGlnLe 600
QY 1998 CTGCGTGAATGTTGAACAAATGACATGTCGAACACCTGTGAGAAATGAATCCCTTACT 2057
DB 600 IlyLeuValGluValGluArgMetGluCysAlaThrProSerAspIlySerGlnIlyMetProVa 620
QY 2058 GTTGATTTTAATTAATTTCTCTGTATATGTAATGTAACAGACATATCATGATGTCAGTGT 2117
DB 620 IleuSerLeu--AsnIleThrCysGlnMetAsnIlySerHISIleIleGlyIlySerValIle 639
QY 2118 CAGTGTGATTTGTGTATCCACTGTAGCATTTTGTGATATACCACTTCTTATTTTCACTGAT 2177

```

Db 639 uSerValIeuValSerValAlaValIeuValTyrIleYSerPheHISLeuMe 659
QY 2178 ACTTATGCTGGCGTGTAAAGTACAGAGAGGAGGAAGATCATGTGATTCATTTGGAT 2237
Db 659 cLeuLeuAlaGlyCysIleuYrStyrgIyArgGlyGlnAsnIleYrAspIaPheValII 679
QY 2238 CTACTCGAGTCAGATGAGGATCGGTGAGAAATGAGCTGGTAAAGATTAGAGAGG 2297
Db 679 eYrSerSerGlnAspGlnAspIuAspTrpValArgAsnGlnLeuValIyAsnLeuGlnGlu 699
QY 2298 AGTACCCCGCTTTCACCTCGCTTCACACAGAGATTTATTCCTGCTGAGCCATGC 2357
Db 699 yValIProProPheGlnIleuYrStyrgIyArgAspPheIIleProGlyValAlaIleAl 719
QY 2358 TGCCAACTCATCATCAGAGAGGCTTCCAGAGAGCGGAGAGTTATGTGTAGTGTAG 2417
Db 719 aAlaAsnIleIleHISGlnGlyPheHISLysSerArgLysValIleValIValIleValSerGI 739
QY 2418 ACACTTATTCAGAGCGGTGTGTATCTTGTATGATGAGATTGCTCAAACTAGCAGTT 2477
Db 739 nHISPheIleGlnSerArgTrpCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPh 759
QY 2478 TCTGAGACGCGCTCTGTCATCATCTTTCATTTGCTTGAAGAGTTGAGAGTCCCTGCT 2537
Db 759 eLeuSerSerArgIaGlyIleIlePheIleValIleGlnIleValGlnIleYrThrLeuLe 779
QY 2538 GAGGACACAGTGAATTGTATGCTTCTTATGAGAAACCTTGAATCTGGAATGGAGGA 2597
Db 779 uArgGlnGlnValGlnIleuYrArgLeuLeuSerArgAsnThrYrIleuGlnTrpGlnAs 799
QY 2598 CAATCTCTGGGGAGGACATCTTCTGAGAGAGCTTAAAGTAAATCCCTATTTGATGAGAA 2657
Db 799 pSerValLeuGlyYrArgHISIlePheTrpArgArgLeuArgLysAlaIleuLeuAspGly 819
QY 2658 AGCCTCGAATCTGAGCAACA 2679
Db 819 sSerTrpAsnProGlnGlyThr 826
RESULT 5
ADD48826
ID ADD48826 standard; protein; 839 AA.
XX ADD48826;
AC
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein AAF05316, SEQ ID NO 14536.
XX
KM Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
KM spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN MO2003016475-A2.
XX
XX 27-FEB-2003.
PD
PF 14-AUG-2002; 2002WO-US025765.
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; AAF05316.
DR

XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017p; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 839 AA;
SQ
Alignment Scores:
Pred. No.: 2,7e-303 Length: 839
Score: 2792.00 Matches: 557
Percent Similarity: 79.35% Conservative: 100
Best Local Similarity: 67.27% Mismatches: 166
Query Match: 53.93% Indels: 6
DB: 7 Gaps: 4
US-09-396-985b-46 (1-2951) x ADD48826 (1-839)
QY 208 ATGATGCTTCCTGCTGCTGCTGAGTCTGATGATGACATG--TTCTTCTCTGCG 264
Db 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIIleProAlaMetAlaPheLeuSerCys 20
QY 265 CTGACACAGAGAGCTTGAATCCCTGACATAGAGGTGTTCTTAATTTACCTACCAATGC 324
Db 21 ValArgProGlnSerTrpGlnProCysValGlnValAlaProAsnIleThrYrGlnCys 40
QY 325 ATGATCAGAAACTCAGCAAGTCCCTGATGACATCTCTTCTTCAACCAAGACATAGAT 384
Db 41 MetGlnLeuAsnPheYrIyStIleProAsnLeuProPheSerThrIyAsnLeuAsp 60
QY 385 CTGAGCTTCAACCCCTTGAAGATCTTAAAGAGTATAGCTTCTTCATTTTTCAGAACTT 444
Db 61 LeuSerPheAsnProLeuArgHISGlnGlySerTyrSerPheSerPheProGlnLeu 80
QY 445 CAGTGGCTGATTTATCCAGGTGTGAAATTTGAAACAAATTGAAGACAGCATGGCATGGC 504
Db 81 GlnValIleuAsnPheuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaYrGlnSer 100
QY 505 TTACACCACTCTCAACTGATGATGACAGAAACCTTATCCAGAGTTTTCCTCCAGCA 564
Db 101 LeuSerHISLeuSerThrIleuIleuThrGlnAsnProIleGlnSerIleuAlaLeuGly 120
QY 565 AGTTTCTTGAGACTTAAAGATTAGCAATCTGCTGCTGCTGAGACAAATTTGGCTCTT 624
Db 121 AlaPheSerGlyLeuSerSerIleuGlnLysLeuValAlaValGlnThrAsnLeuAlaSer 140

Oy		625	CTAGAAGGTCCTCCATTTGGACAGCGCTTAAACTTAAGGAACCAATGGGTCAACAT	684
Db		141	LeugluAenPheProIleGIYhiSleuylsThrlEuLySGlueAunValAlahIsAn	160
Oy		685	TTTATACATTCCTGTAGTTACCTGCACAATATTTTTCAACTTGACCAACCTAGTACATGTG	744
Db		161	LeuilegInserPheyleuPheProclulurZrPheserAenleuthrAshleuGlulhiSleu	180
Oy		745	GATCTTTCTTATACTATATTTCAAACTATTTACTGTCAACGACTTACAGTTTCTACGTAA	804
Db		181	AspleuSerSerAshnlyleIeglInsertleYrCysThrAspleuArGValleuhIsgln	200
Oy		805	AATCCACAAGTCAACTCCTCTTTTACACATNGCTTTGAACGCCAATGTAGCTTCAATCAAC	864
Db		201	MecProleuLeuAenleuSerleuAaspleuSerleuAanPrometAasnPhelIeglInPro	220
Oy		865	CAAGCCTTTCAGGGAAATTAAAGTCATCATGAACSTGCTTAAGAGGAAATTTTAAATGTGCA	924
Db		221	GlylaIarPheLySGluIlleArgleuHiStrysleuthrLeuAArgAasnPhaespeleu	240
Oy		925	AATATATGAAAACCTGGCTTCAAAAACCTGGCTGGTTTACAGTCATCGGTGATCTTG	984
Db		241	AsnValMetCysThrCysIleglIndIyeuAagIyeuGlulValhIeArgleuValleu	260
Oy		985	GGAGAAATTTAAAGATGAAGAAGAAATTTGGAAATTTTGAACCTCTATCATGAGAGACTA	1044
Db		261	GlyguPheArgAengluGIyaSnleuGlulysPheaspLySseArAlaleuGlulngIyeu	280
Oy		1045	TGTGATGTGACCATTTAGTAGTACAGTTAACATATCAATCAAAANGATTTTTCAGATGATTT	1104
Db		281	CysasnleuthrIleglulnPheArgleuAlatYrleuAasPyrTrYrleuAasprIle	300
Oy		1105	GTTAAG--TTTCCATTCGCTTGCGCANCTTTTCTGCAATGTCTTGCGAGGTATCTATA	1161
Db		301	IleaspleuPheaenCysleuthrAshnalBerSerPheSerleuValserValThrIle	320
Oy		1162	AAATATCTAGAAGATGTTCTTAACATTTCCAATGGCAATCCTTATCAATCATTAAGATGT	1221
Db		321	GlulArGValYrVaasPheSerTyxAsnPhelglYrGlnhIsleuGluleuValAsnCys	340
Oy		1222	CAACTAAG-CAGTTTCCAACTCTGGATCTTACCCTTTCTTAAAGTTTGAACTTTAACATAG	1280
Db		341	LysPheglYgluInPheProthrLeuLysleuYserleuLyBaArgleuthrPheThrSer	360
Oy		1281	AACAAAGGCTTATCAGTTTAAAAAAAGTGGCCCTACCAAGTCACTGAGTATCTAGATCTT	1340
Db		361	AsnlysgIyeGIyaSnAlaPheSerGlulValAspleuProSerleuGlulPheAuspheu	380
Oy		1341	AGTAGAAATGACSTGAGCTTTAGTGGTGGCTGTCTTATTCTGATTTGGGAACAAACAGC	1400
Db		381	SerArgAangIyLeuSerPheLyglYocCysSerGlninserAasPheglYThrThrSer	400
Oy		1401	CTGAGACACTTAAGCTCTGAGCTTCAATGATGGCCATCATTAAGATGCCAATTTCAATGGGT	1460
Db		401	LeuYsrYrleuAaspleuSerPheAasnGlYallleThrMetSerSerAasPheleuGlY	420
Oy		1461	CTAGAAGGCTGACGACACCTGAGTTTTTACACASTCACTTAAAGAGGCGCACAGATT	1520
Db		421	LeuGlulInleuGlulhIsleuAasP-PheGlnhIsSerAsnleuLySGlnMetSerGIuPh	440
Oy		1521	CTCAGCGTCTTATCCCTTGAAGAAAGCTACTTACTTCACTGACATCTTTATATACACCAA	1580
Db		440	eSerValPheleuSerleuAArgAandeuIleTYrleuAasPrIleSerhIsthrlhIsthrAr	460
Oy		1581	AATTGACTTCGATGGTATATTTCTTGGCTTGACCAAGTCTCAACACATTTAAATGGCTGG	1640
Db		460	gValAlaPheAasngIyIlePheAasngIyLeuSerSerleuGlulValleuYsmetaGI	480
Oy		1641	CAATTCCTTCAAGACAAACCCCTTTCAAAAGTCTTTGCAAAACACAAACAACTTGACATT	1700
Db		480	YasnSerPheglIndIyuSnPheleuProAspGIlePhehrrGlulYuAArgAenleuthrPh	500

[illegible]

Db	445	Leuabp	pheglnlnhssertanleuylglnmeccserglubheservalpneleuserle	444
Oy	1539	TGAAGAAGCTATTACCTTGAACATCTCTTAATACACAAATTTGACTTCGATGGTAT		1598
Db	444	uarganleuiletyrleuadaprlleserzhlethrthshtrayalalaphenanglyl		464
Oy	1559	ATTTCCTGGCTTGAACAGACTTCACACATTTAAAAATGGCTGGCAATTTCTTCAAAGACA		1658
Db	464	ephenanglyneuserSerleugluValleuylwewerlaaglyanserPheglnGuIs		484
Oy	1659	CACCCCTTCAATATGCTTTGGCAAAACAAACAACTTGACATTCCTGGATCCTTCAATG		1718
Db	484	nphleupProasprliepethrgrluLeuargshneuthrPheueabrylseuglnCy		504
Oy	1719	TCAATTGGACAACAATATCTTGAGGGGGATTTTGACACCCCTGCATAGACTTCATTAATA		1778
Db	504	sglnleudiuglnleuserProthrlalaphenanserleuserSerleuglnValleuIs		524
Oy	1779	TATGAGTCACAACAATCTTATTTGTTTGGATTCATCCATTATACAGCTGTATTCCT		1838
Db	524	meSerthshnshenPheuserSerleuaspbthrPheProtyrlyscyIsleuanserle		544
Oy	1839	CAGACCTGTATTTGCAAGCTTTCATTCGGATAGAGACATCT--AAAGAAATCTGGACA		1895
Db	544	uglnValleuasptryserleuAenhlsllewerthserlysybnglnIuleuGlnhl		564
Oy	1896	TTTTTCCAAGAAGCTAGACCTTTCATATCTTACTTACATCAATTCGTGTGCTGTATATGCA		1955
Db	564	spheProsererleuAlaphelenuAenlthrdlnshnsbPhealacythrCySgl		584
Oy	1956	ACATCAGAAATCTCTGACAGTGGGTCAAGAAACAGAAAGCATTTGTGTGAATGTGAACA		2015
Db	584	whlsglnserPheueglntrpIlelyAsbglnaraglnleuValgluValgluar		604
Oy	2016	AATGACATGTCACACACTGTAGAGATGAATACCTCCTTACTGTGGATTTTAATATTC		2075
Db	604	gmeGlnuysalatrProserabpLySglnGlymeProvalleuserleu--Aasrl		623
Oy	2076	TACCTGTATATGTACACAAACATCATGAGTGTGACGTGCTAGTGTGATGTGATTC		2135
Db	623	ethrCyseImethcanlystrhllelecglyValserValleuserValleuValse		643
Oy	2136	CAGCTAGCAATTTGTGATATACCACTTATATTTTCACTGATACTTATGCTGGCTGTAA		2195
Db	643	rValValAlaValleuValtyrlyIsPhehyleuAenleuAlaglyCysIl		663
Oy	2196	AAAGTACAGACAGAGAAACATCTAGATGCATTTGTGATCTTACCTGAGTCAAGATGA		2255
Db	663	elystrtylyargglyuAenlletyrAspAlaPheVallletyrSerSerGlnasbgl		683
Oy	2256	GGACCTGGGTGGAATAGCTGTGTAAACAAATTTTGAAGAGAGAGCCCGCTTCACCT		2315
Db	683	uaspttryValargshnglnleuValylsasmeuglnludlyalPropropheglnle		703
Oy	2316	CTGCCTTCACTACAGACATTATTTCTGTGTAGCCATTGCTGCCAACATCATCCAGGA		2375
Db	703	ucyueuNhlslyrhrghaphehelleproglYvalAlallehAlaAenllelehlsgl		723
Oy	2376	AGGCTTCCACAAGACCGGAAGGTTATGTGTGATGTGTCTAGACATTTATTCAGACCG		2435
Db	723	uglnPhehlslyserArglyVallleValaValaserGlnhlsPhehleGlnserAr		743
Oy	2436	TTGGGTATCTTTGAATATGAGATTGCTCAAAACATGGAGATTTCTGAGACGCGCTCGG		2495
Db	743	gttPcyAlleheglnlyrGlnllealaglnthrttPclnPhleuserSerArgAlaGl		763
Oy	2496	CATCATCTTCAATGTCTTGAAGAGGTGAGAAGTCCCTGTCTGAGCGACAGCTGAATT		2555
Db	763	yllellePhehleValleuGlnlyValglulubthrleuAenlrglnGlnValgIule		783
Oy	2556	GTATTCGCTTTTAGCAGAAACCTTACCTGGAATGGAGAGACATCTCTGGGGAGGCA		2615

Db	783	uTyfArgLeuLeuSerArgAntHrTrYrLeuGlUTrPgluAspSerValLeuGlyArgHis	803
Qy	2616	CATCTTGTGGAGAAAGCTTAAAAATGCCCTATTGGATGGAAAAAGCCTCGAATCCTGAGCA	2675
Db	803	siLePheTrpArgArgLeuArgIysAlaLeuLeuAspGlyYlssSerTrpAsnProGluGI	823
Qy	2676	AACA 2679	
Db	823	yThr 824	
RESULT 7			
ID	AAB16102	standard; protein; 837 AA.	
AC	AAB16102;		
XX			
DT	26-MAR-2002	(first entry)	
XX			
DE	Human DNAX Toll like receptor (DTLR) 4 #2.		
XX			
KM	Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;		
KM	interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200190151-A2.		
XX			
PD	29-NOV-2001.		
XX			
PF	23-MAY-2001; 2001WO-US016766.		
PR	25-MAY-2000; 2000US-0207558P.		
XX			
PA	(SCHE) SCHERING CORP.		
PI	Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;		
XX			
DR	WPI; 2002-083085/11.		
XX	DR N-PSDB; AAD26292.		
PT	New DNAX Toll like receptor (DTLR) proteins, useful for treating		
PT	conditions exhibiting abnormal expression of the receptors of their		
PT	ligands, particularly abnormalities manifested by immunological		
PT	disorders.		
PS	Claim 3; Page 41; 297pp; English.		
XX			
CC	The invention relates to mammalian receptor proteins, e.g., primate,		
CC	human DNAX Toll like receptor (DTLR) protein and their corresponding		
CC	nucleic acids. The DTLR is useful for treating conditions exhibiting		
CC	abnormal expression of the receptors of their ligands. Such abnormality		
CC	is manifested by immunological disorders. In particular, the DTLR is		
CC	useful for treating various disease or disorders associated with abnormal		
CC	expression or abnormal triggering of response to a ligand. The DTLR is		
CC	also useful as an immunogen for the production of antisera or antibodies		
CC	specific, e.g. capable of distinguishing between other interleukin (IL)-1		
CC	receptor family members, for the DTLR or its various fragments. The		
CC	purified DTLR can be used to screen monoclonal antibodies or antigen-		
CC	binding fragments. The antibodies are useful for screening expression		
CC	libraries for particular expression products. These are useful for		
CC	detecting or diagnosing various immunological conditions related to		
CC	expression of DTLR or cells that express it. The present sequence is		
CC	human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.		
CC	Note: The present sequence SEQ ID NO 26 is stated to be similar to the		
CC	sequence shown in page 240-243 (AAB16116). However these sequences differ		
CC	at several locations		
XX			
SO	Sequence 837 AA;		

Alignment Scores:	4.19e-301	Length:	837
Pred. No.:	2772.50	Matches:	554
Score:	79.56%	Conservative:	100

Best Local Similarity: 67.40% Mismatches: 162
Query Match: 53.55% Indels: 7
DB: 5 Gaps: 5
US-09-396-985b-46 (1-2951) x AAIE102 (1-837)
QY 226 CTGGCTAGAGCTGTGATCATGGCACTG---TTCTTCTCTGCGCTGACCCAGAGAGCTTG 282
DB 6 LeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCysValArgProGlnSerTrp 25
QY 283 AATCCCTGCATAGAGGATGTTCTTAATATTAATCTTACCAATGCATGATCGAAATCTGAC 342
DB 26 GluProCysValGlu---ValProAsnIleThrTyrGlnCysMetGluLeuAsnPheTyr 44
QY 343 AAGTCCCTGATGATTCCTTCTTCAACCAAGACATAGATCGAGCTTCAACCCCTTG 402
DB 45 LysIleProAsnLeuProPheSerThrLysAsnLeuAsnLeuSerPheAsnProLeu 64
QY 403 AAGATCTTAAAGGCTATAGCTTCTCCAAATTTTTCAGAACTTCAGTGGCTGATTTATCC 462
DB 65 ArgHisLeuGlySerTyrSerPhePheSerPheProIleuGlnValLeuAsnLeuSer 84
QY 463 AGGTGTAATTTGAACAATTTGAAGACAGGCAATGCGATGCTTACCACTCTCTCAAC 522
DB 85 ArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuSerThr 104
QY 523 TTGATTAATGACAGAAACCTATCCAGATTTTCCCGAGAAAGTTTCTGTGACTACA 582
DB 105 LeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSer 124
QY 583 AGTTTACACATCTGTGTGCTGTGAGACAAATTTGCGCTCTTACAAAGCTTCCCTATT 642
DB 125 SerIleuGlnLysLeuValAlaValGluThrAsnLeuAlaSerLeuGlnAsnPheProIle 144
QY 643 GGAACCTTTATACCTTAAAGAACTCAATGTGCTCAACATTTTATACATCTCTGTAAG 702
DB 145 GlyHisLeuLysThrIleuLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLys 164
QY 703 TTACCTGATATTTTCCATCTGACGACCTAGACCTAGTACATGGATCTTCTTATATAT 762
DB 165 LeuProIuLysPheSerAsnLeuThrAsnLeuGlnHisLeuAsnLeuSerSerAsnLys 184
QY 763 ATTCAACATATTAATCTGTCACAGCTTACAGTTTTCAGTGAATAATGCAACAAGCTATTC 822
DB 185 IleGlnSerIleTyrCysThrAsnLeuArgValLeuHisGlnMetProLeuLeuAsnLeu 204
QY 823 TCTTTAATCATGTCTTTGAACCAATGACTTCACTTAAGACCAAGCTTTCAGGGAATT 882
DB 205 SerLeuAsnLeuSerIleuAsnProMetAsnPheIleGlnProGlyAlaPheLysGluIle 224
QY 883 AAGCTCATGAACTGATCTAGAGGTAATTTTAATGCTCAATATATATGAATAATGCTGC 942
DB 225 ArgLeuHisLysLeuThrIleuArgAsnAsnPheAsnSerLeuAsnValMetLysThrCys 244
QY 943 CTTCAAAACCTGCGTGGTTTACACGCTCATGCTGTTGATCTTGAGAGATTTAAAGATGAA 1002
DB 245 IleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValIleuGlnGluPheAsnArgGln 264
QY 1003 AGGAATGTGAATTTTGAACCTCTATATCAATGAGAGCATGATGTGATGCCATTGAT 1062
DB 265 GlyAsnLeuGlnLysPheAsnLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGln 284
QY 1063 GAGTTCAAGGTTAAACATATGAATTTTTCAGATGATATGTTAAG---TTCCATATGC 1119
DB 285 GluPheArgLeuAlaTyrLeuAsnLysTyrTyrLeuAsnAspIleIleAsnLeuPheAsnCys 304
QY 1120 TTGGCAATGTTTCTGCAATGCTCTGGCAGGTGATCTATATAATATCAAGATGTT 1179
DB 305 LeuThrAsnValSerSerPheSerPheSerLeuValSerValThrIleGlnGluValLysAsn 324
QY 1180 CTTAAACATTTTCAATGCAATCTTTATCAATCAATTAAGATGCACTAAG-CAGTTTCCA 1238
DB 325 SerTyrAsnPheGlyTyrGlnHisLeuGlnLeuValAsnCysLysPheGlyGlnPhePro 344

QY 1239 ACTGTGATCTACCCCTTTCTTAAAGTTTGACTTTTACTATGACAAAGGCTTATCAGT 1298
DB 345 ThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSerAsnLysGlyGlyAsnAla 364
QY 1299 TTTAAAGGAGGAGCCCTTACCAAGTCTGACATCTTATGATCTTATGTAATGACATGAC 1358
DB 365 PheSerGlnValAsnLeuProSerLeuGlnPheLeuAsnLeuSerArgAsnGlyLeuSer 384
QY 1359 TTTAGGAGGCGCTTATATCTGATTTTGGGAAACAACAGCCTGACACTTACGACCTC 1418
DB 385 PheLysGlyCysGlySerIleAsnSerAsnPheGlyThrThrSerLeuLysTyrLeuAsnLeu 404
QY 1419 AGCTTCAATGAGGCTCATTAATGAGTGCAATTTTCATGAGGCTTACAGAGCTGACAGAC 1478
DB 405 SerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlnGlyLeuGlnLeuGlnHis 424
QY 1479 CTGGATTTTTCAGCACTCTTATTAAGAGGTCACAGAAATTCACGCTTCTTATCCCT 1538
DB 425 LeuAsp-PheGlnHisSerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerIle 444
QY 1539 TGAAGGCTACTTACTTACCTGACATCTCTTATCTAATACCAAAATGACTTGATGCTAT 1598
DB 444 ValArgAsnLeuIleTyrLeuAsnProIleSerHisThrHisThrArgValAlaPheAsnGlyAla 464
QY 1599 ATTCTTGGCTTGACACGCTCTCAACATTTAAAGGCTGCGCAATTTCTTCAAGACAA 1658
DB 464 ePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnLys 484
QY 1659 CACCTTTCAATGTCTTTTGCAAAACAACAACATTTGACATTCCTGATCTTCAATAG 1718
DB 484 nPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPheLeuAsnLeuSerGlnCys 504
QY 1719 TCAATTGGAACAAATATCTTGGGGGATTTTGAACCCCTCAATGACCTTCAATATTAA 1778
DB 504 GlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnAlaLeuAs 524
QY 1779 TATGATCAACAACATCTATTTGTTTGGATTCATCCATTTATTAACAGCTGATTCCT 1838
DB 524 nMetSerHisAsnAsnPhePheSerLeuAsnProIleTyrLysCysLeuAsnSerIle 544
QY 1839 CAGCACTTTGATTTGAGATTTCAATGCAATGACAGACATCT--AAAGAAATCTGCAACA 1895
DB 544 GlnValLeuAspTyrSerIleuAsnHisIleMetThrSerLysGlnGlnLeuGlnHis 564
QY 1896 TTTTCCAAAGAGCTTACGCTTCTTCAATCTTATCAATTCCTGTTGCTGTATATGTA 1955
DB 564 sPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGln 584
QY 1956 ACATCAAGAAATTCCTGACGAGGTCAGGAAGACAGAGAGCTTCTTGATGATTTGAACA 2015
DB 584 uHisGlnSerPheLeuGlnThrIleLysAsnGlnGlnGlnLeuValGluValGluArg 604
QY 2016 AATGACATGTCAACACCTGTAGAGATGAATACCTCTTATGTTGATTTAATAATTC 2075
DB 604 gMetGlnCysAlaThrProSerAsnLysGlnGlnMetProValLeuSerLeu--AsnIle 623
QY 2076 TACCTGTATATGTAACAAGCAATCATCAAGTGTCTCAAGTGTCAAGTGTATTTGGTATC 2135
DB 623 eThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSerValLeuValAlaIse 643
QY 2136 CACTGTGATCTTCTGATATACACTTATTTTCACTGATCTTATTTGCTGCTGCTGTA 2195
DB 643 ValValAlaValLeuValTyrLysPheTyrPheHisLysMetLeuLeuAlaGlySerIle 663
QY 2196 AAGATACAGCAGAGAGAAAGCATCTATGATGCAATTTGTGATCTGATCGACAGATGA 2255
DB 663 eLysTyrGlyArgGlyGluAsnIleTyrAsnAlaPheValIleTyrSerSerGlnAspGln 683
QY 2256 GGACTGGGTGAAAGAGCTGTGTAAGATTTTGAAGAAAGAGTCCCGCTTCACTTCACT 2315
DB 683 uAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlnGlyValProProPheGlnLe 703

QY 2316 CTGCTTCTAGAGAGACTTATTCCTGTGTAGACCATTCCTCCAAATCATTCAGAGA 2315
 Db 703 uCyLeuHisIeYrArGAsPheIleProGlyValAlaIleHlaIaIaSenIleHISGL 723
 QY 2276 AGGCTTCCACAGAGCCGGAAGGTTATTTGGTGTCTAGACATTTATTCAGACCG 2435
 Db 723 uGlyPheHisIeYsErArGlyValIleValValSerGlnHisPheIleGlnSerAr 743
 QY 2436 TTGGTATTCCTTAAATATATGATTCGCAAAACGACGATTCCTGAGCAGCCGCTCG 2495
 Db 743 gTTPCyIlePheIleuYrGluIleAlaGlnThrTrpGlnPheIleuSerArGAlaG 763
 QY 2496 CATCATCTTCATTCCTTGTAGAGAGGTTGAGAGCTCCCTGTGAGCAGCAGTGTGATT 2555
 Db 763 yIleIlePheIleValIeugInuYsValGluYleThrIleuIeArGInuIleValG 783
 QY 2556 GTATCGCTTCTTATGAGAGAAACACTTACCTGGAATGGAGAGACATCTCTGGGGAGCA 2615
 Db 783 uTYrArGleuIeUSeArIeArGAnThrTYrIeUGluTrpGluAspSerValIeUGlyArG 803
 QY 2616 CATCTTCTGAGAGAGACTTAAATAATGCCCTATTCGATGAGAAAGCCTCGAATCCTGAGCA 2675
 Db 803 sIlePheIeTrpArGArGleuArGlySAlaIeUSeArGlyLysSerTrpAsnProGluG 823
 QY 2676 AACA 2679
 Db 823 yThr 824
 RESULT 8
 ABU04776
 ID ABU04776 standard; protein; 837 AA.
 AC ABU04776;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1442.
 XX
 KM Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KM protease; protease inhibitor; transporter; cytoskeletal protein;
 KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN W0200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002W0-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicz RM, Tomlinson AJ, Urban RG;
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1442; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a

CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIP0 at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 837 AA;
 Alignment Scores:
 Pred. No.: 4,19e-301 Length: 837
 Score: 2772.50 Matches: 554
 Percent Similarity: 79.56% Conservative: 100
 Best Local Similarity: 67.40% Mismatches: 162
 Query Match: 53.55% Indels: 7
 DB: 6 Gaps: 5
 US-09-396-985b-46 (1-2951) x ABU04776 (1-837)
 QY 226 CTGCTTCTAGAGAGACTTATTCCTGTGTAGACCATTCCTCCAAATCATTCAGAGA 282
 Db 6 LeuAlaGlyThrIleuIeProAlaMetAlaPheIeUSeArGlyValArGProGluSerTrp 25
 QY 283 AATCCCTGATAGAGAGTGTCTTATTTACTTACCAATGCATGCATGACAAATCAGC 342
 Db 26 GluProCyValGlu--ValProAsnIleThrTYrGlnYsMetGluUSeArPheTYr 44
 QY 343 AAAGCTCCGATGATTCCTTCTTCAACCAAGACATTCGATGAGCTTCAACCCCTTG 402
 Db 45 LysIleProAsnIleUSeArPheSerThrIeYsAsnIeUSeArPheAsnProIleu 64
 QY 403 AAGATCTTAAAGAGTATAGCTTCCAAATTTTTCAGAACTTCAAGTGTGATTTATTC 462
 Db 65 ArgHisIeUGlySerTYrIeSerPhePheSerPheProGluIeUGlnValIeUSeAr 84
 QY 463 AGGTGTGAATTTAAACATTTGAGACAGACGATGCGATGGCTTACACACTTCTCAAC 522
 Db 85 ArgCyGluIleGlnIleThrIleGlnIleAspGlyAlaTYrGlnSerIeUSeArHisIeUSeAr 104
 QY 523 TTGATCTGACAGAAACCTATCCAGAGTTTTCACAGAAAGTTTCTCTGAGCTTACACA 582
 Db 105 LeuIleUSeArHisIeUSeArProIleGlnSerIeUSeArValAlaPheSerGlyIleUSeAr 124
 QY 583 AGTTTGAACAATCTGTGTGTGAGACAAATTTGCGCTTCTAGAAAGCTTCCCTATT 642
 Db 125 SerIeUGlnIleUSeArValAlaValGluThrAsnIleUSeArIeUGlnIleUSeArProIle 144
 QY 643 GGAAGCTTATTAACCTTAAAGAACTCATGTGTGCTCAAAATTTTATCTTCTGTAAG 702
 Db 145 GlyHisIeUSeArThrIeUSeArGlyUSeArValAlaHisIeUSeArIleGlnSerPheIeYs 164
 QY 703 TTACCTGATATTTTCCATCTGAGCAACCTGATGATGTGATCTTCTTATTAATAT 762
 Db 165 LeuProGluTYrPheSerIeUSeArIleUSeArIleUSeArIleUSeArIleUSeArIleUSeAr 184
 QY 763 ATTCAACATATTAATCTGACAGACTTACAGTTTCTAAGTAAATGACAGATCAATCTTC 822
 Db 185 IleGlnSerIleUSeArGlyThrIeUSeArGlyValIleHisIeUSeArProIleUSeArIleUSeAr 204
 QY 823 TCTTTAGACATGCTTGTGAACCAATGACCTTATTCAGAACCAAGCTTTCAGGGAAAT 882
 Db 205 SerIeUSeArIleUSeArIleUSeArIleUSeArIleUSeArIleUSeArIleUSeArIleUSeAr 224

418 TATAGCTTCCCAATTTTTCAGAACTTCAGTGGTGGATTTATTCAGGATGTAATGAA 477
41 TysSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluLeuGln 60
478 ACAATTTGAAGACAGGACATGCGATGGCTTACACCACTTCTCAACTGATGATGACAGA 537
61 ThrIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGly 80
538 AACCCATCCAGAGTTTTCGCCAGAAAGTTTCTGTGACCTAACCAAGTTTATGACAATG 597
81 AsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIlyLeu 100
598 GTGGCTGTGAGACAAATTTGGCTCTCTAGAAAGCTTCCCATTTGACAGCTTAAAC 657
101 ValAlaValGluThrAsnLeuAlaSerLeuGluAsnProIleGlyHisLeuIlyThr 120
658 TTAAGAAATCTCAATGGGCTCACAATTTTATACATTCCTGTAAGTTACCTGACATATTT 717
121 LeuIlyGluLeuAsnValAlaHisAsnLeuIleGlnSerPheIlyLeuProGluIlyrPhe 140
718 TCCATATGACGAAGTCTGATACATGATCTTTTATTAATTAATTAATTAATTAATTAAT 777
141 SerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnIlyHisLeuAsnIlyThr 160
778 GTCAACGACCTTACAGTTTCTACGTGAATTCACAAAGTCATCTCTTTTACAGATGCT 837
161 CysIlyAspLeuGlnValLeuHisLeuIleMetProLeuSerAsnLeuSerLeuAspLeuSer 180
838 TTGAACCAATTTGACTTCAATTCACAGCAAGCTTTTACAGGAATTTAAGCTCCATGACT 897
181 LeuAsnProIleAsnPheIleGlnProGlyAlaPheIlyGluIleArgLeuHisIlyLeu 200
898 ACTTAAGAGTAAATTTTATAGCTCAATATTAATTAAGAAATCTGCTTCAAACTGGCT 957
201 ThrLeuAspSerAsnPheAspAspLeuAsnValMetIlyThrCysIleGlnIlyLeuAla 220
958 GGTTTACAGCTCCATCGGTTGATCTTGGAGAAATTTAAAGATGAAGATCTGGAATTT 1017
221 GlyLeuGlnValHisArgLeuValLeuGlyGluPheArgAsnGlnIlyAsnLeuGlnIly 240
1018 TTGAACCTCTATCATGAGAAAGATATGATGATGATGATGATGATGATGATGATGATGAT 1077
241 PheAspSerSerSerLeuGluGlyLeuCysAsnLeuThrIleGlnIlyPheArgLeuThr 260
1078 TATACAAATGATTTTTCAGATGATATTTGTAAG--TTCCATTTGCTTGGCAATGTTTCT 1134
261 TyrLeuAspIlyTyrLeuAspAsnIleIleAspLeuPheAsnCysLeuAlaAsnValSer 280
1135 GCAATGTCTGGGAGGTGATATTAATAATATCTAGAGATGTTTCCAAACATTTTCAA 1194
281 SerPheSerLeuValSerValSerIleIlyAsnArgValGluAspPheSerTyrAsnPheArg 300
1195 TGGCAATCTTATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1253
301 TrpGlnHisLeuGlnIlyLeuValAsnCysIlySerPheGlnIlyPheProIleGlnIlyLeuGln 320
1254 TTTCTTAAAGTTGATCTTAACTTATGACAAAGGCTTATCAGTTTAAAAAAGTGCC 1313
321 SerLeuIlyAspArgLeuThrPheThrAlaAsnIlySerGlyIlyAsnAlaPheSerGluValAsp 340
1314 CTACCAAGTCTCAGATCTATGATCTTATGTAAGAAATGATGATGATGATGATGATGATGAT 1373
341 LeuProSerLeuGlnIlyPheLeuAspLeuSerArgAsnGlyLeuSerPheIlyCysIly 360
1374 TCTTATTTGATTTGGGAAACAAGCTGAGACATTTAGACTTCAAGCTTCAATGATGCTC 1433
361 SerGlnSerAspPheGlyThrThrSerLeuIlyThrLeuAspLeuSerPheAsnAspVal 380
1434 ATCATTTATGATGCAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1493
381 IleThrMetSerSerAsnPheLeuGlyLeuGlnIlyIlyLeuGlnIlyHisLeuAsp-PheGlnHis 400

1494 CTCTACTTTAAAGAGGTCAAGAAATTTCTCAGCTTCTTATCTCTGAAAGAACTTACTTA 1553
400 sSerAsnLeuIlySerIleMetSerGlnPheSerValPheLeuSerLeuAsnLeuIly 420
1554 CTTTGACATCTCTTATTAACATCAACAAATTTGATGATGATGATGATGATGATGATGATGAT 1613
420 rLeuAspIleSerHisThrHisThrArgValAlaPheAsnIlyIlePheAspGlyLeuIle 440
1614 CAGTCTCAACATTTAAATTTAGCTGGCAATCTTTTCAAGACAAACCCCTTCAATGT 1673
440 uSerLeuIlyValLeuIlySerMetAlaGlyAsnSerPheGlnIlyAsnPheLeuProAspI 460
1674 CTTTGAAACACAAACAACTTACATTCCTGATCTCTTCAATGATGATGATGATGATGATGAT 1733
460 ePheThrAspLeuIlyAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnIle 480
1734 ATCTTGGGGGATTTTGAACACCTCCATGACATTCATTAATTAATTAATGATGACAAACA 1793
480 uSerProThrAlaPheAspThrLeuAsnIlyLeuGlnValLeuAsnMetSerHisAsnAs 500
1794 TCTATTTGTTTGGATTCATCCCATTTATTAACCACTGATATTCCTGACACTTGTGATG 1853
500 nPhePheSerLeuAspThrPheProTyrIlyCysLeuProSerLeuGlnValLeuAspTyr 520
1854 CAGTTTCAATGACATGACATGACATCAAAAGG--ATACGCAACATTTTCCAAAGAGCT 1910
520 rSerLeuAsnHisIleIleMetThrSerAsnAsnGlnIlyLeuGlnHisPheProSerSer 540
1911 AGCTTTCTCAATTTTACTTAACAAATTTGTTGCTTGTATATGTAATGACATGAAATTTCT 1970
540 uAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnIlyGlnSerPheIle 560
1971 GCAATGGGTCAAGAAACAAGAGCTTCTTGTGAATGTTGAACAATGATGATGCAAC 2030
560 uGlnTrpIleIlyAspGlnIlyArgGlnLeuLeuValGlnAlaGlnArgMetGlnCysAlaThr 580
2031 ACTGTGAGATGAATACCTCTTACCTTGAATTTTAAATTTTCACTGATTAATGTA 2090
580 rProSerAspIlyGlnIlyMetProValIleSerLeu--AsnIleThrCysGlnMetHis 599
2091 CAAGACATCATCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2150
599 nIlyThrIleIleGlyIlySerValPheSerValLeuValSerValValAlaValIle 619
2151 GATATACCACTTCTTATTTTCACTGATATCTTATGCTGCTGTATTAAGAAAGTACAGACAG 2210
619 uValTyrIlyPheThrPheHisLeuMetLeuValIleGlyCysIle**TyrGlyArgG 639
2211 AGAAGCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2270
639 yGluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspIlyAspIlyPheValArgAs 659
2271 TGAAGCTGTAAGAAATTTAGAAAGAGAGGCCCCCTTCACTCTGCTTCACTACAG 2330
659 nGluLeuValIlyAsnLeuGlnIlyValProProPheGlnLeuIlyCysIleHisIlyrArg 679
2331 AGACTTTATCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2390
679 gAspPheIleProGlyAlaAlaIleAlaIleAlaAsnIleIleHisGlnIlyPheHisIlySe 699
2391 CCGGAAGGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2450
699 rArgIlyValIleValValIlySerGlnHisPheIleGlnSerArgTrpCysIlePheG 719
2451 ATATGATTTGCTCAACATGACAGTTTCTGACAGCCGCTTGGACATCATCTTCAATGT 2510
719 uTyrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 739
2511 CTTTGAGAAAGTTGAGAAAGCTCTGCTGAGGACGACGATGATGATGATGATGATGATGATGAT 2570
739 IleGlnIlyValGlnIlySerThrLeuLeuArgGlnIlyValGlnLeuIlyrArgLeuIlySe 759
2571 CAGAAACACTTACCTGGAATGGAGAGCAATCTCTTGGGAGGACATCTTCTGAGAGAG 2630


```
Db      759  rAGsAnThrTyLeuGIuTrpGIuaSpSeValLeuGIuInHisIlePheTrpArgAr 779
Qy      2631 ACTTAAATAATGCCCTATTGATGGAAGAAAGCGCTGAGATCCCTGAGCAA 2676
      779  gLeuArgLySaLaLeuLeuAspGIyArGSeTrTPAsnProGIuIn 794

RESULT 11
AD057803
ID      AD057803 standard; protein; 808 AA.
AC      AD057803;
XX      12-AUG-2004 (first entry)
XX      XX
DE      Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX      XX
KW      toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW      immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
KW      sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX      XX
OS      Pan troglodytes.
XX      XX
PN      WO2004042365-A2.
XX      XX
PD      21-MAY-2004.
XX      XX
PF      03-NOV-2003; 2003WO-US036247.
XX      XX
PR      01-NOV-2002; 2002US-0423113P.
XX      XX
PA      (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX      XX
PI      Messier W;
XX      XX
DR      WPI; 2004-400726/37.
DR      N-PSDB; AD057801, AD057802.
XX      XX
PT      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT      sequence of the Old World monkey with that of a human.
XX      XX
PS      Disclosure; SEQ ID NO 24; 111pp; English.
XX      XX
CC      The invention relates to a novel method for identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an old world monkey
CC      comprising comparing the TLR4 polynucleotide sequence of the Old World
CC      monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC      method of the invention has antibacterial, immunosuppressive, and
CC      antiaesthetic activity. The method is useful in identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC      change may be associated with reduced sensitivity to Gram-negative
CC      bacterial infection. The methods, agents and composition are useful in
CC      treating sepsis, severe sepsis or septic shock and asthma. The present
CC      sequence represents chimpanzee TLR4.
XX      XX
SQ      Sequence 808 AA;

Alignment Scores:
Pred. No.:      2,15e-296      Length:      808
Score:          2730.50      Matches:      541
Percent Similarity: 80.18%      Conservative: 98
Best Local Similarity: 67.18%      Mismatches: 154
Query Match:    52.74%      Indels:      5
DB:             8      Gaps:      3

US-09-396-985B-46 (1-2951) x AD057803 (1-808)

Qy      298  GTAGTTCCTAATATTACTACCATGATGATGAGAAACTCAGCAAAAGTCCGATGAC 357
      1  ValAlaProaSnIleThrTyGIuInCysWeGIuLeuAsnPheTyLyValIleProAspSn 20
Db      358  ATTCCCTTCTTCACCAAGAACATAGATCTGAGCTTCAACCCCTTGAAGATCTTAAAAAGC 417
```

```
Db      21  LeuProPheSerThrLySaSnLeuAsnLeuAspLeuSerPheAsnProLeuArgHisLeuGIySer 40
      418  TATAGCTTCCTCCAAATTTTTCAGAACTTCAGTGGCTGATTTATCCAGAGTGAATTTGAA 477
      41  TyrSerPhePheSerPheProGIuLeuGIuValLeuAsnLeuSerPheArgGIuLeuGIu 60
Qy      478  ACAATTGAAGACAAAGCATGGCATGGCTTACACCACTCTCAAACTGATACTGACAGGA 537
      61  ThrIleGIuAspLyAlaTyGIuInSerLeuSerHisLeuSerThrLeuIleLeuThrGIy 80
Db      538  AACCTTATCCAGAGTTTTCCTCCAGAGAGTTTCTCTGACATTAACAAGTTTGAACATTC 597
      81  AsnProIleGIuInSerLeuAlaLeuGIuAlaPheSerGIyLeuSerSerLeuGIuInLySeu 100
Qy      598  GTGGCTGTGGAGACAAATTTGGCTCTCTAGAAAGCTCCCTTGTGACAGCTTATTAAC 657
      101  ValAlaValaGIuThrAsnLeuAlaSerLeuGIuAsnPheProIleGIuHisLeuLyThr 120
      658  TTAAGAAACTCAATGTGGCTCACAATTTATACATTCCTGTGAAGTTACCTGCATATTTT 717
      121  LeuLyGIuLeuAsnValaHisAsnLeuIleGIuInSerPheLySeuProGIuTyRhe 140
Qy      718  TCCAAATCTGACGAACTTACTGATCATGTGATCTTTTATTAATAATTCAACTATTACT 777
      141  SerAsnLeuThrAsnLeuGIuHisLeuAspLeuSerSerAsnLyIleGIuInSerIleTyR 160
Qy      778  GTCAAGACCTTACAGTTTCTACGCTGAAGAAATCCCAAGTCAATCTCTTTAGACATGTC 837
      161  CysThrAspLeuArgValLeuHisGIuMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
      838  TTGAACCAATTAATGACTTCATTCATCAAGACCAAGCCTTTCAGGGAATTAAGCTCCATGA 897
      181  LeuAsnProMetAsnHeIleGIuInProGIuAlaPheLySeuGIuIleArgLeuHisLySeu 200
Qy      898  ACTCTAAGAGGTAATTTTAATAGCTCAATATATATGAAAACTTGCTTCAAAACCTGGCT 957
      201  ThrLeuArgAsnAsnPheAspSerLeuAsnValMetLySerCysIleGIuInLyLeuAla 220
      958  GGTTCACGCTGCATGGTGTGATCTTCTGGAGATTTTAAAGATTAAGAAAGAAATCTGA 1017
      221  GIyLeuGIuValaHisArgLeuValaLeuGIyGIuInPheArgAsnGIuInLeuAsnLeuGIuLy 240
Qy      1018  TTGAACCCCTCTATCATGAGAGACTATGATGATGACCATTAAGATTCAGTGTAAACA 1077
      241  PheAspLySerAlaLeuGIuGIyLeuCysAsnLeuThrIleGIuInPheArgLeuAla 260
      1078  TATACAAATGATTTTTCAGATGATATTGTTAAG--TTCCATTGCTTGGCAATGTTTCT 1134
      261  TyrLeuAspTyRtyrLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnValSer 280
Qy      1135  GCATGTCTGTGGCAGGTGATGATCTATTAATAATCTTAAGAAAGTTTCTTAAACAA 1194
      281  SerPheSerLeuValSerValInThrIleLySerValaLyAspPheSerTyRAsnPheGIy 300
      1195  TGGCAATCCTTATCATCATTAATGATGATGATCACTAAG--CAGTTTCCAACTGATGATCA 1253
      301  TrpGIuHisLeuGIuLeuValaLyCysLyPheGIyGIuInPheProThrLeuLySeuLySe 320
      1254  TTTCTTAAAGATTGACTTAACTTATGAGAACAAAGGCTTATCACTTTTAAAAAAGTGCC 1313
      321  SerLeuLyArgLeuThrPheThrSerAsnLyGIyGIyAsnAlaPheSerGIuValaAsp 340
      1314  CTACCAAGTTCAGGCTATCTAGATCTTAAGTAAGAAAGACCTGAGCTTTAATGGTGGCT 1373
      341  LeuProSerLeuGIuInPheLeuAspLeuSerSerArgAsnGIyLeuSerPheLySGLyCys 360
      1374  TCTTATCTGATTTGGGAACAAAGAGCTGAGACACTTAACCTCAGCTCAATGGTGC 1433
      361  SerGIuInSerAspPheGIyThrThrSerLeuLyTyRLeuAspLeuSerPheAsnGIyVal 380
      1434  ATCATTAATGAGTGCCAATTTTCATGGGTCTAAGAGAGCTGACAGACCTGATTTTTCAGCA 1493
```


Db 381 ILethrMetSerSerAsnPhelLeuGluInLeuGluIleuAsp-PheGlnI 400
 QY 1494 CTCTACTTTAAAGAGGTGACAGAAATCTCAGCGTCTTATCCCTTGAAAGACTTCTTA 1553
 Db 400 sSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTy 420
 QY 1554 CTTTGACATCTCTTATATCTAACACCAAAATTGACTTCGATGATATTTCTTGCGCTTGAC 1613
 Db 420 rLeuAspIleSerIleThrIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSe 440
 QY 1614 CAGCTGACACATTTAAATGCTGCAATCTTTCAAGACCAACACCTTTCAAAATGT 1673
 Db 440 rSerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGluAsnPhelLeuProAspI 460
 QY 1674 CTTTGCAAAACACAACTTGACATCTCGTATCTCTTCAATGATCTTCAATTTGAACAAT 1733
 Db 460 ePheThrGluLeuArgAsnLeuIleThrPheLeuAspLeuSerGlnGluLeuGluIle 480
 QY 1734 ATCTTGAGGGGTATTTGACACCTCCATAGACTTCAATTTAAATATGAGTCAACAA 1793
 Db 480 uSerProThrAlaPheAsnSerLeuSerSerLeuGluValLeuAsnMetSerIleAsnAs 500
 QY 1794 TCATTTGTTTGGATTCATCCCATTTAACACAGCTGATTTCCCTCAGCACTTTGATTG 1853
 Db 500 nPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGluValLeuAspTy 520
 QY 1854 CAGTTTCATCGCTAGACATCT---AAAGAAATCTGGAACATTTTCCAAAGATCT 1910
 Db 520 rSerLeuAsnIleIleMetThrSerLysLysGlnGluLeuGlnIlePheProSerSerLe 540
 QY 1911 AGCCTTCTCAATCTTACTAACATTTCTGTTGATATGATGATGACATGAAATCTCT 1970
 Db 540 uAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnIleSerPheLe 560
 QY 1971 GCAGTGGGTCAAGAACAGAAAGAGTCTTGATGATGATGAAACAAATGACATGTGCAAC 2030
 Db 560 uGlnTrrPileLysAspGlnArgGlnLeuValGluValGluArgMetGluCysAlaIle 580
 QY 2031 ACCGTGAGATGAAATCCCTCCTAGTGGATTTAAATATCTTCACTGTTATATGTA 2090
 Db 580 rProSerAspLysGlnGlyMetProValLeuSerLeu--AsnIleThrCysGlnMetAs 599
 QY 2091 CAAGACATCATCATGATGTGATGATGTGATGATGTGATGATGATGATGATGATGATGAT 2150
 Db 599 nLysThrIleIleIleGlyValSerValLeuSerValLeuValSerValAlaAlaValle 619
 QY 2151 GATATACACTTCTATTTTCACTGATATCTTATGCTGCGCTGTAAGAAAGTACAGCAGAG 2210
 Db 619 uValTyrLysPhePheThrPheIleuMetLeuValGlyCysIleLysTyrGlyArgG 639
 QY 2211 AGAAGCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2270
 Db 639 yGluAsnIleLysAspAlaPheValIleTyrSerSerGlnAspGlnAspIrrValAlaGAs 659
 QY 2271 TGAAGTGTAAAGATTTAG 2330
 Db 659 nGluLeuValLysAsnLeuGlnGlyValProPheGlnLeuGlnCysLeuIleIleTyr 679
 QY 2331 AGACTTATTCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2390
 Db 679 gAspPheIleProGlyAlaIleAlaIleAlaAsnIleIleIleGluGlyPheIleIleS 699
 QY 2391 CCGGAGGTATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2450
 Db 699 rArgLysValIleValValValSerGlnIlePheIleGlnSerArgTrrPyrSlePheG 719
 QY 2451 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2510
 Db 719 uTyrGluIleAlaGlnIleThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVa 739
 QY 2511 CTTTGAGAGGTTGAGAGAGTCCCTGCTGAGCAGCAGAGTGAATGATGATGATGATGATGAT 2570
 Db 739 lLeuGlnLysValGluLysThrLeuLeuArgArgGlnValGluLeuTyrTrpArgLeuLeuSe 759

QY 2571 CAGAAACACCTACCTGATGAGAGCAATCTTGAGGAGCAATCTTGTGAGAG 2630
 Db 759 rArgAsnThrTyrLeuGlnTrrPgluAspSerValLeuGlyArgHisIlePheThrPArg 779
 QY 2631 ACTTAAATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2679
 Db 779 gLeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGluGlyThr 795
 RESULT 12
 AD057797 standard; protein: 801 AA.
 ID AD057797
 AC AD057797;
 DT 12-AUG-2004 (first entry)
 DE Squirrel monkey toll-like receptor 4 SEQ ID NO:18.
 XX
 DE toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KW sepsis; severe sepsis; septic shock; asthma; squirrel monkey.
 XX
 OS Saimiri sciureus.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 14
 FT /label= Leu, Phe
 FT
 PN WO2004042365-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 03-NOV-2003; 2003WO-US036247.
 XX
 PR 01-NOV-2002; 2002US-0423113P.
 XX
 PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
 XX
 PI Meslier W;
 DR WPI; 2004-400726/37.
 DR N-PSDB; AD057795, AD057796.
 XX
 PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX
 PS Disclosure; SEQ ID NO 18; 11pp; English.
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antisthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents squirrel monkey TLR4.
 XX
 SQ Sequence 801 AA;
 Alignment Scores:
 Pred. No.: 3,58e-296 Length: 801
 Score: 2728.50 Matches: 542
 Percent Similarity: 79.17% Conservative: 89
 Best Local Similarity: 68.01% Mismatches: 162
 Query Match: 52.70% Indels: 5
 DB: 8 Gaps: 3
 US-09-396-985B-46 (1-2951) x AD057797 (1-801)

QY	298	GTAGTTCCTAATATATCTTACCAATGCAATGCAAGAACTCACAAGATCCCTGATGAC	357
Db	1	ValValProAnaValThrTyrGlnYsnMetGluLeuAn**TyrLysIleProAspAn	20
QY	358	ATTCCCTTCAACCAAGACATAGATGATGAGCTTCAACCCCTTGAGATCTTAAAAAGC	417
Db	21	IleProPheSerThrLysAsnLeuSprLeuSerPheAnProLeuAghIleuGlySer	40
QY	418	TATAGCTTCTCCAAATTTTTCAGAACTTCAAGTGGCTGGATTTATTCAGGTGTGAATTGA	477
Db	41	HisSerPhePheAsnPheProGluLeuGlnValLeuSprLeuSerArgCysAspIleGln	60
QY	478	ACAATTGAAGCAAGACGATGGCTGTATACACCACTCTCAAACTTATCTAGACAGA	537
Db	61	ThrIleGluAspGlyAlaTyrGlnSerLeuSerThrIleuIleuThrGly	80
QY	538	AACCTTATCCAGAGTTTTCCTCCAGAAAGTTTCTGTGACTACACAGTTTAAACATCTG	597
Db	81	AsnProIleGlnAsnLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLysLeu	100
QY	598	GTGGGTGGAGAGCAAAATTTGGCCCTGTACGAAGCTTCCCTATTGGACACTTATACC	657
Db	101	ValAlaValGluThrHisIleLeuLeuSerLeuGluAsnProIleGlyHisIleuLysThr	120
QY	658	TTAAAGAACTCAATGTGGCTCACAATTTTATACATTCCTGTAAATTACTCTGCATATTTT	717
Db	121	LeuLysAspLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGlyTyrPhe	140
QY	718	TCCATCTGACGAACTAGTACATGTGAGATCTTTTATCTATCTATTCACAACTATTACT	777
Db	141	SerAsnLeuThrAsnLeuGlnHisIleuLeuSprLeuSerSerAsnAsnIleGlnAsnIleLys	160
QY	778	GTCAACGACTTACAGTTTCTACGTGAATAATCCACAGACGATCTCTTTAGACATGCT	837
Db	161	CysLysAspLeuGlnValLeuHisIleGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer	180
QY	838	TTGAACCCAAATGACTTCAATTCACAGACCAAGCCTTTCAAGGGATTAAGCTCCAGACTG	897
Db	181	LeuAsnProIleAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisIleLysLeu	200
QY	898	ACTCTAAGAGGTATTTTATATAGCTCAATTAATAAGAAACCTGGCTCAAAACCTGGCT	957
Db	201	ThrLeuAspGlyAsnAspPheAspSerLeuAsnAlaMetLysTrpCysIleGlnGlyLeuAla	220
QY	958	GGTTTACACGTCATCGTGGTGTACTCTGGAGAAATTTAAAGATGAAGAAGATCTGGAAAT	1017
Db	221	GlyLeuGlnValHisArgLeuValIleuGlyGlnPheArgAsnGlnLysArgAsnIleGlyLys	240
QY	1018	TTTGAACCTCTATCATGAGAAAGCATATGTGATGTGCACATTCAGATTCAGGTTTACA	1077
Db	241	PheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleAsnGlnPheArgLeuAla	260
QY	1078	TATACAAATGATTTTTTCAGATGATATTTGTAAG--TTCCATGGCTGGCCGATTTTCT	1134
Db	261	TyrLeuAspAspPheLeuAspAspArgIleIleAspLeuPheAsnCysLeuAlaAsnValSer	280
QY	1135	GCAATGTCTCTGGACAGGTGTATCTATAAATATCTAAGAAAGATGTTCTTAAACATTTCAA	1199
Db	281	SerPheSerLeuValAsnValHisIleLeuLysValGluAspPheSerTyrLysPheArg	300
QY	1195	TGGCAATCCTTATTCATCATTTAGATGTCA-ACTAAGACAGTTTCCAACTGTGATCTACCC	1255
Db	301	TrpGlnHisIleuGlnLeuValAsnGlyValIleGlnGlnPheProProLeuLysLeuLys	320
QY	1254	TTTCTTAAAGTTTGACTTTAATACTGAACAAAGGTCTATCAGTTTAAAAAGTGGCC	1313
Db	321	SerLeuLysArgLeuThrPheThrAlaAsnLysGlyArgAsnHisPheSerGlyValAsp	340
QY	1314	CTAACAAAGTCCAGCATCTAGATCTTATGTAAATAATGCACTGAGCTTATAGTGTGGCTGT	1373
Db	341	LeuProSerLeuGlnLysLeuAspLeuSerAspArgAsnGlyLysSerPheLysGlyCysCys	360

QY	1374	CTTAATTCGATTTGGGAAACAACAGGCTGAGCACTTAACCTCACTCAATGGTGGCC	1433
Db	361	SeGlnSerIaPheGlyThrThrSerLeuIuYgYLeuAmpLeuSerPheAaAaPVal	380
QY	1434	ATCATTTATGAGTGCACATTTCAATGGGTCTGAAGAAGCTGAGCACTCGGATTTTTCAGCA	1493
Db	381	IleThrMetGlySerAaPheLeuGlyLeuGlnGlnLeuGlnIleAaAaP-PheGlnI	400
QY	1494	CTTAACCTTAAAAAGGGCTCAGACAAATTCGAGCTTGTATTCCTGAAAACTATTTA	1553
Db	400	sSerAaPheLeuGlnMetSerGlnPheSerValPheLeuSerLeuAaPheIleuIleTy	420
QY	1554	CCTTGACATCTCTTATCTAAACACAAATTTGACTTGAGGTATATTTCCTGGCTGAC	1613
Db	420	rLeuAaPrlLeSerIleThrIleStrIaAValAlaPheAaGlnGlyIlePheAaGlnGlyLeuP	440
QY	1614	CAGTCTCAACACATTTAAAAATGCTGGCAATTCCTTCAAGAACAACACCCCTTCGAATGT	1673
Db	440	eSerIleuIuValLeuIuYsMetAlaGlyAaPheSerPheGlnGlnAaPheLeuGlnAaPrl	460
QY	1674	CTTTCGAAACAACAACAACTTGACATTCCTGGATCTCTTGAATGCAATTTGGAAACAAT	1733
Db	460	ePheThrAaPheLeuAaPheLeuIlePheLeuAaPLeuSerGlnCysGlnLeuGlnGlnIle	480
QY	1734	ATCTTGGGGGGTATTTGACACCCCTCCATGACTTCATATTAATTAATGAGTCAACA	1793
Db	480	uSerProThrAlaPheAaPserLeuProGlyLeuAaGlyIleLeuAaPheSerIleAaAaAa	500
QY	1794	TCTATGTTTGGATTCATCCCAATTATTAACACCTGTATTCCTCTGACACTCTTGATTG	1853
Db	500	nPhePheAlaLeuAaPheThrPheProGlyGlyAaIleuTyIserLeuGlnAlaLeuAaPrl	520
QY	1854	CAGTTTCATCGCATAGACATGTAAGA -- ATACTGCACATTTTCCAAAGCT	1910
Db	520	rSerLeuAaPheIleGlyThrSerIuYsAaGlnGlnIleuGlnIlePheProSerSerIe	540
QY	1911	AGCCTTCTCAATCTTACTAACAATTCGTGCTTGTAATGTAACATCAAGAAATTCCT	1970
Db	540	uAlaPheLeuAaPheLeuThrGlnAaAaPheAlaCysThrTyGlnIleGlnSerPheIle	560
QY	1971	GCAGTGGGTCAAGAAACAAGACAGTCTTGCTGTAAAGTTGTAACAATTAAGACATGCAAC	2030
Db	560	uGlnTrpIleuYsAaPrlAaGlyLeuLeuValGlnValGlnIleMetGlnCysAlaIleTh	580
QY	2031	ACCTGTAGAGATGCAATACCTCTCTTATGCTGGATTTTAATTAATTCATCTGTATATGTA	2090
Db	580	rProLeuAaPheAaPheGlyIleProValLeuSerLeu -- AaIleThrCysGlnMetSe	599
QY	2091	CAGAACAATCATCACTGTGTCACTGAGTGTGATGTGTGTATGTGTATTCACATGACATTTCT	2156
Db	599	rTySerThrIleIleGlyValSerValLeuSerValLeuValSerValAlaAlaValIle	619
QY	2151	GATATACCACTTATTTCACTGATCACTTAATGCTGGCGGTAAAGTAAGTACACAGAG	2210
Db	619	uValIuTyIuYsPheIuTyPheAaIleMetLeuLeuAlaIuYsIleuTyIuGlyAaGln	639
QY	2211	AGAAAGCACTATGATGATTTGTGATCTTACAGTGCAGATGCAGATGAGCACTGGGTGAGAA	2270
Db	639	yGlnAaPheThrTyAaPheAlaPheValIleTyIserSerGlnIaPheGlnAaPrlAaGlyAa	659
QY	2271	TGAGCTGTGAAGAATTTGAAGAAGAGTGGCCGGCTTCACTCTTGCCTTCACTACAG	2330
Db	659	ngIuLeuValIuYsAaPheLeuGlnGlnGlnIuYValProProPheGlnIleuTyCysVleuAaIuTyAa	679
QY	2331	AGACTTTATTCCTGTGTAGCACTTGGCGGCAACAATATCCAGAAAGCTTCCCAAGAG	2390
Db	679	gAaPheIleProGlyValAlaIleAlaAaPheIleIleIleGlnGlyPheAaIleYsSe	699
QY	2391	CCGAAAGGTATTTGGTAGTGTCTAGACATTTATTCAGACCGTGGTATCTTTGA	2450
Db	699	rAaGlyAaValIleValAlaSerGlnIlePheIleGlnIleAaPrlAaGlyIlePheGln	719
QY	2451	ATATAGATTGCTCAACATGGCACTTTCTGAGACCGGCTCTGGCATCATCTTCATTTGT	2510

```

Db      719  uTyrGluIleAlaGlnThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 739
Qy      2511 CCTGAGAGGTTGAGAGTCCCTGCTGAGCAGCAGAGTGAATTTGATCCCTTTCTAG 2570
Db      739  IleGlnIleValGluIleValSerLeuLeuValGlnGlnIleValGluIleuValArgLeuLeuSe 759
Qy      2571 CAGAAACACCTACCTGAGATGGAGACATCTCTGGGAGAGCAGATCTTCTGGAGAG 2630
Db      759  rArgAsnThrTyrIleuGluIleuValGlnPheSerValIleuGlyArgHisIlePheIlePheArg 779
Qy      2631 ACTTAAATGCTTATTTGATGAGAAAACCTCGAATCTGAGCAACA 2679
Db      779  gLeuArgIleValIleuLeuAspGlyArgProIlePheProGluIleuThr 795

RESULT 13
AD057782
ID      AD057782 standard; protein; 808 AA.
AC
XX      AD057782;
DT      12-AUG-2004 (first entry)
XX
DE      Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KM      toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW      immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX      sepsis; severe sepsis; septic shock; asthma; chimpanzee.
OS      Pan troglodytes.
XX
FN      WO2004042365-A2.
XX
PD      21-MAY-2004.
XX
PF      03-NOV-2003; 2003WO-US036247.
XX
PR      01-NOV-2002; 2002US-0423113P.
XX
PA      (EVOLO-) EVOLUTIONARY GENOMICS LLC.
XX
PI      Messier W;
XX
DR      WPI: 2004-400726/37.
DR      N-PSDB: AD057780, AD057781.
XX
PT      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT      sequence of the Old World monkey with that of a human.
XX
PS      Example 1; SEQ ID NO 3; 111pp; English.
XX
CC      The invention relates to a novel method for identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an old world monkey
CC      comprising comparing the TLR4 polynucleotide sequence of a human. The
CC      monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC      method of the invention has antibacterial, immunosuppressive, and
CC      antiasthmatic activity. The method is useful in identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an Old World monkey where
CC      change may be associated with reduced sensitivity to Gram-negative
CC      bacterial infection. The methods, agents and composition are useful in
CC      treating sepsis, severe sepsis or septic shock and asthma. The present
CC      sequence represents chimpanzee TLR4.
XX
SQ      Sequence 808 AA;

Alignment Scores:
Pred. No.:      6,05e-296      Length:      808
Score:          2726.50      Matches:     541
Percent Similarity: 80.05%      Conservative: 97
Best Local Similarity: 67.88%      Mismatches: 155
Query Match:    52.67%      Indels:      5
DB:             8      Gaps:         3

```

```

US-09-396-985b-46 (1-2951) x AD057782 (1-808)
Qy      298  GTAGTCTCTAATATTACCTTACCAATGATGATGATCAGAAATCTCAGCAAAAGTCCCTGATGAC 357
Db      1    ValValProAsnIleThrTyrGlnCysMetGlnLeuAsnIlePheTyrIleIleProAspAsn 20
Qy      358  ATTCCCTCTTCAACCAAGAACATAGATCTAGGCTTCAACCCCTTGAAGATCTTAAAGC 417
Db      21  LeuProPheSerThrIleuValAsnLeuAspLeuSerPheAsnProLeuAlaGlnIleuGlySer 40
Qy      418  TATAGCTTCTCAGATTTTTCAGAACTTCACTGAGCTGAGATTATTCAGGTGTAATTGAA 477
Db      41  TyrSerPhePheSerPheProGluIleuGlnValIleuAspLeuSerArgGlyIleGln 60
Qy      478  ACAATTAAGACAAAGGATGAGCATGGCTTACACCACTCTCAAACTTGATTCAGACGGA 537
Db      61  ThrIleGluAspGlyAlaTyrGlnSerLeuSerHisIleuSerThrIleuIleuThrGly 80
Qy      538  AACCTTACAGAGTTTTCCTCCAGAGAGTTTCTGGAATTAACAAGTTTGAACAATCTG 597
Db      81  AsnProIleGlnSerIleuAlaLeuGlyAlaPheSerIleuSerIleuSerIleuGlnIleu 100
Qy      598  GTGGCTGTGAGACAAAAATGGCTCTCTAGAAAGCTTCCCTATTGGACAGCTTATTAAC 657
Db      101  ValAlaValGlnThrAsnLeuAlaSerLeuGluAsnIleuProIleGlyHisIleuIleuThr 120
Qy      658  TTAAGAAATCTCAATGGCTGCTCAATTTTATATCTCTGTAAGTTAAGTTAAGTTATTT 717
Db      121  LeuIleGluIleuAsnValAlaHisIleuIleGlnSerPheIleuProGluIleuPhe 140
Qy      718  TCCAATCTGACGAACCTAGTACATGAGATCTTCTTATATATATTAATTAACAATTAAT 777
Db      141  SerAsnIleuThrAsnIleuGluHisIleuAspLeuSerSerAsnIleuIleGlnSerIleuTyr 160
Qy      778  GTCAACGACTTACAGTTTCTACGTGAATTCACAAGATCAATCTCTTTAGACATGCT 837
Db      161  CysThrAspLeuArgValIleuHisGlnMetProIleuLeuAsnIleuSerIleuAspLeuSer 180
Qy      838  TTGAACCAATTTGACTTCAATTCAGAACCAAGCTTTTCAGGAAATTAAAGCTTCATGAAC 897
Db      181  LeuAsnProMetAsnIleuIleGlnProGlyAlaPheIleuGlnIleuArgLeuHisIleu 200
Qy      898  ACTCTAAGAGTAAATTTTATAGCTCAATATATATGAAGAACTTGCCCTCAAAACCTGGCT 957
Db      201  ThrLeuArgAsnAsnIleuAspSerLeuAsnValMetCysThrCysIleGlnIleuAla 220
Qy      958  GGTTCACAGCTTCATGCTGATCTTGGAGAAATTTAAAGATGAAGAAATCTGGAATTT 1017
Db      221  GlysLeuGluValHisIleuArgLeuValIleuGlyGluPheArgAsnIleuGluAsnIleuGly 240
Qy      1018  TTTGAACCTCTTATCATGAGAGACATATGATGACCATGATGATGATTCAGGTTAACA 1077
Db      241  PheAspIleuSerIleuAlaLeuGluGlyLeuCysAsnIleuThrIleGluIleuPheArgLeuAla 260
Qy      1078  TATTAACAATATTTTTCAGATGATGATTTTAAAG---TTTCATGCTTGGGGAATGTTTCT 1134
Db      261  TyrLeuAspIleuTyrIleuAspAspIleuIleAspLeuPheAsnIleuCysIleuThrAsnValSer 280
Qy      1135  GCAATGCTCTGAGAGGTTGATCTATTAATAATATCTTGAAGATGTTCTTAAACATTTCAAA 1194
Db      281  SerPheSerIleuValSerValThrIleuIleuSerValIleuAspPheSerIleuAsnIleuGly 300
Qy      1195  TGGCAATCTTATCAATCATTAAGATGCAACTAAG-CAGTTTCAACTGTGATCTTAACC 1253
Db      301  TrpGlnHisIleuGluIleuValIleuValIleuValIleuGlyIleuPheProThrIleuIleu 320
Qy      1254  TTTCTTAAAGTTTGACTTTAATCAATGAACAAGAGGCTATCGTTTAAAGAGTGCC 1313
Db      321  SerLeuIleuArgLeuThrPheThrSerAsnIleuGlyGlyAsnIleuPheSerGluValAsp 340
Qy      1314  CTACCAAGTCTCAGATCTAGATCTTAGTAGAAAGCACTGAGCTTATGATGCTGCTG 1373

```

Db 341 LeuProSerLeuGluIupheLeuAspLeuSerAArgAnGlyLeuSerPheGlyCySeCySe 360
 QY 1374 TCTTATTCTGATTGGGAAACAAGCCTGAGACACTTGAAGCTTCACTGATGGTCC 1433
 Db 361 SerInSerAspPheGlyThrThrSerLeuIysThrLeuAspLeuSerPheAsnGlyVal 380
 QY 1434 ATCATTTTGGAGTGCATTTTCAATTCAGATAGAGAGTGCAGACCTGGATTTTTCAGA 1493
 Db 381 IleThrMetSerSerAsnPheLeuGlyLeuGluGlnLeuGlnIleuAspPheGlnIle 400
 QY 1494 CTCTACTTTTAAAAAGGTCACAGAAATTCAGCGTCTTATCCCTTGAAGAACTACTTTA 1553
 Db 400 SerAsnLeuIysGlnMetSerGluPheSerValPheLeuSerLeuArgLeuIleTy 420
 QY 1554 CCTTGACATCTCTTATCTAACAACCAAAATTCAGTGGATGATATTTCTTGCTTGAC 1613
 Db 420 rLeuAspIleSerThrIleThrIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSe 440
 QY 1614 CAGTCTCAACACATTTAAAAATGGCTGGCAATTTCTTCAAGACAAACCCCTTCAAAATGT 1673
 Db 440 rSerLeuGluValLeuIysMetAlaGlyAsnSerPheGlnGlnIleuAsnProAspIle 460
 QY 1674 CTTCGAAACAAACAACCTTACATTCCTTGATCTCTTAAATGTCAATTGAAACAAT 1733
 Db 460 ePheThrGluLeuArgLeuLeuThrPheLeuAspLeuSerGlnCySglnLeuGluGlnLe 480
 QY 1734 ATCTTGGGGGGTATTGACACCCCTCCATGACTTCAATTATTAATATGAGTCAACA 1793
 Db 480 uSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerIleAsnAs 500
 QY 1794 TCTATTGTTTGGATTCATCCCATTTAAACAGCTGATTCCTCCAGCACTCTTGATTTG 1853
 Db 500 nPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAspTyr 520
 QY 1854 CAGTTTCAATGCAATAGACATCT--AAAGAAATATGCAACATTTCCAAAGAGTCT 1910
 Db 520 rSerLeuAsnIleSileMetThrSerLysGlnGlnLeuGlnIlePheProSerSerLe 540
 QY 1911 AGCCTTCTTCAATCTTACTAACAATTCGTGCTTGTATGTATGTAACATCGAAATTCCT 1970
 Db 540 uAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnIleGlnSerPheLe 560
 QY 1971 GCAGTGGGTCAAGACAGAGAGAGTCTTGATGATTTGAACAATGATGATGCAAC 2030
 Db 560 uGlnThrIleLysAspGlnArgGlnLeuLeuValGluValGlnArgMetGluCysAlaThr 580
 QY 2031 ACCTGTAGATGAAATACCTCTTATGTTGATTTTAATTAATCTTATATATGTA 2090
 Db 580 rProSerAspLysGlnGlyMetProValLeuSerLeu--AsnIleThrCysGlnMetAs 599
 QY 2091 CAAGACATCATCAGTGTGTGATGTCAGTGTGATTTGTGATTCACCTGATGACATTTCT 2150
 Db 599 nLysThrIleIleGlyValSerValLeuSerValLeuValSerValAlaAlaValLe 619
 QY 2151 GATATACCATCTTATTTTACCTGATCTTATGCTGCTGTTAAAAAGTTCACAGAGAG 2210
 Db 619 uValTyrIleLysPheThrPheIleSileMetLeuLeuAlaGlyCysIleLysTyrGlyArgG 639
 QY 2211 AGAAGACATCATGATGATTTGTGATCTACTGATGATGATGATGATGATGATGATGAT 2270
 Db 639 yGluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGluAspTyrValArgAs 659
 QY 2271 TGAGTGTGTAAGAAATTTGAAGAGAGAGTCCCGCTTTCACCTCTGCTTCACTACAG 2330
 Db 659 nGluLeuValLysAsnLeuGluGlnGlyValProProPheGlnLeuCysLeuIleTyrAs 679
 QY 2331 AGACTTATTCCTGTTAGCATGTCGATGTCGCAACATCATCCAGAGAGCTTCCCAAGAG 2390
 Db 679 gAspPheIleProGlyValAlaIleAlaAlaAsnIleIleHISglnGlyPheAsnLysSe 699
 QY 2391 CCGAAGAGTTATTTGTGATGTCATGACATTTATTCAGAGCCCTTGATGATCTTGA 2450
 Db 699 rArgLysValIleValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGln 719

QY 2451 ATATGAGATTGCTCAACATGGCAGTTCCTGAGCAGCCGCTGCGCATCTTATGTG 2510
 Db 719 uTyrGluIleAlaGlnThrThrPheLeuSerSerArgAlaGlyIleIlePheLeuVal 739
 QY 2511 CCTTGAAGAGTGTGAGAAGTCCCTGCTGAGGACAGATGGAATTTATCGCTTTTGA 2570
 Db 739 IleGlnLysValGlnLysThrLeuLeuArgArgGlnValGluLeuTyrArgLeuLeuSe 759
 QY 2571 CAGAAACACCTTACCTGGAATGGAGAGCAATCTCTGGGGAGACATCTTCGAGAGAG 2630
 Db 759 rArgAsnThrTyrLeuGluThrPheGlnAspSerValLeuGlyArgHisIlePheThrArg 779
 QY 2631 ACTTAAAAATGCGCTTATGATGAAAGCTGCAATCCTGAGCAACA 2679
 Db 779 gLeuArgLysAlaLeuLeuAspIleLysSerThrAsnProGluGlyThr 795
 RESULT 14
 ID AD057800 standard; protein; 795 AA.
 AC AD057800;
 DT 12-AUG-2004 (first entry)
 XX
 DE Hamadryas baboon toll-like receptor 4 SEQ ID NO:21.
 XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KM sepsis; severe sepsis; septic shock; asthma; hamadryas baboon.
 XX
 OS Papio hamadryas.
 XX
 FN W02004042365-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 03-NOV-2003; 2003W0-US036247.
 XX
 FR 01-NOV-2002; 2002US-0423113P.
 XX
 PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
 XX
 PI Mesleier W;
 XX
 DR WPI; 2004-400726/37.
 DR N-PSDB; AD057798, AD057799.
 DR
 PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX
 PS Disclosure; SEQ ID NO 21; 111pp; English.
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The method, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents hamadryas baboon TLR4.
 XX
 SQ Sequence 795 AA;
 Alignment Scores:
 Pred. No.: 2,83e-295 Length: 795
 Score: 2720.50 Matches: 540
 Percent Similarity: 79.65% Conservative: 94
 Best Local Similarity: 67.84% Mismatches: 158

Query Match: 52.55% Indels: 5
 DB: 8 Gaps: 3
 US-09-396-985b-46 (1-2951) x AD057800 (1-795)

QY 298 GTAAGTCTTAATATTAATCAATGCAATGATGAGAAATCAAGCAAAATGCTGATGAC 357
 1 ValValProAsnIleThrTyGlnCysMetCgluLeuAsnPhetyrLysIleProAspAsn 20
 QY 358 ATTCCCTTCAACCAAGACATAGATCTGAGCTTCAACCCCTTGAAGATCTTAAAGC 417
 21 IleProheSerThrLysAsnLeuAspLeuSerPheAsnProLeuAaGhLsleuGlySer 40
 QY 418 TATAGCTTCTCAATTTTTCAGAACTTCAGTGCCTGATTTATCCAGGTGAAATGAA 477
 41 TySerPheLeuAaGpHeProGluLeuGlnValLeuAspLeuSerAaGyGgluIleGln 60
 QY 478 ACAATTGAAGCAAGGATGAGATGCTTACACCACTTCAAACTTGATTAAGTACAGA 537
 61 ThrIleGluAspGlyAlaTyGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGly 80
 QY 538 AACCTTATCCAGAGTTTTCCTCCAGAAATGTTCTCTGACATTAACAATTTAGCAATCTG 597
 81 AsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLysLeu 100
 QY 598 GTGGCTGTGAGACAAATGAGCTCTCTGAAGAGCTCCCTATTTGACAGCTTAAAC 657
 101 ValAlaValGlnThrAsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuLysThr 120
 QY 658 TTAAGAACTCAATGTGGCTCACAATTTTATACATTCCTGTAAAGTACCTGATATTTT 717
 121 LeuLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluLysPhe 140
 QY 718 TCCATCTTGACGAACCTTAAGTATGATGATTTTCTTATTAATCTATTAATCAATTTACT 777
 141 SerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnAsnIleTyL 160
 QY 778 GTCAAGCACTTACAGTTTCTACGTAAGAAATCCACAGTCAATCTCTGTTAGACATGCT 837
 161 CysLysAspLeuGlnValAlaHisGlnMetProLeuProAsnLeuSerLeuAspLeuSer 180
 QY 838 TTGAACCAATTAAGCTTCAATTCAGAACCAAGCTTTGAGGAAATTAAGCTTCATGAATG 897
 181 LeuAsnProIleAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLysLeu 200
 QY 898 ACTTAAGAGGATATTTTATAGCTCAAAATTAATGAAGAACTTCCCTTCAAACTGGCT 957
 201 ThrLeuAspSerAsnPheAspAspLeuAsnValMetLysThrCysIleGlnGlyLeuAla 220
 QY 958 GGTTTACAGTCCATCGGTTGATCTTGAGAAATTTTAAAGTGAAGAAATTCGGAATT 1017
 221 GlyLeuGlnValAlaHisArgLeuValLeuGlyGlnPheArgAsnGlnValGlnAsnLeuGln 240
 QY 1018 TTGAACCTCTATCATGAGAAAGATATGATGATGACATTTGATGATTCAGTTTAA 1077
 241 PheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGluPheArgLeuThr 260
 QY 1078 TATACAAATGATTTTTCAGATGATATGTTAG--TTCCATTCCTTGGCAATGTTTCT 1134
 261 TyLeuAspTyLysTyLeuAspAsnIleIleAspLeuPheAsnCysLeuAlaAsnAlaSer 280
 QY 1135 GCATGCTCTGGAGAGTATATTAATAATATTAAGATGTTTCTTAAACATTTGAA 1194
 281 SerPheSerLeuValSerValAsnIleLysArgValGlnAspPheSerTyAsnPheArg 300
 QY 1195 TGGCAATCTTATCATCATTAAGATGATCACT--AAGCAGTTTCCAACTGATCTTACCC 1253
 301 TrpGlnHisLeuGlnLysLeuValAsnCysLysPheGlnGluPheProHisLeuGlnLys 320
 QY 1254 TTTCTTAAAGTTGACTTATTAATGAACAAGAGGCTTATCACTTTTAAAGAGTGGCC 1313
 321 SerLeuLysArgLeuThrPheThrAlaAsnLysGlyGlnLysAsnAlaPheSerGlnValAsp 340

QY 1314 CTACCAAGTCTCAGCTATCTAGATCTTATAGAAATGCACTGAGCTTATGCTGCTGT 1373
 341 LeuProSerLeuGlnPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCysCys 360
 QY 1374 TCTTATTTGATTTGGGACAAACAGCTGAGACACTTGAACCTCAGCTTCAATGCTGCC 1433
 361 SerGlnSerAspPheGlyThrThrSerLeuLysTyLeuAspLeuSerPheAsnAspVal 380
 QY 1434 ATCATTAATGAGTCCCAATTTCAATGCTTGAAGAGTGCAGACCTTGATTTTTCGCA 1493
 381 IleThrMetCysSerAsnPheLeuGlyLeuGlnGlnMetCylHisLeuAsp-PheGlnHis 400
 QY 1494 CTCTACTTTTAAAGAGGTCAAGAAATTCAGAGCTTCTTATCCCTTGAAGAACTACTTTA 1553
 400 SerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTy 420
 QY 1554 CTTTGACATCTCTTATTAATCAACCAAAATTAAGTACCTGATGATATTTCTTGCTTGAC 1613
 420 IleuAspIleSerHisThrHisThrThrValAlaPheAsnGlyIlePheAspGlyLeuLe 440
 QY 1614 CAGTTCACACATTAATAAATGCTGCAATTCCTTCAAAAGACACCCCTTCAAAATGT 1673
 440 uSerLeuLysValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspI 460
 QY 1674 CTTTGCAACACAAACAACTTGACATTCCTGATCTCTTAAATGTCATTTGACAAAT 1733
 460 ePheThrAspLeuLysAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnLe 480
 QY 1734 ATCTTGAGGAGGATTTTGACACCTCCATAGACTTCAATTTATTAATTAATGATCAACAA 1793
 480 uSerProThrAlaPheAspThrLeuAsnLysLysGlnValLeuAsnMetSerHisAsnAs 500
 QY 1794 TCTATGTTTTCGATTCATCCCATTAACACAGCTGATTCCTCAGACCTCTGATTTG 1853
 500 nPhePheSerLeuAspValPheProTyLysCysLeuProSerLeuGlnValLeuAspTy 520
 QY 1854 CAGTTTCAATCGCATGAGACATCTTAAAGAA--ATATCTGCAACATTTTCCAAAGAGCT 1910
 520 rSerLeuAsnHisIleMetThrSerLysAsnGlnGluProGlnHisPheProSerSerLe 540
 QY 1911 AGCTTCTTCAATCTTATCAACAAATTCGTTGCTTGTATATGTCACATCAAGAAATTCCT 1970
 540 uAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisIleGlnSerPheLe 560
 QY 1971 GCAGTGGGTCAAGAAACAGAAAGAGTTCCTGCGAATGTTGAACAATGACATGTGGAAC 2030
 560 uGlnTrpIleLysAspGlnArgIleLeuLeuValGluAlaGluArgMetGluCysAlaThr 580
 QY 2031 ACCTGTAAGATGAATAACCTCCTTAGTGTGATTTTAAATTTCACTGATTAATGTA 2090
 580 rProSerAspLysGlnGlyMetProValLeuSerVal--AsnIleThrCysGlnMetCAs 599
 QY 2091 CAAGACATCATCAGTGTGTCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 2150
 599 nLysThrIleIleGlyValSerValPheSerValLeuValValSerValValAlaValLe 619
 QY 2151 GATATACACTTATTTTCACTGATACCTGATATCTTATGCTGCTGCTGTAAGAAAGTACAGAG 2210
 619 uValTyLysPheTyPheHisLeuMetCysLeuLeuAlaGlyCysIleLysTyIleTyArgI 639
 QY 2211 AGAAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2270
 639 yGlnAsnIleTyAspAlaPheValIleTySerSerGlnAspGlnAspTrpValArgAs 659
 QY 2271 TGAAGTGTAAAGAAATTTGAAGAAAGAGAGTCCCGCTTACCTTGCCTTCACTAAG 2330
 659 nGlnLeuValLysAsnLeuGlnGlnGlyValProporPheGlnLeuCysLeuHisTyArg 679
 QY 2331 AGACTTTATTCCTGCTGATGAGCTTGTGTCGACATCATTCACAGAAAGGCTTCCACAAAG 2390
 679 gaPhePheIleProGlyValAlaIleAlaIleAlaIleHisGlnGlyPheHisLysSer 699
 QY 2391 CCGAAGGTTATGTGTAGTGTCTAGACACTTATTCAGAGCGCTTGATGATCTTTGA 2450

Db 699 rarglyvalillevaivalserginhisphenileclnserargtrypcyllepegl 719
 QY 2451 ATATGAGATTGCTCAACATGAGCAGTTTCTGAGCAGCCGCTGGCATCATCTTCATTGT 2510
 Db 719 uTYGluil1a1aglnthrtprglnpheleuserserarg1a1c1ylellephenileva 739
 QY 2511 CCTTGAGAGGTTGAGAGGTCCTGAGGAGCAGAGGAGTGTATGATGCTTCTAG 2570
 Db 739 l1euglnlyvalc1u1ystrh1eulnarg1nglnvalc1u1euty1rarg1euln 759
 QY 2571 CAGAAACACCTACCTGAGATGAGAGCAATCCTCTGGGAGCAGCATCTTCTGAGAG 2630
 Db 759 rArgAenThrtYrleuclun1rpg1uapservalleucl1ygl1nhi1le1hetrpargar 779
 QY 2631 ACTTAAAAATGCCCTATTGATGAGAAAACCTCGAATCTTGAGCA 2676
 Db 779 glenArglyalaleu1eulnspg1yArgser1rpsAnproglucln 794
 RESULT 15
 ADOS7785 ID ADOS7785 standard; protein; 808 AA.
 AC ADOS7785;
 DT 12-AUG-2004 (first entry)
 XX
 DE Gorilla toll-like receptor 4 SEQ ID NO:6.
 XX
 KW toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KM sepsis; severe sepsis; septic shock; asthma; gorilla.
 XX
 OS Gorilla gorilla.
 XX
 PN WO2004042365-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 03-NOV-2003; 2003WO-US036247.
 XX
 PR 01-NOV-2002; 2002US-0423113P.
 XX
 PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
 XX
 PI Messier W;
 XX
 DR WPI; 2004-400726/37.
 DR N-PSDB; ADOS7783, ADOS7784.
 XX
 PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX
 PS Example 1; SEQ ID NO 6; 111pp; English.
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents gorilla TLR4.
 XX
 SQ Sequence 808 AA;
 Alignment Scores: 6.38e-294 Length: 808
 Pred. No.: 2708.50 Matches: 538
 Score:

Percent Similarity: 79.80% Conservative: 98
 Best Local Similarity: 67.50% Mismatches: 157
 Query Match: 52.32% Indels: 5
 DB: 8 Gaps: 3
 US-09-396-985b-46 (1-2951) x ADOS7785 (1-808)
 QY 298 GTAGTCCCAATATTTACCTACCAATGATGATCAGAAATCAGAAAGTCCATGAC 357
 Db 1 ValValProksn1leThrtYr1ng1ncYsweGlu1eulnAenPhe1rY1s1leP1roApsn 20
 QY 358 ATTCTCTTCAACCAAGAACATATGATCTGAGCTTCAACCCCTTGAAGATCTTAAAGC 417
 Db 21 leuProPheSer1hrtYr1s1nleu1eulnAenPhe1s1rPhe1s1nPro1euln1rgh1s1leu1g1s1er 40
 QY 418 TATAGCTTCCCAATTTTCAAGAACTTCAGTGCTGATTTATCCAGGTGTAATGAA 477
 Db 41 TyrSerPhePheSer1hrtYr1s1nleu1eulnAenPhe1s1rPhe1s1nPro1euln1rgh1s1leu1g1s1er 60
 QY 478 ACAATTGAAGACAAAGGATGAGCATGGCTTACACCTCTCAAACTTGATGACAGCA 537
 Db 61 Thr1leGlu1nspolYal1atYr1ng1nser1eulnser1h1eulnser1h1euln1euln1rgh1s1er 80
 QY 538 AACCTATCCAGAGTTTTCCTCCAGAGATTTCTGAGATTAACAAGTTTGAACAATCTG 597
 Db 81 AsnPro1leGlnser1euln1aleu1g1yAlaPheSer1d1y1eulnser1euln1g1n1s1eul 100
 QY 598 GTGCTGTGAGACAAATTTGGCTCTTGAAGAGCTTCCCTTGTGACAGCTTATAAC 657
 Db 101 ValAlaValAlGluThrs1nleu1eulnA1s1er1eulnA1s1nPh1e1r1leG1y1s1leu1s1tr 120
 QY 658 TTAAGAAACTCAATGTGGCTCACAATTTATCATCTTCTGTAAGTACCTGATATTTT 717
 Db 121 leu1y1s1euln1euln1Val1ah1s1nleu1leGln1s1er1Phe1y1s1eulnPro1g1u1Yr1Phe 140
 QY 718 TCCAACTGACGAACTAGTACATGTGATCTTCTTATATCATATTAATTAATTAAT 777
 Db 141 SerAsnleuThrs1nleu1g1u1Yr1eulnA1s1er1euln1s1er1euln1s1er1euln1s1er 160
 QY 778 GTCAAGCATTTACAGTTTCTGACGTAATCCCAAGTCAATCTCTTTAGCATGTCT 837
 Db 161 CysThrs1rAs1euln1rgh1Val1euln1s1g1n1s1er1Pro1leu1euln1s1er1eulnA1s1er 180
 QY 838 TTGAACCAATGATCTTCAATTCAGCAAGACCTTCAAGGATTAAGCTCCATGAC 897
 Db 181 leuAsnPro1eulnThrs1nleGln1rgh1AlaPhe1y1s1euln1le1arg1euln1s1tr1s1eul 200
 QY 898 ACTTAAGAGTAAATTTATAGCTCAATATATATGAAAACTTGCTTCAAACTGGCT 957
 Db 201 Thr1euln1rgh1s1n1s1n1Phe1s1er1eulnA1s1er1eulnA1s1er1eulnA1s1er 220
 QY 958 GGTTTACAGCTCCATGCTGATCTTGGGAGATTTTAAAGATGAAAGATCTGGAAT 1017
 Db 221 Gly1euln1Val1Arg1rgh1euln1Val1euln1g1y1u1Phe1rgh1s1n1g1y1euln1g1u1s1 240
 QY 1018 TTTGAACCCCTCATGAGAGGATGATGATGATGATGATGATGATGATGATGATGAT 1077
 Db 241 Phe1s1r1s1er1euln1euln1g1y1euln1s1er1euln1s1er1euln1s1er1euln1s1er 260
 QY 1078 TATACAAATGATTTTTCAGATATGTTAG--TTCCATGCTTGGGAAATGTTCT 1134
 Db 261 Tyr1eulnA1s1rYr1r1eulnA1s1r1le1le1As1Phe1s1n1Cys1eulnThrs1nVal1s1er 280
 QY 1135 GCATGTCTTGGCAGGTATCTATTAATATCTGAAGATGTCTCTAAACATTTCAA 1194
 Db 281 SerPheSer1eulnVal1s1erVal1Thr1leGln1rgh1s1rgh1s1rgh1s1rgh1s1rgh1s1r 300
 QY 1195 TGGCAATCCTTATCATCATTAATGATGACAACTAAG--CAGTTTCAACTCTGATCTACCC 1253
 Db 301 TrpGln1h1s1euln1euln1Val1euln1s1er1euln1s1er1euln1s1er1euln1s1er1euln1s1er 320
 QY 1254 TTTCTTAAAGTTTGAATTAATGATGACAAAGGCTTATCAGTTTAAAGAGTGCC 1313

Db 321 SerLeuYsArGLeuThrPheThrSerAsnIysGlyAlaAsnAlaPheSerGluValAsp 340
 QY 1314 CTACCAAGTCTCAGCTATCTAGATCTTAGTAAGAATGCAGTGAAGTTAGTGGCGT 1373
 Db 341 LeuTrSerLeuGluPheLeuAspLeuSerArGAsnGlyLeuSerPheIysGlyCysAs 360
 QY 1374 TCTTATTCGATTTGGGAACAACAGCTGAGACCTTAGACCTCAGCTTCATGTGCC 1433
 Db 361 SerGInSerAspPheGlyThrThrSerLeuYsTrIleuAspLeuSerPheAsnGlyVal 380
 QY 1434 ATCATATAGATGCCAATTTAGAGGTTAGAAAGCTGCGACACCTGGATTTTTCAGCA 1493
 Db 381 IleThrMetSerSerAsnPheLeuGlyLeuGlnIleuGlnIleuAsp-PheGlnI 400
 QY 1494 CTCTACTTAAAGGGGTCAAGAAATTCAGCGTCTTATCCCTGGAAGAAAGCTACTTA 1553
 Db 400 SSerAsnLeuYsGlnMetSerGluPheSerValPheLeuSerLeuArGAsnIleuY 420
 QY 1554 CCTTGACATCTCTTATTAACAACCAAAATTCAGTGTGATATTTCTTGCGCTTGAC 1613
 Db 420 rLeuAspIleSerIsthristhriArgValAlaPheAsnGlyIlePheAsnGlyLeuSe 440
 QY 1614 CAGTCTCAACATTTAAATGCTGCGCAATTCCTTCAAGACAACACCTTCAAAATG 1673
 Db 440 rSerLeuGluValIleuYsMetAlaGlyAsnSerPheGlnIleuAsnPheLeuProAspI 460
 QY 1674 CTTTGCAAAACACAACAACTTGATCTCCGTGATCCTTCAATGCAATTTGGAACAAAT 1733
 Db 460 ePheThrGluLeuArGAsnLeuTrnPheLeuAspLeuSerGlnCysGlnLeuGlnIle 480
 QY 1734 ATCTTGGGGGTATTTGACACCTTCATAGACTTCATTAATTAATATGAGTCAACA 1793
 Db 480 uSerProThrAlaPheAsnSerLeuSerSerLeuGlnValIleuAsnMetSerIleAsnAs 500
 QY 1794 TCTATTGTTTGGATTCATCCATTAATACACAGCTGATTCCTCAGACACTTGTGATG 1853
 Db 500 nPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuArGValIleuAspTy 520
 QY 1854 CAGTTCAATGCGATAGACATCT--AAAGAAATCTGCAACATTTCCAAAGAGCT 1910
 Db 520 rSerLeuAsnIsthIleMetThrSerLysGlnGlnIleuGlnIsthPheProSerSerLe 540
 QY 1911 AGCTTCTTCATCTTACTTAACAATTCGTTGTTGATTAATGATACATGAAATTCCT 1970
 Db 540 uAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnIsthIleGlnSerPheLe 560
 QY 1971 GCAGTGGGTCAAGACAGACAGAGCTTGTGTAATGTTGAACAAATGACATGTGCAC 2030
 Db 560 uGlnTrpIleLysAspGlnArgGlnLeuLeuValGluValGluArgMetGlnCysAlaTh 580
 QY 2031 ACCGTAGAGATGAATACCTCCTTAGTGTGATTTAATATTAATTCCTGTTATANGTA 2090
 Db 580 rProSerAspLysGlnIleMetProValIleuSerLeu--AsnIleThrCysGlnMetAs 599
 QY 2091 CAAGACAATCATCAGTGCAGGTCAGGTCAGGTCAGTGTGATTCACCTGAGACATTCCT 2150
 Db 599 nLysThrIleIleGlyValSerValIleuSerValIleuValSerValAlaIleValIle 619
 QY 2151 GATATACACTTCTATTTTCACTGATATCTTATGCTGCTGTAAAAAGTACAGACAGAG 2210
 Db 619 uValIlyLysPheThrPheIsthIleuMetLeuLeuAlaGlyCysrIleLysTrpGlyArgG 639
 QY 2211 AGAAGATCTATGATGATTTGATGATCTAGATCAGATCAGATGAGATGAGGTGAGAAA 2270
 Db 639 yGluAsnValIlyAspAlaPheValIleYrSerSerGlnAspGlnAspTrpValArgAs 659
 QY 2271 TGAAGTGTAAAGATTAGAGAGAGAGAGGCGCGCTTTCACCTGCGCTTCATACAG 2330
 Db 659 nGluLeuValIlyAsnLeuGlnGlyValProProPheGlnLeuYsIleuHsTrpAr 679
 QY 2331 AGACTTATTCCTGCTGATGACATGCTGCCAATCATCATCAGGAAGGCTTCCACAAAG 2390
 Db 679 gAspPheIleProGlyValAlaIleAlaAsnIleIsthIleGlnIlyPheHsIlySe 699

QY 2291 CCGAAGATTATGTTGGTAGTGTCTAGACATTTATCAGAGCGGTGGTGTATCTTGA 2450
 Db 699 rArgIyValIleValValIsthIsthIsthIsthIsthIsthIsthIsthIsthIsthIsth 719
 QY 2451 ATATGATATGCTCAACATGCGAGTTCGTGAGCAGCGCTCGGCATCATCTTCATGT 2510
 Db 719 uTyrGluIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIsthIsthIsthIsth 739
 QY 2511 CCTTGAGAAGTTGAGAAATCCCTGCTGAGCAGCAGAGTGAATTTGATGCTTCTTAG 2570
 Db 739 IleuGlnLysValGluLysThrLeuLeuArgGlnGlnValGluLeuYrArGLeuLeuSe 759
 QY 2571 CAGAAACACCTACCTGGAATGGAGAGCAATCCTGTGGAGAGGACATCTTGTGAGAG 2630
 Db 759 rArgAsnThrTrpLeuGlnTrpGlnAspSerValIleuGlyArgIsthIsthIsthIsthIsth 779
 QY 2631 ACTTAAATGATCCCTATTTGATGGAAGAAAGCTCGAATCCTGAGCAACA 2679
 Db 779 gLeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlyThr 795

Search completed: March 29, 2005, 17:03:32
 Job time : 193.387 secs

This Page Blank (uspto)


```

Db      |||||
36  GluValAlProbenilIethrIyGlnCywecoluleuabnpheIyIysIleProAsp 55
Qy      355 GACATTCCTCTTCACCAAGAAATGATGTGAGCTTCAACCCCTGGAAGATCTTAAAA 414
Db      56 AsnLeuProbeserIthrIyAsnLeuAspLeuSerPheAsnProLeuAlaPheGlnIys 75
Qy      415 AGCATATGCTTCTCAATTTTTCAGACTTCAGTGGCTGATTTATTCAGGTGGAAT 474
Db      76 SerIySerPhePheSerPheProGlnLeuGlnValLeuAspLeuSerAlaGysGlnIle 95
Qy      475 GAAACAATGAAACAAGGATGGCATGGCTTACACACCTCTCAAACTTGATATGACA 534
Db      96 GlnThrIleGlnAspGlyAlaIyGlnSerIleuSerIleuSerThrIleuIleLeuThr 115
Qy      535 GGAACCTCTATCCAGAGTTTTCACCAAGAGTTTCTGTGACATACAAAGTTTATGACAA 594
Db      116 GlysAsnProIleGlnSerIleuAlaLeuGlnAlaPheSerGlyLeuSerSerIleuGlnIys 135
Qy      595 CTGGTGGCTGTGAGACAAAAATGGCTCTAGAAAGCTTCCCTATTTGACAGCTTATA 654
Db      136 LeuValAlaValAlaGlnThrAsnLeuAlaSerIleuGlnAsnPheProIleGlnIleuIys 155
Qy      655 ACCTTAAAGAACTCAATGGTGGCTCACAAATTTATACATTTCTGTGATTAAGTTACCTGACAT 714
Db      156 ThrIleuGlnIleuAsnValAlaAlaAsnLeuIleGlnSerPheIySleuProGlnIyIy 175
Qy      715 TTTTCSAATCTGACGAACTAGTACATGGATGCTTTCTTATATCATATTAATCAACATAT 774
Db      176 PheSerAsnLeuThrAsnLeuGlnIleuAspLeuSerSerAlaIySleGlnIleuIys 195
Qy      775 ACTGTCAACGACTTACAGTTTCTACGTGAAATCCACAAAGCATCTCTTTAGACATG 834
Db      196 TyIySerIthrAspLeuAlaGlnValLeuAlaGlnIleuProIleuAsnLeuSerIleuAspLeu 215
Qy      835 TCTTTGAACCCCAATGACCTTCATTCACAAACCAAGCTTTGACGGAATTAAGCTTCATGAA 894
Db      216 SerIleuAsnProMetAsnPheIleGlnProGlyAlaPheIySleuIleAlaGlnIleuIys 235
Qy      895 CTGACTTAAAGAGTAATTTTAAAGCTCAAAATTAATGAAGAACTTCCCTTCAAAACCTG 954
Db      236 LeuThrIleuAlaGlnAsnPheAspSerIleuAsnValMetClyThrIySleGlnIleuIys 255
Qy      955 GCTGTTTAAACGCTCACTCGGTGATCTTGGAGAAATTTAAAGATGAAGAACTGTGAA 1014
Db      256 AlaGlnIleuGlnValAlaGlnLeuValLeuGlnIyGlnPheArgAsnGlnIyAsnLeuGln 275
Qy      1015 ATTTTGAACCTCTATCATGAAAGAACTATGTGATGACCATGTGATGATGATGATGAT 1074
Db      276 LysPheAspLysSerAlaLeuGlnIyGlnIyCysAsnLeuThrIleGlnIyPheArgLeu 295
Qy      1075 ACATATACAAATGATTTTTCAGATGATTTGTGAAG---TTCCATTCCTTGGCAATGTT 1131
Db      296 AlaIyIleuAspIyTyIyLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnVal 315
Qy      1132 TCTGCAATGTCTGCGAGAGTGTATCTATAAATATCTAGAAAGATGTTCCATCAATTC 1191
Db      316 SerSerPheSerIleuValSerValThrIleGlnIyAlaIyAspPheSerTyIyAsnPhe 335
Qy      1192 AAATGCAATCTTATCATGATCATTAAGTGCATTAAG-CAGTTTCAACTCTGATCTTA 1250
Db      336 GlnIyGlnIleuGlnIleuValAlaAsnCysIySleuGlnPheProThrIleuIySleu 355
Qy      1251 CCCTTTCTTAAATTTGACCTTAACTATGAACAAGGCTATCAAGTTTAAAAAGTG 1310
Db      356 LysSerIleuIySasGlnIleuThrPheThrSerAsnIySleGlnIyAsnAlaPheSerGlnVal 375
Qy      1311 GCCCTACCAAGTCTCAGCTATCTAGATCTTATGAAATGCACTGAGCTTATGAGTGGC 1370
Db      376 AspLeuProSerIleuGlnIyPheLeuAspLeuSerIyArgAsnGlnIyLeuSerPheIyGlnIyCys 395
Qy      1371 TGTTCATATCTGATTTGGGAAACAACAGCTGAGACACTTGAAGCTTCAGCTCAATGTT 1430

```

```

Db      396 CysSerGlnSerAspPheGlnIyThrIleuSerIleuIyTyIyLeuAspLeuSerPheAsnGlnIy 415
Qy      1431 GCCATCATTTATGAGTCCCAATTTTCATGGGCTCAGAGAGCTGACAGCTGATTTTTC 1490
Db      416 ValIleThrMetSerSerAsnPheLeuGlnIyLeuGlnIleuGlnIleuIySleuAsp-PheGln 435
Qy      1491 GCACTACTACTTTTAAAAAGGTCACAGAAATTCACAGGCTTCTTATCCCTTGAAGAACTACT 1550
Db      435 nHisSerAsnLeuIyGlnIleuSerGlnIyPheSerValPheIleuSerIleuAlaGlnIleuI 455
Qy      1551 TTACCTTGACATCTCTTATPCTAACACCAAAATGACTTGATGTGATATTTCTTGCTT 1610
Db      455 eTyIleuAspIleSerIleuThrIleuThrIyAlaAlaPheAsnGlnIyIlePheAsnIyIle 475
Qy      1611 GACCACTTCAACAACATTTAAATAGCTGGCAATCTTTCAAAGACAACACCTTTCAA 1670
Db      475 uSerSerIleuGlnValLeuIySleuMetAlaGlyAsnSerPheGlnIyAsnPheLeuProAs 495
Qy      1671 TGTCTTTGCAACAACAACAACAACTTGACATTCCTGATTCCTTAAATGTCAATTTGAAACA 1730
Db      495 pIlePheThrGlnLeuAlaGlnAsnLeuThrPheIleuAspLeuSerGlnIyGlnIleuGlnI 515
Qy      1731 AATATCTTGGGGGGGTATTGACACCTCCATAGACTTCAATTTATTAATGATGACACA 1790
Db      515 nLeuSerProThrAlaPheAsnSerIleuSerSerIleuGlnValLeuAsnMetSerIleuSAs 535
Qy      1791 CAATCATATGTTTGTGATTCATCCCATTAATACAGCTGATTTCCCTGACAGACTTGA 1850
Db      535 nAsnPhePheSerIleuAspIthrPheProTyIySasIleuAsnSerIleuGlnValLeuAs 555
Qy      1851 TTGAGTTTCAATCGCATAGACACATCT--AAAGAAATAGTCAACATTTTCCAAAGAG 1907
Db      555 pTyIySerIleuAsnIleGlnMetThrSerIySleuGlnIleuGlnIleuGlnIleuPheProSer 575
Qy      1908 TCTAGCTTCTTCAATCTTACTAACAAATCTGTCTGTGATATGTAAGACATGAAAT 1967
Db      575 rIleuAlaPheLeuAsnLeuThrGlnIyAsnAspPheAlaCysThrCysGlnIleuIleuSerP 595
Qy      1968 CTGCAAGTGGGTCAAGAACAGAAAGAGTTCTTGGGAATGTGGAACAATGACATGTGC 2027
Db      595 eIleuGlnIyPThrIleuAspIleuAlaGlnIleuLeuValAlaGlnIyGlnIleuIyCysAl 615
Qy      2028 AACACCTGTAGAGATGAATACCTCTTATGTTGATTTTAAATATCTTACCTGATATAT 2087
Db      615 aThrProSerAspLysGlnIyMetProValLeuSerIleu--AsnIleuThrCysGlnIle 634
Qy      2088 GTACAAAGACATATCATGATGTGACAGTGTGATGTGATGTGATGTGATGTGATGTGAT 2147
Db      634 tAsnIySleuThrIleIleGlnIyAlaSerValLeuSerValLeuValAlaSerValAlaIyAla 654
Qy      2148 TGTGATATACACCTTCATTTTACCTGATATCTTATGCTGAGCTGTGAAAGATGACAGCAG 2207
Db      654 lIleuValTyIyLysPheIyThrPheIleuMetLeuLeuAlaGlnIyCysAlIeIySleuTyIyGln 674
Qy      2208 AGGAAAGACATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2267
Db      674 gGlnIyGlnAsnIleTyIyAspIlePheValIleTyIySerSerGlnAspIyAspIyAlaIy 694
Qy      2268 AAATGACTGTGAAAGATTTGAAGAAGAGAGTCCCGCTTTCACCTCTGCTCTCACTA 2327
Db      694 gAsnGlnIleuValIyAsnIleuGlnIyGlnIyAlaProProPheGlnIleuIyCysIleuIy 714
Qy      2328 CAGAGACTTATTCCTGGTGTAGCACTGTGCAACATGATCAGAGGAGGCTTCCACAA 2387
Db      714 rArgAspPheIleProGlnIyAlaIleAlaIleAlaIleAlaIleIleIleIleIleIleIle 734
Qy      2388 GAGCGGAGAGTATTTGTGATGTCTAGACACTTATTTACAGAGCGGTGTGATCTT 2447
Db      734 sSerAlaGlnIyValIleValIyAlaSerGlnIleuIleGlnIleuSerArgIyCysIlePhe 754
Qy      2448 TGAATATGATGATGCTCAAAACATGAGCATTTCTGAGACAGCGCTCTGGACATCATTTGAT 2507
Db      754 eGlnIyGlnIleAlaGlnIleThrIyGlnIleuSerSerArgAlaGlnIyIleIlePheIle 774

```

QY 2508 TGTCTTGAGAGGTTGAGAGTCCCTGAGGAGAGGTTGGAATTTGATCGCTTCT 2567
 Db 774 eValLeuGlnlyslValGlysthrLeuArgGlnValGlnLeuTyraGlyLeu 794
 QY 2568 TAGGAGAAACCTTACCTGAGTGGAGAGCAATCTCTGGAGGACATCTTCTGAG 2627
 Db 794 userArgAsnthrTyrlLeuGlnTprGluAspserValLeuGlyArgHisIlePheTpr 814
 QY 2628 AAGCTTAAAAATGCCCTTATGATGAGAAAAGCTCGAATCTGAGCAAA 2679
 Db 814 gArGleuArglyslAleuLeuAspGlyLysserTprAsnProGlnGlyThr 831
 RESULT 2
 US-08-514-014-4
 Sequence 4, Application US/08514014
 Patent No. 5707829
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth
 APPLICANT: McCoy, John
 APPLICANT: Kelleher, Kerry
 APPLICANT: Carlin, McKenough
 TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 NUMBER OF INVENTION: ENCODED THEREBY
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
 STREET: 87 Cambridgepark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/514,014
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724
 REFERENCE/DOCKET NUMBER: G16000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-8224
 TELEFAX: (617) 876-5851
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 661 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-514-014-4
 Alignment Scores:
 Pred. No.: 4,59e-53 Length: 661
 Score: 579.50 Matches: 185
 Percent Similarity: 47.54% Conservative: 124
 Best Local Similarity: 28.46% Mismatches: 305
 Query Match: 11.19% Indels: 37
 DB: Gaps: 16
 US-09-396-985B-46 (1-2951) x US-08-514-014-4 (1-661)
 QY 289 TGCATAGAGTAGTTCCTATATATACCTACCAATGATGATGAGAAATCTGAGAAAGTC 348
 Db 28 CysIleGlyuylsGluAlaAsnlyThrTyraGlyuylsGlnLeuGlyLeuSerGlnIle 47
 QY 349 CCGATGACATCTCTCTTCAACCAAGAAACATAGATCTGACCTTCAACCCCTGAAAGTC 408
 Db 48 ProAspThrLeuProAsnThrThrGlnPheLeuGlnPheSerPheAsnPheLeuProThr 67

QY 409 TTAAGAGCTATAGCTTCTCCAAATTTTTCAGAACTTCAGTGGAGATTATTCAGAGTGT 468
 Db 68 IleHisAsnArgThrPheSerAlaGlyLeuMetAsnLeuThrPheLeuAspLeuThrArgCys 87
 QY 469 GAAATTTGAAACAAATTGAGAGCAAGGATGGCATGGCTTACCAACCTCTCAAACTTGATA 528
 Db 88 GlnIleAsnThrPheIleGlnAspThrPheGlnSerHisIleGlnLeuSerThrLeuVal 107
 QY 529 CTGACAGAAACCTTATCCAGAGTCTTCCCGAGAAAGTTCTCTGACCTAACAAGTTTA 588
 Db 108 LeuThrTyAsnProLeuIlePheMetAlaGlnThrSerLeuAsnGlyProLysSerLeu 127
 QY 589 GACATCTGGTGGCTGGAGACAAATTTGCGCTCTGAGAAAGCTTCCATTTGACAG 648
 Db 128 LysHisLeuPheLeuIleGlnThrGlyIleSerAsnLeuIlePheIleProValHisAsn 147
 QY 649 CTATTAACCTTAAAGAAACTCAATGGGCTCACAAATTTTATACATTCCTGTAAGTTACCT 708
 Db 148 LeuGlnAsnLeuGlnSerLeuTyrlGlySerAsnHisIleSerSerIleLysPhePro 167
 QY 709 GCATATTTTCCAACTGACGAACCTTATGATGATGATCTTCTTATTACTATATTCAA 768
 Db 168 LysAspPhePro--AlaArgAsnLeuLysValLeuAspPheGlnAsnAlaIleHis 186
 QY 769 ACTATTAAGTCAACGACTTACAGTTTCTACGTGAAATCCACAAAGTCATCTCTTTA 828
 Db 187 TyrlSerArgGluAspMetArgSerLeuGln-----AlaIleAsnLeuSerLeu 204
 QY 829 GACATGCTTTTGAACCAATTTGACTTCAATTCACAAACCAACCTTTCAGGAAATTAAGCTC 888
 Db 205 AsnPheAsnGlyAsnAsnValLysGlyIleGlnLeuGlyAlaPheAspSerThrValPhe 224
 QY 889 CATGAACTGACTTAAGAGTAAATTTTATAGCTCAATATTAATGAAGAACTTGCTTCAA 948
 Db 225 GlnSerLeuAsnPheGlyGlyThrProAsnLeuSerValIlePheAsnGly--LeuGln 243
 QY 949 AACCTGGCTGTTTACACGTCACGTCATCGTATGCTGAGAAATTTAAAGATGAAGAAGT 1008
 Db 244 AsnSerThr-----ThrGlnSerLeuThrPheGlnAspIleAspAsp 260
 QY 1009 CTGAAATTTTGAACCTCTATCATGAGAGACTATGATGATGACATTTGATGATGCTT 1068
 Db 261 GlnAspIle--SerSerAlaMetLeuLysGlyLeuCysGlnMetSerValGlnSerLeu 279
 QY 1069 AGGTTAACATATCAAAATGATTTTTCAGAT--GATATTTGTAAGTTCCATGCTGGCG 1125
 Db 280 AsnLeu--GlnGlnHisArgPheSerAspIleSerSerThrThrPheGlnCysPheThr 298
 QY 1126 AATGTTTTCGCAATGCTCTGCGAGGATGATCTATATAAATATAGTAAGAAGTGTCCATA 1185
 Db 299 GlnLeuGlnGlnLeuAspLeuThrAlaThrHisLeuLysGlyLeuProSerGlyMetLys 318
 QY 1186 CATTT-----CAATGCAATCTCTTATCATCAT-----TAG 1217
 Db 319 GlyLeuAsnLeuLeuLysIleLeuValLeuSerValAsnHisPheAspGlnLeuCysGln 338
 QY 1218 ATGTCAATAGAGATTTCCAACTGTGATCTACCTTTTAAAGTTGAACTTTAACT 1277
 Db 339 IleSerAlaIleAsnPheProSerLeuThrHisLeuTyrlLeuArgIleAsnValLysLys 358
 QY 1278 ATGAACAAGGGCTATCAATTTTAAAGATGGCCCTTACCAAGTCTCAGCTATGAT 1337
 Db 359 LeuHisLeuGlyAlaGlyCysLeuGlnLys-----LeuGlyAsnLeuGlnThrLeuAsp 376
 QY 1338 CTATAGTAATGCACTGACCTTATGATGAGCTGTCTTATTTCTGATTTGGAGACAAC 1397
 Db 377 LeuSerHisAsnAspIleGlnAlaSerAspCysCysSerLeuGlnLeuLysAsnLeuSer 396
 QY 1398 AGCCTGAGACCTTAAAGCTGACCTTCAATGATGATGCAATC--ATTATGATGCAATTTTC 1454
 Db 397 HisLeuGlnThrLeuAsnLeuSerHisAsnGlnProLeuGlyLeuGlnSerGlnAlaPhe 416

```

OY      1555 ATGGGTCATGAAGAAGCTCACACACCTGGATTTTTCAGACACTCTATTAAGAAAGGCTAC 1574
Db      417  LysGIuCySPrgInLnuGIuLeuLeuAspLeuAla -PheThrArgLeuHisIleAsnAl 436
OY      1515 AGAAATTCACAGCTTTCTTATCCCTTGAAGAAAGCTACTTATCCCTTGACATCTCTTACTAA 1574
Db      436  aPrgInSerProPheGlnAenLeuHisPheLeuGlnAlaLeuAsnLeuThrTyCysPrh 456
OY      1575 CACCAAAATTGACTTCGATGGATATTTCTTGCGCTTGACCAAGTGCACACATTTTAAAAAT 1634
Db      456  eleuAspThrSerArgSnGlnHisIleLeuAlaGlyLeuProValLeuArgHisIleAsnIle 476
OY      1635 GGCTGGCAATCTCTTCAAGACACACACCTT-----TCAATGCTCTTGGAAACACACAC 1688
Db      476  uLysGIuAsnHisPheGlnAenPrgGlyThrIleThrIleThrArgAsnLeuGlnThrIleValGI 496
OY      1689 AAACCTTGACATTCCTCGAGATCCCTTCAATATGTCATATGGACAAATATCTTGAGGGGATTT 1748
Db      496  ySerLeuGlnValLeuIleLeuSerSerCysGlyLeuLeuSerIleAspGlnGlnAlaPrh 516
OY      1749 TGACACCCCTGCATAGACTTCATATTAATTAATGATGACACAACTATTTG-----TT 1802
Db      516  eHisSerLeuGlyLysMetSerHisValAspLeuSerHisAsnSerLeuThrCysAspSre 536
OY      1803 TTTCGATTCAC---TCCCATTTATACACACTGATATCCCTCAGACACTCTTGATGACATTT 1858
Db      536  rIleAspSerLeuSerHisIleLeuLysGlyIleTyL-----LeuAsnLeuAlaAl 552
OY      1860 CAATGCGCATGAGACATCATTAAGAAATCTGCACACATTTTCCAAAGAGTCTAGCCTTCTT 1919
Db      552  aAsnSerIleAsnIleIleSerProArgLeuLeuProIleLeuSerGlnGlnSerThrI 572
OY      1920 CAATCTTACTAACAAATCTGTTGCTTGATATGTCATGACATCAGAAATTCCTGCAGTGGT 1979
Db      572  eAsnLeuSerHisAsnProLeuAspCysThrCysSerAsnIleHisPheLeuThrTpy 592
OY      1980 CAAGAACACGAAGACGCTCTTGCGTAATGTCAGAAATGACATGTCAGAACCTGTAGA 2039
Db      592  rLysGIuAsnLeuHisLysLeuGlnGlySerGlnIleThrThrCysAlaAsnProSre 612
OY      2040 GATGCAAT-----ACCTCCTTAGTGCTTGATTTTAATAATCTTACCTGTTATAT 2087
Db      612  rLeuArgGlyValLysLeuSerAspValLysLeuSerCysGlyIleThrAlaIleGlyI 632
OY      2088 GTACAAACAATCATCAGTGTGTGCAGTGTGCAGTGTGATGTCAGTATCCAGTATGACAT 2147
Db      632  ePhePheLeuIleValPheLeuLeuLeuAlaIleLeuLeuPhePheAlaValIleTy 652
OY      2148 TCTGATATACCACTTCTATTTTCACCTG 2175
Db      652  rLeuLeuArgTrpLysTyGlnHisIle 661

RESULT 3
US-08-833-823-4
: Sequence 4, Application US/08833823
: Patent No. 5969093
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: APPLICANT: McCoy, John
: APPLICANT: Kelleher, Kerry
: APPLICANT: Carlinh, McKeough
: TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
: TITLE OF INVENTION: ENCODED THEREBY
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
: STREET: 87 CambridgePark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
/

```

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,823
FILING DATE: 10-APR-1997
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/514,014
FILING DATE: 11-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-823-4

Alignment Scores:
Pred. No.: 4,59e-53 Length: 661
Score: 579.50 Matches: 185
Percent Similarity: 47.54% Conservative: 124
Best Local Similarity: 28.46% Mismatches: 305
Query Match: 11.19% Indels: 37
DB: 2 Gaps: 16

US-09-396-985B-46 (1-2951) x US-08-833-823-4 (1-661)
QY 289 TGCATGAGAGTGTGTTCCCTAATATATCAACCAATGCATGCATGAGAACTCAGAAATC 348
DB 28 CysllsgllslgsluAlahslmsylthrltyrslncysgluaslntleugllylslsegluile 47
QY 349 CCTGATGACATTCCTCTTCTTCAACCAAGAACATAGATCTGAGCTTCAACCCCTTGAAATC 408
DB 48 ProslrthrlleuproslrlnthrlthrglupheluglupheserPhelanphleuprothr 67
QY 409 TTAATAAGCTAATGCTTCTCCAAATTTTTCAGAACTTCAGTGGCTGAGATTATCCAGGTG 468
DB 68 llhllslasAlrgthrlpheserArgluemeArslnleuthrlPhelaulerleuthrlArgCys 87
QY 469 GAATTTGAAACAATGGAAGACCAAGCATGGCATGCTTACACCAACCTCTCAAACTTGATA 528
DB 88 GlnllaslntrlllellsgllslsprthrlPheglnserrhlshlsgllnleuSerthrlleuAl 107
QY 529 CTGACAGAAACCCCTATCCAGAGATTTTCCACAGAAATTTCTTGACCTAACAAAGTTTA 588
DB 108 leuthrlGlyslsnProleuilelhelmetAlaqluthrlsrleuAaenlglyProlyseSerleu 127
QY 589 GACAAATCTGGTGGCTGTGAGACAACAATTTGGCTCTTAGAAAGCTTCCCTAATTGACAG 648
DB 128 lyeHllslsluPhelullelglntnhrgllyleserAaenleuglupheilleProvalnlslsn 147
QY 649 CTTATTAACCTTAAGAAATCAATGAGCTGCTACAAATTTTATACATCTCTGTAAGTTAC 708
DB 148 leuGlulslsluendlsuSerleuylrleugllyserlnhlslleSerSerlleVslrPhelro 167
QY 709 GCATATTTTTCCTCAATGCTGACGAACCTAGTACATGAGATCTTTCTTATTAATATATCA 768
DB 168 lyeAspPhelro---AlArghslneulysVallleuAspPhelglnAsnAsnAlilleHls 166
QY 769 ACTATTAATCTGTCAACGACTTACAGATTGTACGAGTAAATTCACAAAGCTCAATCTCTTTA 828
DB 187 TyrllelserArglulslsPrmetArghserleuEnglunlgn-----AlAlleAaenleuSerleu 204
QY 829 GACATGCTTTTGAACCAATTCATTCATTAAGACCAAGCTTTCACGGAATTTAACTC 888
DB 829

```

Db 205 AsnDheAngIyAsnAsnValIySgIyIleGluLeuGlyAlaPheAspSerThrValPhe 224
 QY 889 CATGAACTGACTCTAAGAGTAATTTATAGCTCAATATATAGAAACTTGCTTCA 948
 Db 225 GlnSerLeuAsnPhgIyGlyThrProAsnLeuSerValIlePheAsnGly---LeuGln 243
 QY 949 AACCTGGCTGGTTTACACGTCATCGTTGATCTTGGAGAAATTTAAAGATGAAGAAAT 1008
 Db 244 AsnSerThr-----ThrGlnSerLeuThrPheGluAspIleAspAsp 260
 QY 1009 CTGAAATTTTGAACCTCTATCATGAGACATATATGATGACCATTTGATGATTC 1068
 Db 261 GluAspIle---SerSerAlaMetLeuIySgIyLeuCySgluMetSerValGluSerLeu 279
 QY 1069 AGGTTAACAATATACAAATGATTTTCAGAT---GATATTTGTAAGTTCCATTTGCGC 1125
 Db 280 AsnLeu---GlnGluHisArgPheSerAspIleSerSerThrThrPheGlnCyPheThr 298
 QY 1126 AATGTTTCTGCATATGCTCTGGCAGGTGTATCTATAAATATCTAGAAAGATGTTCTTAA 1185
 Db 299 GlnLeuGlnGluLeuAspLeuThrAlaThrHisLeuIySgIyLeuProSerGlyMetIyS 318
 QY 1186 CATTT-----CAATGCAATCTTATCAATCAT-----TAG 1217
 Db 319 GlyLeuAsnLeuLeuIySgIyLeuValLeuSerValAsnHisPheAspGlnLeuCySglu 338
 QY 1218 ATGTCAACTAAGACATTTCCAACTCTGATCTACCCCTTTCTTAAAGTTGACTTTACT 1277
 Db 339 IleSerAlaAlaAsnPhgProSerLeuThrHisLeuTyrlleArgGlyAsnValIySlys 358
 QY 1278 ATGACAAGAGGCTATCATGATTTTAAAAAAGTGCCCTACCAAGTTCTAGATCTAGAT 1337
 Db 359 LeuHisLeuGlyValGlyCySleuGlnIyS-----LeuGlyAsnLeuGlnThrLeuAsp 376
 QY 1338 CTTAGTGAATATGACATGAGCTTATAGTGGCTGCTTTTATTTGATTTGGAAACAAC 1397
 Db 377 LeuSerHisAsnAspIleGluAlaSerAspCySserSerLeuGlnLeuIySAsnLeuSer 396
 QY 1398 AGCCTGAGACACTTACAGCTTCAAGTTCAGTGCATC---ATTATGAGGCCAATTTG 1454
 Db 397 HisLeuGlnThrLeuAsnLeuSerHisAsnGluProLeuGlyLeuGlnSerGlnAlaPhe 416
 QY 1455 ATGGGCTTAGAAGAGCTGACAGACCTGATTTTTCAGACATCTTATTAAGAGGCTCAC 1514
 Db 417 LysGluCySProGlnLeuGluLeuAspLeuAla-PheThrArgLeuHisIleAsnAl 436
 QY 1515 AGAATTTCTACGCGTTCTTATCCCTTGAAGACTTACTTACCTTACATCTTACTTAA 1574
 Db 436 AProGlnSerProGlnAsnLeuHisPheLeuGlnValLeuAsnLeuThrTyCySph 456
 QY 1575 CACCAAAATGACTCGATGTATATTTCTTGGCTTACCGCTCAACATTAATAAT 1634
 Db 456 GluAspThrSerAsnGlnHisLeuLeuAlaGlyLeuProValLeuArgHisLeuAsnLe 476
 QY 1635 GGGTGGCAATTTCTTCAAGACAACACCTT-----TCAATGTCTTGGCAACACACAC 1688
 Db 476 uIySgIyAsnHisPheGlnAspGlyThrIleThrIySAsnLeuGlnThrValG 496
 QY 1689 AACTTGAATCTCTGATCTCTTAAATGTCAATTTGGAACAATATCTGGGGGATTT 1748
 Db 496 ySerLeuGlnValLeuLeuLeuSerSerCySgIyLeuLeuSerIleAspGlnAlaPhe 516
 QY 1749 TGACACCTCATGACTTCAATATATTAATATAGTCAACAACATTAATTTG-----TT 1802
 Db 516 eHisSerLeuGlyIySAsnSerHisValAspLeuSerHisAsnSerLeuThrCySAspSe 536
 QY 1803 TTGGATTTCA---TCCATTATTAACAGCTGATTTCCCTCAGACACTTGTGATCAGTTT 1859
 Db 536 rIleAspSerLeuSerHisLeuIySgIyIleTy-----LeuAsnLeuAlaAl 552
 QY 1860 CAATCGCATGAGACATCTTAAAGAAATCTGCAACATTTTCCAAAGAGTCAAGCTTCTT 1919
 Db 552 aAsnSerIleAsnIleSerProArgLeuLeuProIleLeuSerGlnGlnSerThrI 572

QY 1920 CAATCTTACTAACAATTTCTGTGCTGTATATGGAACATCAGAAATTCCTGACGTGGT 1979
 Db 572 eAsnLeuSerHisAsnProLeuAspCySThrCySAsnHisIleHisPheLeuThrTy 592
 QY 1980 CAAAGAAACAGAGCATTTCTTGGTAAATGTTGAACAAATGACATGTCGAACCTGTAGA 2039
 Db 592 rIySgIyAsnLeuHisIySAsnLeuGlnIySAsnGlnIySAsnThrThrCySAlaAsnProSe 612
 QY 2040 GATGAAAT-----ACCTCCTTAGTGTGATTTTAAATATCTTACCTGTATAT 2087
 Db 612 rLeuArgGlyValIySLeuSerAspValIySLeuSerCySgIyIleThrAlaIleGlyI 632
 QY 2088 GTACAAACATCATCATGATGTGATGATGATGATGATGATGATGATGATGATGATGAT 2147
 Db 632 ePhePheLeuIleValPheLeuLeuLeuLeuAlaIleLeuLeuPheAlaValIyS 652
 QY 2148 TCTGATATACCACTTCTTATTTTCACTG 2175
 Db 652 rLeuLeuArgTyIySArgIySHisIle 661
 RESULT 4
 US-09-396-308B-23
 / Sequence 23, Application US/09982308B
 / Patent No. 6531290
 / GENERAL INFORMATION:
 / APPLICANT: DaiIe, Barbara
 / APPLICANT: Fan, Xuedong
 / APPLICANT: Lundell, Daniel
 / APPLICANT: Lunn, Charles A.
 / APPLICANT: Tan, Jimmy C.
 / APPLICANT: Zavadny, Paul J.
 / TITLE OF INVENTION: Mammalian TNF-alpha Convertases
 / FILE REFERENCE: JB0601QC
 / CURRENT APPLICATION NUMBER: US/09/982,308B
 / CURRENT FILING DATE: 2001-10-17
 / PRIOR APPLICATION NUMBER: 09/156,163
 / PRIOR FILING DATE: 1998-09-17
 / PRIOR APPLICATION NUMBER: 08/889,909
 / PRIOR FILING DATE: 1997-07-10
 / PRIOR APPLICATION NUMBER: 60/021,710
 / NUMBER OF SEQ ID NOS: 23
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 23
 / LENGTH: 784
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-09-396-308B-23
 Alignment Scores:
 Pred. No.: 1,9e-40 Length: 784
 Score: 463.00 Matches: 218
 Percent Similarity: 41.64% Conservative: 133
 Best Local Similarity: 25.86% Mismatches: 317
 Query Match: 8.94% Indels: 176
 DB: 4 Gaps: 34
 US-09-396-985B-46 (1-2951) x US-09-982-308B-23 (1-784)
 QY 337 CTGACAAAGTCCCTGATGACTTCTTTCACACCAAGACATGATGAGCTTCAAC 396
 Db 43 LeuAsnSerIleProSerGlyLeuThrGluAlaValIySAsnLeuAspLeuSerAsn 62
 QY 397 CCCTTGAAAGTCTTAAAGCTTATAGCTTCTCCAAATTTTTCAGAACTTCAAGTGGCTGAT 456
 Db 63 ArgIleThrTyrlleSerAsn-----SerAsp 71
 QY 457 TTATCAGATGTGAAATTTGAAACATTTGAAGACAGGATGGATGGCTTACACCACTC 516
 Db 72 LeuGlnArgCySVal-----AsnLeu 78
 QY 517 TCAAACTGATGATGACAGAAACCTTATCCAGATTTTCCACAGAAAGTTTCTCTGCA 576

Db	79	GlinalLeuValLeuThrSerAsnGlyIleAsnThrIleGluGluAspSerPheSerSer	98
Oy	577	TTAACCAATGTATAGACAATCTGTGTGGCTGTGGAGACAATAATGTGGCTCTTGAGAAAGCTTC	636
Db	99	LeuGlySerLeuGluIleLeuAspLeuSerGlyAsnGlyLeuSerAsnLeuSerSerSer	118
Oy	637	CCATATGGACAGACTTATATACTTTAAGAAACTCAATGTGGCTCACAAATTTTATACATTC	696
Db	119	TrpPheLysProLeuSerSerLeuThrPheLeuAsnLeuLeuGlyAsnProGlyLeuThr	138
Oy	697	TGTAAGTACCGCATTTTTCCAATGTGAGCAACCTGATACATGTGGATCTT	750
Db	139	LeuGlyGluThrSerLeuPheSerIleLeuThrLysLeuGluIleLeuArgValGlyAsn	158
Oy	751	-----TCCTTAACCTATATTCAAACTATTATCTGTCAACAGACTTACAGTTTCTACGTGAA	804
Db	159	MetAspThrPheThrLysIleGlnArgLysAspPheIleGlyLeuThrPheLeuGluGlu	178
Oy	805	AATCCACAAGTCATCTCTCTTTAGACACATGCTTTGAAACCAATGACTTCAATTCAAAGAC	864
Db	179	-----LeuGluIleAspAlaSerAspLeuGlnSerGlyGluPro	191
Oy	865	CAAGCTTTCAGGGAAT-----AACTCCATGCA	894
Db	192	LysSerLeuLysSerIleGlnAsnValSerIleLeuIleuHisMetLysGlnHisIle	211
Oy	895	CTGACTCTAAGAGGTAATTTTAATAGCTCAATATATAGAAACAGTGGCTTCA-----	948
Db	212	LeuLeuLeuGluIlePheValAspValIleThrSerSerValGlu-----CysLeuGluLeuArg	230
Oy	949	-----AACTGGCTGGTTTACACGCTCATCGGTTGATCTTGGAGAAATTTAAAGAT--	999
Db	231	AspThrAspLeuAspThrPheHisPheSerGluLeuSerThrGlyGluThrAsnSerLeu	250
Oy	1000	-----GAAGAAATCTGGAAATTTTGAACCCCTCATCATGGA-----	1038
Db	251	IleLysLysPheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMet	270
Oy	1039	-----GAACTATGTATGATGACCATTTGATGATGAGTTGACAGTTTAA	1077
Db	271	LysLeuLeuAsnGlnIleSerGlyLeuLeuGluLeuGluPheAspAspCysThrLeuAsn	290
Oy	1078	TATACAAATGATTTT-----TCAGATGATATTTGTTAAGTTCCATTGGCTGGCAATGTT	1131
Db	291	GlyValGlyAsnPheArgAlaSerAspAsn-----	300
Oy	1132	TCTGCAATGTCTCTGGACAGGTATCTATAAAATCTAGAAAGATGTTCTTAAACATTTCC	1191
Db	301	-----AspArgValIleAspProGly	307
Oy	1192	AAATGGCAATCCTTATTCATCATTTAGATGTCAACTAGACAGTGTTCACATCTGTG-----GAT	1247
Db	308	LysValGluThrLeuThrIleLeuArgLysHisIleProLysPheGlyLeuPheLysAsp	327
Oy	1248	CTACCCCTTCTTAAAGTTTGAAGTTTAACTATAGAACAAAGGGCTATCATGTTTAAAAAA	1307
Db	328	LeuSerThrLeuLysSerLeuThrGluArgValLysArgIleThrValGluAsnSerLys	347
Oy	1308	GTG-----GCCCTACCAAGTCTCAGCTATCTAGATTTT	1340
Db	348	ValPheLeuValProCysLeuLeuSerGlnHisLeuLysSerLeuGluLysLeuAspLeu	367
Oy	1341	AGTAACAATGCACGTG-----AGCTTTAGTGGAGGCTG-----TCCTATCTT	1382
Db	368	SerGluAsnLeuMetValGluGluLysLysAsnSerAlaCysGlnAspAlaIlePro	387
Oy	1383	GATTGGGAACAACAAGCTGTGAGA-----CACTTA-----GACCTCAGCTTCAATAGTGTCC	1433
Db	388	SerLeuGlnThrLeuIleLeuArgGlnAsnHisLeuAlaSerLeuGluLysThrCysGlu	407
Oy	1434	ATCATTAATGAGTGCCAATTTTCATGGGCTCTAGAAAGCTTGACAGACCTGAGATTTTTCAGCA	1493

Db 408 Thrileuethr-----LeuIysAsnLeuThrAsnIleAspIleSer-Ly 422

Qy 1494 CTCTACTTTAAAGAGGTCAACAGATTCTCAGCGTCTTAATCCCTTGAAAAGCTACTTTA 1553
::: :::: ||| :::: ||| :::: ||| :::: |||

Db 422 SAsnSerPheHisSerMetProGluThrCysGlnTrp-----ProGluCysMetIleSly 440
::: :::: ||| ::: ||| ::: ||| ::: ||| ::: |||

Qy 1554 CCTTGACATCTCTTAATCTAACACCAAAATTGACTTGATGATATTTCTGGCTTGAC 1613
||| :::: ||| ::: ||| ::: ||| ::: ||| ::: |||

Db 440 rLeuAsnLeuSer-----SerThrArgIleHis----- 449

Qy 1614 CAGCTCTCAACACATTTAAATAGGTGGCTGCAATTTCTTCAAGACAAACCCCTTCAATGT 1673
::: ||| ::: ||| ::: ||| ::: |||

Db 450 -----SerValThrGlyCysIleProIylSerThrleuIuIleuAspVa 464
::: ||| ::: ||| ::: ||| ::: |||

Qy 1674 CTTCGCAAAACAACAACACTTGACATTCCTCGAGATCCTTCAATGTCAATTTGGAACAAT 1733
||| ||| ||| ||| ::: |||

Db 464 lSerAsnAsnAsnLeuAsnLeuPheSerLeuAsn----- 475

Qy 1734 ATCTTGGGGGGTATTGACACCCCTCCATAGCTTCATTTAATATGTAGTCAACAAC 1793
||| ||| ||| ||| ::: ||| ::: ||| ::: |||

Db 476 -----LeuProGlnLeuLysGlnLeuIlyrIleSerArgAsnLys 488

Qy 1794 TCTATTGTTTTGGATTTCATCCCATTTAAACACAGCTATATTCCTGACAGCTCTTGATTG 1853
||| :::: ||| ::: ||| ::: ||| ::: |||

Db 488 sIleuMetThrleuProAspAla-----SerleuLeuProMetleuLeuValIleuSly 506
||| :::: ||| ::: ||| ::: ||| ::: |||

Qy 1854 CAGTTTCATTCGCTAGAGACA--TCTAAAGAAATCTGCACATTTTCCAAAGAGCT 1910
||| ||| ||| ||| ::: |||

Db 506 eSerArgAsnAlaIleThrThrPheSerLysGlnGlnLeuAspSerPhe--HisThrIle 525
||| ||| ||| ||| ::: |||

Qy 1911 AGCCTTCTTCAATCTTACTAACATCTTCGTGCTTGATATGTGAACATCAGAAATTCCT 1970
||| ||| ||| ||| ::: |||

Db 525 uIylSerThrleuGluIuIaGlyIysAsnAsnPheIleCysSerCysGln-----PheLe 542

Qy 1971 GCAGNGGGGTCAAGAGACGAGAAAGCGTTCTGGTGAATGTT-----GAACA 2015
||| :::: ||| ::: ||| ::: |||

Db 542 uSerPheThrGlnGlnGln--GlnAlaLeuAlaIylValleuIleAspTrpProAlaAs 561
||| :::: ||| ::: ||| ::: |||

Qy 2016 AATGACATGTGCAACACCTGTAGAGATGAATACCTCCTTAGTGTGGAT-----TTAA 2069
||| :::: ||| ::: ||| ::: |||

Db 561 nTylLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSe 581

Qy 2070 TAAATTCACCTGTTATATATGACAGACATCATCATGATGTGTCAAGTGTCACTGTGATGT 2129
||| ||| ||| ||| ::: |||

Db 581 rValSerGlnCysHisArgIleAlaLeuValSerGlyMetCysCysAlaLeuPheLeuLe 601

Qy 2130 GGATTCACCTGATACATTTCTGATATACCACTT-----TATTTCACCTGAT 2177
||| :::: ||| ::: ||| ::: |||

Db 601 uIleLeuLeuThrGlyValIleuCysHisArgPheHisGlyLeuTrpTyrMetLysMetWe 621
||| :::: ||| ::: ||| ::: |||

Qy 2178 A-----CTTATTCCTGGCTGTAATAAAGTACAGACAGAGAGAAAGC-----ATCTA 2232
::: :::: ||| ::: ||| ::: |||

Db 621 tTrpAlaIleThrleuGlnIalylsArgLysProIylLysAlaIleProSerThrArgAsnIleCysIly 641

Qy 2223 TGATGCATTTGTGATCTATCTGAGTCAAGATGAAGATCGGTGAGAAATGAGCTGTAA 2282
||| ||| ||| ||| ::: ||| ::: |||

Db 641 rAspAlaPheValSerTyrSerGlnArgAspAlaTyrTrpValGlnAsnLeuMetValG 661

Qy 2283 GAATTTGAAAGAAGAGAGTGGCCGCTTCACTCTGCTTCACTACATACAGAGCTTATATCC 2342
||| ||| ||| ||| ::: |||

Db 661 nGlnLeuGlnAsnPheAsnProProPheLysLysCysLeuHisLysArgAspPheIlePr 681

Qy 2343 TGGTGTAAGCAATTCCTGCAACATATTCACAGAAAGGCTTCCACAAGAGCCGGAAGTTAT 2402
||| ||| ||| ||| ::: ||| ::: |||

Db 681 oGlyLysTrpIleIleAspAsnIleIle--AspSerIleGluLysSerHisLysTrpVa 700

Qy 2403 TGTGGTAGTCTTAGACACTTATTCAGAGCGGTGTGTATCTTTGAATATGAGATTC 2462
||| :::: ||| ::: ||| ::: |||

Db 700 lPheValIleuSerGlnAsnPheValLysSerGlnTrpCysLysTyrGlnLeuAspPheSe 720

Qy 2463 TCAAAACATGACAGTTTCTGAGCAGCGCTCGGATCATCTTCAATGTCTTGAGAAAGT 2522
||| :::: ||| ::: ||| ::: |||

Db 720 rHisPheArgLeuPheAspGlnAsnAspAlaAlaIleuIleuLeuGlnTrpIle 740

```

QY 2523 TGAGAGTCCTCGTCAGGACAGC---GTGAATGTGTATCGGCTTCTTAAGCAAAAC 2579
Db ||||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
740 eGluYslySaIaIlePrGlnInrGheCySlySyleuAaGlySylleMeCantHrlyStn 760
QY 2580 CTACCTGAATGGAGAGCAATCTCTGGGAGGACATCTTGTGAGAACTTAATAA 2639
Db ||||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
760 rTyrlreuglUtrPrCMeTAspJulaGlnrGlyglUgLyPheTrpValaMleuHrGAl 780
QY 2640 TGCCCTCA 2646
Db ||||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
780 aAlaIle 782

RESULT 5
US-09-949-016-8799
; Sequence 8799; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

Alignment Scores:
Pred. No.: 2,36e-34 Length: 775
Percent Similarity: 406.50 Matches: 207
Score: 39.88 Conservative: 118
Best Local Similarity: 25.40% Mismatches: 288
Query Match: 7.85% Indels: 203
DB: 4 Gaps: 33

US-09-396-985B-46 (1-2351) x US-09-949-016-8799 (1-775)
QY 337 CTCAGCAAAAGTCCTCGATGACATTCCTTCTTAACCAAGCAAGATAGTCTGACCTTCAAC 396
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
78 leuAaSerlePrSerSerGlyleuHrGAlaVallySerleuAaSpLeuSerAaSen 97
QY 337 CCCTTGAAAGACTTTAAAGACTATAGCTTCTCCAAATTTTTCAGAACTTCAAGTGGCTGGAT 456
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
98 ArgIleHrTyrlrIleSerAaSen-----SerAsp 106
QY 457 TTATCCAGGTGGAATTAATAACAATTGAAGACAAGGATGCGATGGCTTACACACCTTC 516
Db ||||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
107 leuGlnAaGyCySVal-----AaMleu 113
QY 517 TCMAACTGTATACGTACAGAGAAACCCTATTCAGAGTTTTCGCCAGAACTTCTCTGGA 576
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
114 GlnAlaIleValleuHrSerSerenglyIleAaHrIleGluGluAaSpSerPheSer 133
QY 577 CTAAACAAGTTTGAACAATCTGTGGGCTGTGGAGACAAATTTGGCCTCTTAAGAAAGCTTC 636
Db ||||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
134 leuGlySerleuGlnHrSleuAaSpLeuSerTyraHrTyrlleuSerAaSenleuSerSer 153
QY 637 CCTATGAGACACTTATACCTTTAAAGAAACCAATGAGTGAGCTACAAATTTTATACATTC 696
Db ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
154 TrpHleYsPrIleuSerSerleuHrHrPheleuAaSenleuGlyAaHrProTyrlYsTrHr 173
QY 697 TGTAAGTATCGTCATATTTTTCAAATCTGAGCAACCTATGATACATGATGATCTT----- 750

```

Db	174	LeuGlyGluThrSerLeuPheSerHisLeuThrIleuSerGluIleLeuArgValGlyAsn	193
Qy	751	-----TCCTAATCACTAATTCAACACTATTACTGTCAACGACTTACAGTTTCACTGAA	804
Db	194	MetAspThrPheThrIleValIleGlnArgGlyAspPheAlaGlyLeuThrPheLeuGluGlu	213
Qy	805	AATCCACAAGCAATCTCTCTTTAGACATGCTTTGAACCCCAATTTGACTTCATTCACAAAC	864
Db	214	-----LeuGluIleAspAlaSerAspLeuGlnSerTyrGluPro	226
Qy	865	CAAGCTTTCAGGGAAATT-----AAGCTCCATGAA	894
Db	227	LyserIleuYsSerIleGlnAsnValSerHisLeuIleLeuHisIleMetGlyGlnHisIle	246
Qy	895	CTGACTCTAGAGGTAAATTTTAATAGCTCAATATTAATGAAACTGTGCTTCAA-----	948
Db	247	LeuIleuGluIlePheValAspValThrSerSerValGlu---CysLeuGluIleuArg	265
Qy	949	-----AACCTGGCTGTTTACAGTCCATCGGTTGATCTTGGAGAAATTTAAAGAT---	999
Db	266	AspThrAspLeuAspThrPheHisPheSerGluLeuSerThrGlyGluThrAsnSerLeu	285
Qy	1000	-----GAAGGAATCTGGAAATTTTGAACCTCTATCATGGA-----	1038
Db	286	IleIleYsPheThrPheArgAsnValIleIleThrAspGluSerLeuPheGlnValMet	305
Qy	1039	-----GCACTATGTCATGTCACCATTTGATGAGTTTCAGTTTACA	1077
Db	306	LyseIleuAsnGlnIleSerGlyLeuIleuGluIleuGluPheAspAspCysThrLeuAsn	325
Qy	1078	TATACAAATGATTTT-----TCAGATGATATTGTTAAGTTCCATTGCTTGGCGAATGT	1131
Db	326	GlyValGlyAsnPheArgAlaSerAspAsn-----	335
Qy	1132	TCGTCAATGTCTCGGACGTCATCTAATAAATCTAGAGAGATGTTCCAAACATTTC	1191
Db	336	-----AspArgValIleAspProGly	342
Qy	1192	AAATGGCAATCTTATCAATCATTTAGATGTCACATTAAGCACTTTCAACTCTG---GAT	1247
Db	343	LyseValGluThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyrAsp	362
Qy	1248	CTACCTCTTTCTTAAAGTTGACTTTAATCTATGACAACAAAGGCTCATCAGTTTAAAAA	1307
Db	363	LeuSerThrLeuTyrSerLeuThrGluArgValYsArgIleThrValGluAsnSerYs	382
Qy	1308	GTG-----GCCCTACCAAGTCTCAGTATCTAGATTTT	1340
Db	383	ValPheLeuValProCysLeuLeuSerGlnHisIleuYsSerLeuGluTyrLeuAspLeu	402
Qy	1341	AGTGAATATGACGTG-----AGCTTTAGGTGTGCTGT-----TCCTAATCT	1382
Db	403	SerGluAsnLeuMetValGluGluTyrLeuYsAsnSerAlaCysGluAspAlaTyrPro	422
Qy	1383	GATTGGGAAACAAACAGCTGAGA-----CACTTA---GACCTCAGCTTCAATGTGCC	1433
Db	423	SerLeuGlnThrIleuIleLeuArgGlnAsnHisIleuIleAserLeuGluTyrThrGlyGlu	442
Qy	1434	ATCATTTATAGATGCCAATTTTCATGGGTCTAGAAAGCTGCAGCACCTGGAATTTTTCAGA	1499
Db	443	ThrLeuLeuThr-----LeuYsAsnLeuThrAsnIleAspIleSer---Iy	457
Qy	1494	CTTACCTTTAAAAAGGTCACAGAATTTCTCAGCTTCTATTCCTTGAAAGTCACTTTA	1553
Db	457	AsnSerPheHisSerMetProGluThrCysGlnTyr-----ProGluYsMetLeuTyrIy	475
Qy	1554	CTTTGACATCTCTTATATCTAACACAAATTTGACTTCGATGATATATTTCTTGACTTGAC	1613
Db	475	IleuAsnLeuSer-----SerThrArgIleHis-----	484
Qy	1614	CAGTCTCAACACATTAATAATGCTGGCAATTTCTTTCAAGACAAACCCCTTCAAAATGT	1673

485 -----SerValThrGlyCysIleProIysThrLeuGluIleLeuAspVa 499
QY 1674 CTTTGCAACGACCAACAACTTGACATCTCGATCCTTCAATATGTCATTTGGAACAAAT 1733
Db 499 lSerAsnAsnAsnLeuAsnLeuPheSerIleAsn----- 510
QY 1734 ATCTTGGGGGTATTTGACACCTTCATAGACTTCATTTAATAATGAGTCACAA 1793
Db 511 -----LeuProGlnLeuIleGluLeuIleGluLeuIleSerArgAsnIly 523
QY 1794 TCTATTGTTTGGATTCAATCCATTATTAACAGCTGATATTCCTCAGCACTCTTGATTG 1853
Db 523 sLeuMetThrLeuProAspAla-----SerLeuLeuProMetLeuLeuValLeuIly 541
QY 1854 CAGTTTCAATCGCATAGACACA---TCTAAAGAAATCTGCACATTTTCCAAAGAGTCT 1910
Db 541 eSerArgAsnAlaIleThrThrPheSerIlyGluGlnLeuAspSerPhe--HisThrIle 560
QY 1911 AGCCTTCTTCATCTTACTAACAATCTGTGCTTGATATGTGACATCAGAAATTCCT 1970
Db 560 ulysThrLeuGlnIleGlyIleAsnAsnPheIleCysSerCysGlu-----PheIle 577
QY 1971 GCAGTGGGTCAAGAACGACGATCTTGCTGAATGTT-----GACA 2015
Db 577 userPheThrGlnGlnGln--GlnAlaLeuAlaIlyValLeuIleAspTrpProAlaAs 596
QY 2016 AATGACATGTGACACCTGTAGAGATGAAATACCTCTAGTGTGATTTTAAATATTC 2075
Db 596 nIlyLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSe 616
QY 2076 TACCTGTATATGTACAGACAAACATCATCAGTGTGTCAGTGTGATTTGTGATTC 2135
Db 616 rValSerGluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeu----- 633
QY 2136 CACTGTAGCATTTTGTATATACCACTTCTATTTTCACTGATATCTTATGCTGGC----- 2190
Db 634 -----PheLeuLeuIleLeuLeuThrGlyValIle 643
QY 2191 -TGTAAGAGTAC----- 2202
Db 643 uCysHisArgPheHisGlyLeuTrpIlyrMetLeuMetCysTrpAlaTrpLeuGlnAlaIly 663
QY 2203 -----ACGAGAGAGAAAGCATCTATGATGATGATTTGATCTA 2240
Db 663 sArgIlyrProArgIlyAspAlaProSerArg--AsnIleCysTrpAspAlaPheValSerIly 682
QY 2241 CTCGATGCAGATAGAGACTGGGTGAGAAATGAGCTGTGAAGATTTAGAGAGAGAGT 2300
Db 682 rSerGluArgAspAlaIlyrTrpValGluAsnLeuMetValGlnGlnLeuGluAsnPheAs 702
QY 2301 GCCCGGCTTCACTGCTGCTCTCACTACAGAGACTTATTCCTGCTGAGCCATTGCTGC 2360
Db 702 nProPheProPheIlyLeuCysLeuHisIlyAspAspPheIleProGlyIlyStrpIleIleAs 722
QY 2361 CAACATATCCAGAGAGGCTTCCACAGAGCCGAGAGGTTATTTGTGATGCTGTAGCA 2420
Db 722 pAsnIleIle---AspSerIleGluIlySerHisIlySerThrValPheValIleLeuSerGluAs 741
QY 2421 CTTTATTCAGAGCCGCTGTATCTTGAATATGAGATTGCTCAACATGCGAGTTTCT 2480
Db 741 nPheValIlySerGluTrpCysIlyrGluLeuAspPheSerHisPheArgLeuPheAs 761
QY 2481 GAGAGCCGCTGTGACATCTTCACTGCTGAGAGGTT 2523
Db 761 pGluAsnAsnAspAlaAlaIleLeuIleLeuLeuGlnProIle 775

/ TITLE OF INVENTION: THEREFOR
/ FILE REFERENCE: MEI-019
/ CURRENT APPLICATION NUMBER: US/09/063,950C
/ CURRENT FILING DATE: 1998-04-21
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ TYPE: PR1
/ ORGANISM: Papilio hamadryas
US-09-063-950-5
Alignment Scores:
Pred. No.: 2,32e-21 Length: 605
Score: 285.50 Matches: 144
Percent Similarity: 36.06% Conservative: 94
Best Local Similarity: 21.82% Mismatches: 240
Query Match: 5.51% Indels: 183
DB: Gaps: 17
US-09-396-985b-46 (1-2951) x US-09-063-950-5 (1-605)
QY 301 GTTCTTAATATTACCTACCATGATGATCAGAAACTCAGCAAGTCCCTGATGACATT 360
Db 53 ValAsnGluLeuSerValPheCysSerSerArgAsnLeuThrArgLeuProAspGlyIle 72
QY 361 CCTTCTTCAACCAAGAACATATGATCTGAGCTTCAACCCCTTGAAGATCTTAAAGCTAT 420
Db 73 ProGlyGlyThrGlnAlaLeuTrpLeuAspSerHisAsnLeuSerIleProProAla 92
QY 421 AGCTTCCAAATTTTTCAGAACTTCAGTGGCTGATTTATCCAGTGTGATTTAAAGAAC 480
Db 93 AlaPheArgAsnLeuSerSerIleuAlaPheLeuAsnLeuGlnIlyGlyGlnLeuGlySer 112
QY 481 ATTGAAGACAGGCAAGCAAGCTGCTTACACCACTTCAACTTGAATCTGACAGAGAAC 540
Db 113 LeuGlnProGlnAlaLeuLeuGlyLeuGluAsnLeuCysHisIleuHisIleuGluArgAsn 132
QY 541 CCTATCAGAGTTTTCCCGCAGGAAGTTCTCTGACATAACAAGTTTATGACAAATCTGGT 600
Db 133 GlnLeuArgSerLeuAlaValGlyThrPheAlaIlyrThrProAlaLeuAlaLeuGly 152
QY 601 GCTGTGAGACAAATTTGGCTCTTGAAGAGCTTCCATTGAGACGTTATTAACCTTA 660
Db 153 LeuSerAsnAsnArgLeuSerArgLeuGluAsp----- 163
QY 661 AAGAACTCAATGTGGCTCAAAATTTATATCATTTCTGTAGTTACTGCATATTTTCC 720
Db 164 -----GlyLeuPheGlu 167
QY 721 AATCTGCAACCTAGTACATGTGATCTTCTTATATCTATATTCAACTATTTACTGTC 780
Db 168 GlyLeuGlyAsnLeuTrpAspLeuAsnLeuGlyTrpAsnSerIleuAlaVal----- 184
QY 781 AACGACTTACAGTTTCTACGTGAATTCACAAATCATCTCTTTAGACATGCTTTTG 840
Db 184 ----- 184
QY 841 AACCAATTGATCTTCAATCAAGCAAGCTTTCAGGGAATT---AAGCTCATGAACAG 897
Db 185 -----LeuProAspAlaAlaPheArgGlyLeuGlyIlyLeuArgGluLeu 199
QY 898 ACTCTAAGAGTATTTTATATAGCTCAATATATGAAACTTGCCCTTCAAAACCTGGCT 957
Db 200 ValLeuAlaGlyAsn----- 204
QY 958 GATTACACGTCATCGGTGATCTTGAGAGAAATTAAGATGAAAGAAATCTGGAATTT 1017
Db 205 -----ArgLeuAlaIlyr 208
QY 1018 TTGAACCTCTATCATGAGAGACTATGTGATGTGACCAATTGATGATTCAGGTTTACA 1077
Db 209 LeuGlnProAlaLeuPheSerGlyLeuAlaGluLeuArg----- 221

RESULT 6

US-09-063-950-5
; Sequence 5, Application US/09063950C
; Patent No. 6225085
; GENERAL INFORMATION:
; APPLICANT: Holzman, Douglas A.
; TITLE OF INVENTION: NOVEL LRSG PROTEIN AND NUCLEIC ACID MOLECULES AND USES

QY 1078 TATCAATATGATTTTTCAGATGATATGTTAAGTTCCATGCTGGGCAATGTTTCGCA 1137
 Db 222 -----GluLeuAspLeuSerArg 227
 QY 1138 ATGCTCTGGCAGGATGATCTATAAATATCTAGAACAGTGTCTTAAACATTTCAATGG 1197
 Db 228 AsnAlaLeuArgAlaIleLeuAlaAsnValPheAlaGlnLeuPro-----ArgLeu 244
 QY 1198 CAATCTTATCAATCATTTAGATGTCACATAAGCTTTCCAACT-----CTGGAT 1247
 Db 245 GlnLeuLeuTyrLeuAspArgAsnLeuLeuAlaValAlaProGlyAlaPheLeuGly 264
 QY 1248 CTACCCCTTTCTTAAAGTTTCACTTAACTTGAACAA-----GGCTCATGAGTTT 1301
 Db 265 LeuLeuAlaLeuArgTyrPheLeuAspLeuSerHisAsnArgValAlaGlyLeuLeuGlnAsp 284
 QY 1302 AAAAAAGTGCCCTACCAAGTCTCAGCTATCTAGATCTTATAGAAATGACAGCTGCTT 1361
 Db 285 ThrPheProGlyLeuLeuGlyLeuArgValLeuArgLeuSerHisAsnAlaIleAlaSer 304
 QY 1362 AGTGTGGCTCTTCTTATCTGAT-----TTGGGAACAAC 1397
 Db 305 LeuArgProArgTyrThrPheGluAspLeuHisPheLeuGlnLeuGlnLeuGlyHisAsn 324
 QY 1398 AGCCTGAGACACTTAAAGCTCAGCTCAATGATGATGATGATGATGATGATGATGATG 1457
 Db 325 ArgIleArgGlnLeu-----AlaGluArgSerPheGln 335
 QY 1458 GGTCTAGAACAGCTGACGACACTGATTTTTCAGCACTCTTAAAGGCTGACAGA 1517
 Db 336 GlyLeuGlnGlnLeuGlnValLeu-ThrLeuAspHisAsnGlnLeuGlnVal--Ly 354
 QY 1518 ATTCTAGCGCTTCTTATCCTTGAAGAACTTACCTTGAACCTTCTTACTTAAACAC 1577
 Db 354 sValGlyAlaPheLeuGlyLeuThrAsnValAlaValMetAsnLeuSerGlyAsnCysLe 374
 QY 1578 CAAATGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1637
 Db 374 ValArgAsnLeuProGlnValPheArgGlyLeuGlyLeuLeuHisSerLeuHisLeu 394
 QY 1638 TGGCAATTCCT----- 1647
 Db 394 uGlySerCysLeuGlyArgIleArgProHisThrPheAlaGlyLeuSerGlyLeuArg 414
 QY 1648 -----TTCAAGACAAACACCTTTTCAATGCTTTGCAACA-----AC 1668
 Db 414 GluPheLeuLeuAspAsnGlyLeuValGlyIleGlnGlnLeuSerLeuTyrGlyLeuAl 434
 QY 1689 AAACCTGACATTCCTGATCCTCTTAATGTCATGGAACAATATCTGGGGGATATT 1748
 Db 434 agLLeuLeuGlnLeuAspLeuThrSerAsnGlnLeuThrHisLeuProHisGlnLeuPhe 454
 QY 1749 TGACACCCCTCATGACTTCAATATTAAATATGATGATGATGATGATGATGATGATG 1808
 Db 454 eGlnGlyLeuGlyLeuGlnGlyLeuGlnLeuLeuSerHisAsnArgValAlaGlyLeuP 474
 QY 1809 TTATCCCATTAATACAGCTGATTCCTCAGACACTTGTATGACGTTTCAATTCGAT 1868
 Db 474 cAlaAspAlaLeuGlyProLeuGlnArgAlaPheThrLeuAspValSerHisAsnArgLe 494
 QY 1869 AGAGACATCTAAAGATATCTGCAACATTTTCCAAAAGTGTACCTTTTCATCTTAC 1928
 Db 494 uGluAlaLeuProGlySerLeuLeuAlaSerLeuGlyArgLeuArgTyrLeuAsnLeuArg 514
 QY 1929 TAAACATTCCTGCTTGTATATGATGAAACATCAGAAATTCCTGACG-----TGGGTCAA 1982
 Db 514 gAsnAsnSerLeuArgThrPheThrProGlnProGlnProGlnProGlnProGlnProGln 534
 QY 1983 GAAACAGACAGCTTCTTGTAAGTGTGAACAATGACATGTCACACCTGTAGAG-- 2040
 Db 534 uGly-----AsnProTyrAspCysGlnProCysProLeuVal 546

QY 2041 -----ATGATACCTCTTACTGATGATGATGATGATGATGATGATGATGATG 2081
 Db 546 AlaLeuArgAspPheAlaLeuGlnAsnProSerAlaValProArgPheValGlnAlaIleC 566
 QY 2082 T-----TATATGTACAGACAAATCATCAGTGTGTC 2112
 Db 566 sGluGlyAspAspCysGlnProProValTyrThrTyrAsnAsnIleThrCysAlaSer 585
 RESULT 7
 US-08-190-802A-50
 ; Sequence 50, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; APPLICANT: Ron, Dorit
 ; TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
 ; TITLE OF INVENTION: Theoreof
 ; NUMBER OF SEQUENCES: 265
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Delinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/190,802A
 ; FILING DATE: 01-FEB-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 8600-0139
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 603 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 ; INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
 ; US-08-190-802A-50
 Alignment Scores:
 Pred. No.: 9 07e-21 Length: 603
 Score: 280.00 Matches: 163
 Percent Similarity: 38.12% Conservative: 81
 Best Local Similarity: 25.47% Mismatches: 221
 Query Match: 5.41% Indels: 176
 DB: 1 Gaps: 26
 US-09-396-985b-46 (1-2951) x US-08-190-802A-50 (1-603)
 QY 322 TGCATGATCAGAAACTCAGCAAGTCCCTGATGACATTCCTTTCACCAAGACATA 381
 Db 60 CysSerSerIysAsnLeuThrHisLeuProAspAspIleProValSerThrArgAlaLeu 79
 QY 382 GATCTGAGCTTCAACCCCTTGAAGATCTTAAAGCTTATGCTTCCAAATTTTTCGAA 441
 Db 80 TrpLeuAspGlyAsnLeuLeuSerSerIleProSerAlaAlaPheGlnAsnLeuSer 99
 QY 442 CTTCAGTGGCTGATTTATCCAGGTGTAATTAAGAAACATTTGAAGCAAGGATGCAT 501

APPLICATION NUMBER: 08/487,072
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: MURASHIGE, KATE H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 2550-0025.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-0763
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 603 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 HYPOTHESES: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
 US-08-477-346-50

Alignment Scores:
 Pred. No.: 9.07e-21 Length: 603
 Score: 280.00 Matches: 163
 Percent Similarity: 38.12% Conservative: 81
 Best Local Similarity: 25.47% Mismatches: 221
 Query Match: 5.41% Indels: 176
 DB: Gaps: 26

US-09-396-985b-46 (1-2951) x US-08-477-346-50 (1-603)

322 TGCATGATGAGAAAGTCCGATGATGATCTTCTTCAACCAAGACATA 381
 60 Cyssererlysaenleuthrhisleuproaspapilprovalserthraalaleu 79
 382 GATCTGAGCTTCAACCCCTGAGATCTTAAAGCTATAGCTTCCCAATTTTCAAA 441
 80 Trepulsapgluanaenleuserserleproseralialaheglnaenleuser 99
 442 CTTCAGTGGCTGATTTATCCAGGTGGAATTGAACATTTGAAGACAGCATGGCAT 501
 100 LeuaspheleuanaenleuglnlyserTrepulargserleuglnproglinalaleu 119
 502 GGCTTAACCAACCTCTGAACTGATGACAGAAACCTATCCAGATTTTCCCA 561
 120 GlyleuaglnaenleuYrTyleuhisleuaglnaargnaargleuaglnaleu 139
 562 GGAAGTTCTCTGACTCAACAGTTTGAACATCTGCTGCTGAGACAAAATGGCC 621
 140 GlyleuetherhrhsthrProserleuhalaserleuserleuseraserleu 159
 622 TCTCTAAGAACTTCCCTATTGACAGCTTAACTTAAAGAACTCAATGTGGCTCAC 681
 160 ArgleuaglnuglyleuPheglnlyleuserhisleuTpaapleuanaenleu 179
 682 AATTTT-----ATACATTCCTGT 699
 180 AsherleuValValleuproaspThValPheglnlyleuglyasnlleuhisleu 199
 700 AAGTTA-----CTGCATATTTTTCATCTGACGAC 732
 200 ValleuhalaglyaenlyleuThrTyleuaglnprohalaleuPheCysglyleuagln 219
 733 CTAGTACATGTGATCTTTTATTACTATTAATCAACTATTACTGTCAACGACTTACAG 792
 220 LeuargileuanaenleuserargasnlaleuargserValysalaasnlValPheVal 239
 793 TTCTAGTGAATAATCCACAGTC---AATCTCTTTAGACAGTCTTTGAACCCAT 849
 240 Hisleu-----ProargleuaglnlyleuYrleuaspargasnlleu-----Ile 254
 850 GACTTCATTCAGACCAAGCCTTTCAGGAAATTAAG---CTGCATGAAGTCACTTACAG 906

255 ThrzlaValaIaProglialaPheleuglyMetlysaIaleuargTrepLeuaspLeuser 274
 907 GGTAAATTTTATAGCTCAAAATATATAGAACTGCGCTTCAAAACCTGGCTGTACAC 966
 275 Hisasn---ArgValaIaGlyleuMeGlnsprThrPheproGlyleuGlyleuHis 293
 967 GTCCATCGGTGATCTTGGGA-----GAATTTAAAGATGAA 1002
 294 ValleuargleuanaIahIsaenlaIalealaserleuargProargThrPheLyaspLeu 313
 1003 AGGAATCTGAAATTTTGA-----CCCTTATC 1032
 314 HisPheleuglnuglyleuaglnleuglnlyIsaasnargIleaarglnleuglnargThr 333
 1033 ATGAAGACTATGTAT-----GTACACCTTATAGATTCAGGTTAATACATATACA 1083
 334 PheglnlyleuaglnleuglnleuaglnValleuThreusasnaspanglnIleThrGluVal 353
 1084 AATGATTTTTCAGATGATATTTGTTAAGTTCATGCTGGCGAATGTTCTGC---AAT 1139
 354 Arg-----ValGlyAlaPheSerGlyleuPheasnValaIaValMetasn 368
 1140 GTCTCTGACAGGTATCTATTAATAATATCTAAGAGATGTTCTTAACATTTCAAAATGACA 1199
 369 LeuserGlyasnCyseleuargserleuProgluArg-----ValPhegln----- 383
 1200 ATCTTTCATATCTTATGATGTCAACTAGACAGTTTCCAACTGTGATCTTACCTTTCTT 1259
 383 ----- 383
 1260 AAAAGTTGACTTAACTATGACAAAGGCTATCATGTTTAAAAAAGGCCCTTACA 1319
 384 -----Glyleuasp 386
 1320 AGTCTGACTATCTAGATCTTATAGAAATGACCTGAGCTTATAGTGGCTGTCTTAT 1379
 387 LyeleuThIsaserleuThIsleuaglnIsaserCyseleuaglnlyIsValaArgleuHisThrPhe 406
 1380 TCTGATTTGGGAACAAACACCTGACACCTTGAACCTGACCTGACCTTACATGTG---GCCATC 1436
 407 Ala-----GlyleuSerGlyleuArgyleuPheleuargaspasnSerIleSerSer 424
 1437 ATATGAGTGCATATTCATGAGGCTGTAGAGAGCTGACAGCTGATTTTTCAGCACTC 1496
 425 IleuglnuglnserleuhalaglyleuserGlyleuaglnleuasp-----Leu 441
 1497 TACTTTAAAAAGGTCACAGAAATTC-----TCAGCCTTCTTATCCCTGAAAAGCTACT 1550
 442 -ThrThraasnargleuThrhIsleuProargGlnleuPheglnlyleuaglnHisleuGln 461
 1551 TTACCTTGACATCTCTTATACTTAACACCAAAATGACTTGATGATGATATTTCTGGCTT 1610
 461 uTyyleuThleuSerTyraangln-----Le 470
 1611 GACCAAGTCAACACATTAATAAATGCTGGCAATTTCTTCAAGACAAACCTTTGAAA 1670
 470 uThrThrLeuser-----AlaGln 476
 1671 TGCTCTTGAAACAACAACAACTTGACATTCCTGATCTTCTTAATGTAATTGACAA 1730
 476 uValleuaglyProleuaglnarglaPheThrepLeuaspIleSerhIsaasnHisleuagln 496
 1731 AATATCTTGGGGGATATTTGACACCTTCATAGACTTCAATTAATATAGATGACAA 1790
 496 rleuhalaglnlyleuPheSerSerleuaglyArgValaIargTyleuSerleuargasnl 516
 1791 CAATCTA-----TGTCTTTGGATTCATGCCA 1817
 516 nSerleuaglnThrPheSerProglInProgllyleuaglnargleuThrleuaspIaasnPr 536
 1818 TTATTAACCAAGCTATTCCTCAGACACTTGTATGCAAGTTTCAATGCAATGACATC 1877

Db 536 cTrrp-----AspCyseSer----- 540
Qy 1878 TAAAGAACTACTGCAACATTTCGA---AAGAGCTAGCCTTCTTCATCTTACTACAA 1934
Db 541 -----CysProLeuYsAlaLeuArgAspPheAlaLeuGlnAsnPr 554
Qy 1935 TTCCTGTCCTGTATATGATGCAACATTCCTGCAAGTGGCTCAAGAA-----CA 1988
Db 554 ogYValVal-----ProArgPheValGlnThrValCysGlnuGlyAspAs 569
Qy 1989 GAACCACTCTTCTGTAATGTGAACAAATGCAATGTCACACCTGTAGATGAAT 2046
Db 569 pCyGlnProValYrThrTyraAsnAlaLeuThrCysAlaGlyProAlaAsnValSer 588
RESULT 9
US-08-473-089-50
Sequence 50, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
INDIVIDUAL ISOLATE: pro. complex-rac, Fig. 33
US-08-473-089-50
Alignment Scores:
Pred. No.: 9.07e-21 Length: 603
Score: 280.00 Matches: 163
Percent Similarity: 38.12% Conservative: 81
Best Local Similarity: 25.47% Mismatches: 221
Query Match: 5.41% Indels: 176
DB: 3 Gaps: 26
US-09-396-985B-46 (1-2951) x US-08-473-089-50 (1-603)
Qy 322 TGCATGATCAAGAACTCAGCAAGAGTCCCTGATGATGATCTTCTTCAACCAAGAACTA 381
Db 60 CysSerSerLyAsnLeuThrHisLeuProAspPheIleProValSerThrArgAlaLeu 79

Qy 382 GATCTGAGCTTCAACCCCTTGAAGATCTTAAAGCTATAGCTTCCATTTTTCAGAA 441
Db 80 TrpLeuAspGlyAsnAsnLeuSerSerIleProSerAlaAlaPheGlnAsnLeuSerSer 99
Qy 442 CTTCAGTGGCTGATTTATTCAGAGTGTGAATTTGAACAAATTGAACAAAGCATGGCAT 501
Db 100 LeuAspPheLeuAsnLeuGlnGlySerTrpLeuArgSerLeuGlnProGlnAlaLeu 119
Qy 502 GCGTTACACACCTTCCAACTTGATACACAGAAACCTTCCAGAGTTTTCOCOA 561
Db 120 GlyLeuGlnAsnLeuYrThrLeuHisLeuGlnArgAsnArgLeuArgAsnLeuAlaVal 139
Qy 562 GGAAGTTTCTCTGAGCTTAACAACTTGAACAATCTGTGGCTGTGAGACAAATTTGGCC 621
Db 140 GlyLeuPheThrHisIsthProSerLeuAlaSerLeuSerSerAsnLeuGly 159
Qy 622 TCTCTAGAAAGCTTCCCTATTTGACAGCTTATTAACCTTAAGAACTCAATGTGGCTCAC 681
Db 160 ArgLeuGlnGlyLeuPheGlnGlyLeuSerHisLeuThrAspLeuAsnLeuGlyTrp 179
Qy 682 AATTTT-----ATACATTCTCTG 639
Db 180 AsnSerLeuValValLeuProAspThrValPheGlnGlyLeuGlyAsnLeuHisGlyLeu 199
Qy 700 AAGTTA-----CTGCATATTTTCCAACTGACGAAAC 732
Db 200 ValLeuAlaGlyAsnLeuYrThrTyrlLeuGlnProAlaLeuPheCysGlyLeuGlyGly 219
Qy 733 CTAGTACATGATGATCTTCTTAACTATATTAACCTTAACTGACAAAGCATTAACAG 792
Db 220 LeuArgGlyLeuAspLeuSerArgAsnAlaLeuArgSerValIysAlaAsnValPheVal 239
Qy 793 TTCTTAGTGAATTCACAAAGTC---AATCTCTTTTACATGCTTTGAACCCAT 849
Db 240 HisLeu-----ProArgLeuGlnLysLeuTyrlLeuAspArgAsnLeu-----Ile 254
Qy 850 GACTTCACTCAAGACCAAGCCTTTCAGGAAATTAG---CTCCATGAACTGACTCTAAGA 906
Db 255 ThrAlaValAlaProGlyAlaPheLeuGlyMetLysAlaLeuArgTrpLeuAspLeuSer 274
Qy 907 GGTAAATTTAATAGCTCAAAATATATGAATAAATCTGCTTCAAACTGCTGTTTACAC 966
Db 275 HisAsn---ArgValAlaGlyLeuMetGlyAspThrPheProGlyLeuGlyLeuHis 293
Qy 967 GTCCATGCTTGTGATCTTGGCA-----GAATTTAAGATGAA 1002
Db 294 ValLeuArgLeuAlaHisAsnAlaIleAlaSerLeuArgProArgThrPheLysAspLeu 313
Qy 1003 AGGAATCTGGAATTTTGA-----CCCTTATC 1032
Db 314 HisPheLeuGlnGlyLeuGlnLeuGlyHisAsnArgIleArgGlnLeuGlyGlyArgThr 333
Qy 1033 ATGGAAGACTATGTGAT-----GTGACCATGATGATGATGATGATTAACATATACA 1083
Db 334 PheGlnGlyLeuGlyGlnLeuGlnValLeuThrLeuAsnAspGlnGlnIleThrGlnVal 353
Qy 1084 AATGATTTTTCAGATGATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1139
Db 354 Arg-----ValGlyAlaPheSerSerLysLeuPheAsnValAlaValMetAsn 368
Qy 1140 GTCCTGGCAGGTGATCTAATAAATATCTAGAAGAGTTCCTTAACATTTTCAATGGCA 1199
Db 369 LeuSerLysLeuAsnLeuArgSerLeuProGlnArg-----ValPheGln----- 383
Qy 1200 ATCTTATCATCATTTAGATGTCACATTAACAGATTTTCAACTGATCTTACCTTTCT 1259
Db 383 ----- 383
Qy 1260 AAAAGTTGACTTTAATTAAGAACAAAGGCTTATCATGTTTAAAAAAGGCCCTTACA 1319
Db 384 -----GlyLeuAsp 386

[illegible][illegible]

Db 240 HisLeu-----ProArgLeuGlnIleuLeuArgLeuSerLeu-----Ile 254
 QY 850 GACTTCATTCAGAACCAAGCTTTCAGGAATTAG---CTCCATGAACTGACTCTAGA 906
 Db 255 ThrAlaValAlaProGlnAlaPheLeuGlnIleuLeuArgLeuGlnIleuLeuSer 274
 QY 907 GGTATTTTAAATGATCAATATATGATAAACTGCTCAAACTGCTGCTTACAC 966
 Db 275 HisAsn---ArgValAlaGlnLeuMetGlnAspThrPheProGlnLeuGlnIleuHis 293
 QY 967 GTCCATCGTGTGATCTTGGGA-----GAATTTAAAGATGAA 1002
 Db 294 ValLeuArgLeuAlaHisAsnAlaIleAlaSerLeuArgProArgThrPheLeuAspLeu 313
 QY 1003 AGGAATCGGAATTTTGA-----CCCTCATC 1032
 Db 314 HisPheLeuGlnIleuGlnLeuGlnIleuAsnArgIleArgGlnLeuGlnValArgThr 333
 QY 1033 ATGACAGACTATGTGAT-----GTGACATGATGATGATTCAGTTAACTATACA 1083
 Db 334 PheGlnIleuLeuGlnIleuGlnValLeuThrLeuAsnAspAsnGlnIleuThrGlnVal 353
 QY 1084 AATGATTTTTCAGATGATGTTTAACTTCATTCCTTGGCGAATGTTTCTGC---AAT 1139
 Db 354 Arg-----ValGlnAlaPheSerGlnLeuPheAsnValAlaValMetAsn 368
 QY 1140 GTCTCTGCGACGCTATCTATATAATCTAGAAAGATGTTCTTAACATTTCAAAATGCA 1199
 Db 369 LeuSerGlnIleuAsnCysLeuArgSerLeuProGlnArg-----ValPheGln----- 383
 QY 1200 ATCTTATCAATCATTTAGATGTCAACTAGACAGTTTCAACTGTGATCTTACTCTT 1259
 Db 383 ----- 383
 QY 1260 AAAAGTTGACTTAACTAGAACAAAGGCTTATCATCTTTAAAAAGTGGCCCTTACA 1319
 Db 384 -----GlyLeuAsp 386
 QY 1320 AGTCTCAGTATCTAGATCTTATAGAAATGCACTGACCTTATGCTGCTGCTTCTAT 1379
 Db 387 LysLeuHisSerLeuHisLeuGlnHisSerCysLeuGlnIleValArgLeuHisSerPhe 406
 QY 1380 TCTGATTTGGGAAACAAACAGCTGAGACACTTACAGCTTCAATGCT---GCCATC 1436
 Db 407 Ala-----GlyLeuSerGlnLeuArgArgLeuPheLeuArgAspAsnSerIleSerSer 424
 QY 1437 ATTATGATGCGCAATTTTCATGCGCTTAAAGAGCTGACGACCTGGAATTTTTCAGACATC 1496
 Db 425 IleGlnIleuGlnIleuSerLeuAlaGlyLeuSerGlnLeuLeuGlnLeuAsp-----Leu 441
 QY 1497 TACTTTAAAAAGGCTCACGAATTC-----TCAGCGTCTTATCCCTTGAAGAGCTACT 1550
 Db 442 -ThrThrAsnArgLeuThrHisLeuProArgGlnLeuPheGlnIleuGlnIleuGlnIleu 461
 QY 1551 TTACCTTGACATCTCTTATATCTAACACAAATTTGACTGATGATATTTTGGCTT 1610
 Db 461 uTyrlLeuLeuLeuSerTyrAsnGln-----Le 470
 QY 1611 GACCACTGTCAACACATTTAAAAATGCTGCAATTTCTTCAAGACAAACCTTTGAAA 1670
 Db 470 uThrThrLeuSer-----AlaGln 476
 QY 1671 TGTCTTTGCAAAACAAACAACTTGACATTCCTGGATCCTTCTTAATGTAATTGAAACA 1730
 Db 476 uValLeuGlnIleuProLeuGlnArgAlaPheTyrPheLeuAspIleSerHisAsnHisLeuGlnIleu 496
 QY 1731 AATATCTTGGGGGATTTGACACCCCTCATAGACTCAATTAATTAATAGATGACAA 1790
 Db 496 rLeuAlaGlnIleuPheSerSerLeuGlnArgValArgTyrLeuSerLeuArgAsnAs 516
 QY 1791 CAATCTA-----TTGTTTGTGATTCATCCA 1817
 Db 516 nSerLeuGlnThrPheSerProGlnProGlnArgLeuArgLeuThrPheLeuAspAlaAsnPr 536

QY 1818 TTATTAACAGCTGATTTCCCTCAGCACTCTTATGACAGTTTCAATGCAATAGACATC 1877
 Db 536 oTTP-----AspCysSer----- 540
 QY 1878 TAAAGAACTACTGCAACATTTTCCA---AAGACTTACGCTTCTTCAATCTTACTACAA 1934
 Db 541 -----CysProLeuHisAlaLeuArgAspPheAlaLeuGlnAsnPr 554
 QY 1935 TTCTGTGCTTGTATATGTGACATCAGAAATTCCTGACGTGGCTCAAGGA-----CA 1988
 Db 554 oGlyVal-----ProArgPheValGlnThrValCysGlnIleuLysAspAs 569
 QY 1989 GAACGATCTCTGTGATGTAATGTGACAAATGTGACATGTGCAACCTGTGAGATGAT 2046
 Db 569 pCysGlnProValTyrThrAsnAsnIleuMetCysAlaGlyProAlaAsnValSer 588
 RESULT 11
 US-09-353-585-2
 ; Sequence 2, Application US/09353585
 ; Patent No. 6287865
 ; GENERAL INFORMATION:
 ; APPLICANT: Dixon, Mark S
 ; Jones, David A
 ; Jones, Jonathan DG
 ; TITLE OF INVENTION: Plant pathogen resistance genes and uses
 ; thereof
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Nixon & Vanderhye PC
 ; STREET: 8th Floor, 1100 No. 6287865th Glebe Road
 ; CITY: Arlington
 ; STATE: Virginia
 ; COUNTRY: United States of America
 ; ZIP: 22201-4714
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/353,585
 ; FILING DATE: 15-Jul-1999
 ; CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
 ; 1/68
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/930,277
 ; FILING DATE: 27-OCT-1997
 ; APPLICATION NUMBER: PCY/GB96/00785
 ; FILING DATE: 01-APR-1996
 ; APPLICATION NUMBER: GB 950658.5
 ; FILING DATE: 31-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ms Mary J Wilson
 ; REGISTRATION NUMBER: 32,955
 ; REFERENCE/DOCKET NUMBER: 620-69
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 816-4100
 ; TELEFAX: (703) 816-4100
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1112 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: YES
 ; ORIGINAL SOURCE:
 ; ORGANISM: Tomato
 ; STRAIN: Cf2
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-353-585-2

Alignment Scores:

Pred. No.: 3,56e-20 Length: 1112
 Score: 276.00 Matches: 201
 Percent Similarity: 36.05% Conservative: 118
 Best Local Similarity: 22.71% Mismatches: 312
 Query Match: 5.33% Indels: 255
 DB: 3 Gaps: 37

US-09-396-985B-46 (1-2951) x US-09-353-585-2 (1-1112)

```

QY 42 AGTAGAATGCTAAGGTTGGACCTCTCACTTCCTCT----- 77
DB 319 SerIuSnAlaLeuAnSgLySerIleProAlaSerLeuGlyAenLeuLyAsnLeuSer 338
QY 78 ----TTGAATATAGTACTTGAGAGGGGACCCAGGAGGAGAGAGGAGGAGTGTCCAG 134
DB 339 ArgLeuAnLeuVal-----AsnAnSgInLeuSerGlySerIleProAlaSerLeu 355
QY 135 GGAAGCTGCGCTGCGCACCAGT-----TACAGATGTCATGTCATGTCATGCGCTCACT 188
DB 356 GlyAnLeuAnLeuAnLeuSerMetLeuLyryrAnAnSgInLeuSerGlySerIle 375
QY 189 GGTTCAGAAAATGCCAGATGATGCTCCCTGCTCCTGCTGCTAGAGCTTGATCATGCGC 248
DB 376 -----ProAlaSerLeuGlyAn-LeuAnAnSgInLeuSerMetLe 388
QY 249 ACTGTTCTTCCTCGCTGACACAGAGGTTGAATCCCTGCATAGAGTATGCTCTAA 308
DB 388 uTyrLeuLyryrAnAnSgInLeuSerGlySerIleProAlaSerLeuGlyAnLeuAnAs 408
QY 309 TATTAC-----TACCAATGATGATGAGAAACTCAGCAAACTCCCTGATGATCC 362
DB 408 nLeuSerArgLeuLyryrAnAnSgInLeuSerGlySerIleProGluGluIleGly 428
QY 363 T-----TCTTCAACCAAGAACATAGATCTGAGCTTCAACCTTGAAAGATCTTAAAG 416
DB 428 yTyrLeuSerSerLeuThryrLeuAnSgInLeuSerArgAnSerIleAnSgInPheIlePr 448
QY 417 CTATAGCTTCTCCATTTTTCAGAACTTTCAGTGCTGATTTATCCAGGTGTAATGA 476
DB 448 AlaSerPheGlyAnSgInLeuSerAnLeuAlaPheLeuPheLeuLyryrGluAnSgInLeuAl 468
QY 477 AACCAATGAAGACAGGATGCGATGCTTACACCACTCTCAAACTTGATGATGACAGG 536
DB 468 aSerSerValProGluGluIleGlyLyryrLeuAnSgInLeuSerAnLeuAnSgInLeuSerGly 488
QY 537 AAACCTTATCCAGAGTTTTCCTCCAGAGAGTTTCTGAGACTTAAACAAGTTTGAACAATCT 596
DB 488 uAnSgInLeuAnSgInLeuSerIleProAlaSerPheGlyAnSgInLeuAnSgInLeuSerArgLe 508
QY 597 GGTGCTGTGGAGACAAATTTGGCTCTCTAGAAAGCTTCCCTATTTGACAGCTTATTAAC 656
DB 508 uAnSgInLeuValAnSgInLeuSerGlySerIleProGluGluIleGlyLyryrLeuAnSgIn 528
QY 657 CTTAAAGAACTCAATGGCTCACAATTTTATATACATTTCTGTAAGTACCTGCATATTT 716
DB 528 rLeuAnSgInLeuAnSgInLeuSerGlyAnSgInLeuAnSgInLeuSerIleProAlaSerPh 547
QY 717 TTCCAATCTGACAGAACTTGAATGATGATCTTTCTTATATATATATTAACAATATTAAC 776
DB 547 eGlyAnLeuAnSgInLeuSerArgLeuAnSgInLeuValAnSgInLeuAnSgInLeuSerGlySerIle 567
QY 777 TGTCACGACTTACAGTTTCTAGCTGAAATCCACAAGTCAATTTCTCT----- 825
DB 567 eProGluGluIleGlyLyryrLeuAnSgInLeuSerAnSgInLeuSerGlyAnSgInLeuAla 587
QY 826 -----TTAGACAG----- 834
DB 587 uAnSgInLeuSerIleProAlaSerLeuGlyAnSgInLeuAnSgInLeuSerMetLeuLyryrLeuLy 607
QY 834 ----- 834
DB 607 rAnAnSgInLeuSerGlySerIleProGluGluIleGlyLyryrLeuSerSerLeuThryr 627
  
```

```

QY 835 -----TCTTTGAC-----CCAATTGACTTCATTTCAAGACA 866
DB 627 rLeuSerLeuGlyAnSgInLeuSerAnSgInLeuAnSgInLeuIleProAlaSerPheAlaAnMetAr 647
QY 867 AGCTTTTCAAGGAATTAAGTCCATGAACTGACTTAAAGATTAATTTTAAATGACTCA-- 924
DB 647 gAnSgInLeuAlaLeuIleLeuAnSgInLeuAnSgInLeuIleGlyGluIleProSerSerVa 667
QY 925 -----AATTAATGAAA----- 936
DB 667 lCyAnSgInLeuThSerLeuGluValLeuLyryrMetProArgAnSgInLeuAnSgInLeuLyryrVa 687
QY 937 -----ACTTGCTTCAAAACCGGCTGCTTACACGTCATCGGTGATCTTGAGAGATT 992
DB 687 lProGInCyAnSgInLeuAnSgInLeuSerAnSgInLeuValLeuSerMetSerSerAnSgInPh 707
QY 993 TAAAGATGAAAGGAATGTGAAATTTTGAACCTCTATCATGAGAGACTATGTGATGT 1052
DB 707 eSerGlyGluLeu-----ProSerSerIleSerAnSgInLeuThSerLe 721
QY 1053 GACCATTTGATGAGTTTCAAGTTAATATATACAAATGATTTTTCAGATGATTTGTAAGTT 1112
DB 721 uGInIleLeuAnSgInLeu-----ArgAnSgInLeuGluGluIleProGIn-- 737
QY 1113 CCAATGCTTGCGGAATGTTCTGCAANTGCTCTG----- 1146
DB 738 ----CySPheGlyAnSgInLeuSerSerLeuGluValPheAnSgInLeuAnSgInLeuSgInLeuSe 756
QY 1147 -----GCAGGTGATCTTATTAATATCTA----- 1170
DB 756 rGlyThrLeuProThrAnSgInLeuSerIleGlyCySerLeuIleSerLeuAnSgInLeuHISgI 776
QY 1171 -----GAGATGTTCTTAAACATTTT-----AAATGCAATCTT 1205
DB 776 yAnSgInLeuGluAnSgInLeuIleProArgSerLeuAnSgInLeuCySerLeuGluValLe 796
QY 1206 ATCAATCATTAAGATGATCAATAAGC---AGTTTCCAACTGAT-----CTACCTT 1255
DB 796 uAnSgInLeuGlyAnSgInLeuAnSgInLeuAnSgInLeuPheProMetIzrLeuGlyThrLeuProG 816
QY 1256 TCTTAAAGTTGACTTAACTTAACTGAAACAA-----GGGTCTATC-----AGTTTAA 1303
DB 816 uLeuArgValLeuAnSgInLeuThrSerAnSgInLeuHISgIProIleArgSerSerArgAl 836
QY 1304 AAAAGTGCCCTTCAAGATGTCAGCTATCTAGATCTTATGAGAAATGACACTGAGCTTTAG 1363
DB 836 aGluIleMetPheProAnSgInLeuArgIleIleAnSgInLeuSerArgAnSgInLeuPheSer----- 854
QY 1364 TGTGCTGCTTCTTATTTGATTTGGAAACAAACAGCTGAGACACTTAACCTCACACTT 1423
DB 855 -----GInAnSgInLeuProThrSerLeuPheGluHISgInLeu----- 865
QY 1424 CAATGGTCCATATTATGATGATGATGATTTCAATGGCTGATGAGAGCTGACACCTGGA 1483
DB 866 -LySgInLeuMetArgThrValAnSgInLeuMetGluGluProSerTyryrGluSerTyryrAs 885
QY 1484 TTTTTCAGCACTTACTTAAAGAGGTCACAGAAATTTGAGGTTCTTATCCCTTGAA 1543
DB 885 pAnSgInLeuValValThrLyryrGly-LeuGlu-----LeuGluIleValA 901
QY 1544 AGCTACTTATCTTGAATCTTATTAATCAACCAAAATTTGACTTGATGATATATTC 1603
DB 901 rGlyLeuSerLeu-----TyThr----- 907
QY 1604 TTGGCTTGAACAGTCTCAACATTAATAAATGCTGCAATTTCTTCAAGACACACACC 1663
DB 908 -----ValIleAnSgInLeuSerSerAnSgInLeuPheGluGlyHISgIle- 920
QY 1664 TTTCAATGCTTTTGCAACACAAACAACTTGACATTTCTGATCTTCAATGTCAT 1723
DB 921 -----ProSer----- 922
  
```


537 AAACCTATCCAGAGTTTTCCTGAGTCTGCACTAACAAGTTTACCAACT 596
 488 uasnalaenugnglserrleProAlaserPheglYasnleuasnleuSerArgle 508
 597 GGTGGCTGTGAGACAAATGGCTCTCTAGAAAAGCTTCCCTATTGACAGCTTATAC 656
 508 uasnleuvalasnnglnleuSerGlySerleProgluInilegIlyrleuAsgse 528
 657 CTTAAGAACTCAATGCTGCTCAACATTTTATACATCTGTAAAGTACGCAATATT 716
 528 rleuasnValleuasnleuSerGluasnalaenugngly--SerleProAlaserPh 547
 717 TTCATCTGACGAACCTAGTATGATGAGATCTTTCTTATACATATATCAACTATAC 776
 547 eglyAsnleuasnleuSerArgleuasnleuValAsnnglnleuSerGlySerle 567
 777 TGTCACGACTTACAGTTTCTACGTTGAAATCCACAGTCAATCTCTT 825
 567 eProgluInilegIlyrleuArgSerleuasnAsnpleuGlyleuSerGluasnala 587
 826 -----TTAGACATG----- 834
 587 uasnGlySerleProAlaserleuGlyAsnleuasnAsnleuSerMetleuTyrlleuTy 607
 834 ----- 834
 607 rAsnAsnGlnleuSerGlySerleProgluInilegIlyrleuSerleuThrTy 627
 835 -----TCTTTGAC-----CCAATTGACTTCAATCAAGACA 866
 627 rleuSerleuGlyAsnAsnSerleuAsnGlyleuIleProAlaserPheglYasnMetAr 647
 867 AGCTTCAAGGAGATTAACTCCATGAACTGACTTAAGAGTATTTATATAGCTCA-- 924
 647 gAsnleuGlnIleuIleleuasnAsnAsnleuIleglYleuIleProSerSerVa 667
 925 -----AATAATATGAAA----- 936
 667 lCyAsnleuThrSerleuGlnValleuTyMetProArgAsnAsnleuTySgIlySva 687
 937 ----ACTTGCCTTCAAACTGGCTGGTTTACAGTCCATCGGTTGATCTTGGAGAAAT 992
 687 lProGlnCysleuIleYasnIleSerAsnleuGlnValleuSerMetSerSerAsnSerPh 707
 993 TAAAGATGAAGAATCTGAAATTTTGAACCTCATCATGAGAGCAATGATGATGT 1052
 707 eSerGlyGlnleu-----ProSerSerleSerAsnleuThrSerle 721
 1053 GACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1112
 721 uGlnIleleuAsnAsnleuGly-----ArgAsnAsnleuGlnIleAlleProGln-- 737
 1113 CCATTGCTGGCGCAATGTTTCTGCAATGCTCTG-- 1146
 738 ----CysPheglYasnIleSerSerleuGlnValPheAsnMetGlnAsnAsnIlyleuSe 756
 1147 -----GCAGGTATCTATAAATAATCA----- 1170
 756 rGlyThrleuProThrAsnPheSerleGlyCysSerleuIleSerleuAsnleuHISgl 776
 1171 -----GAGATGTTCTTAAACATTTT-----AAATGGCAATGCTT 1205
 776 yAsnGlnleuGlnAsnProglIleProArgSerleuAsnAsnCySyllySylleuGlnValle 796
 1206 ATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1255
 796 uAsnleuGlyAsnAsnGlnleuAsnAsnThrPheProMetTrpleuGlyThrleuProgl 816
 1256 TCTTAAAGTTGACTTAACTATGACAA-----GGGTATC-----AGTTTAA 1303
 816 uleuArgValleuArgleuThrSerAsnIlyleuHISglProIleArgSerSerArgAl 836
 1304 AAAAGTGGCCCTTACCAAGTCTCAGCTATCTAGATCTTATGAGAAATGCACTGAGCTTAG 1363

836 agluIleMetPheProAsnpleuArgIleIleAsnleuSerArgAsnAlaPheSer----- 854
 1364 TGTGGCTGTTCCTTATCTGATTTTGGAGACAAACAGCTGAGACCTTACAGCTTACACT 1423
 855 -----GlnAsnpleuProThrSerleuPhegluInileu----- 865
 1424 CAATGTCGACATCATTTATGAGTGCATTTTCAATGGTCTAGAAAGAGTGCAGCACTGGA 1483
 866 -lySgIlyMetArgThrValAsnlySthrMetGlnIleuProSerTyrlleuSerTyrlAs 885
 1484 TTTTCGACACTTACTTTTAAAGGCTGCAGAAATTTCTAGCGCTTCTTATCCCTTGAA 1543
 885 pAsnSerValValValThrIlySgIly-leuGln-----leuGlnIleVala 901
 1544 AGCTACTTTCATCTTGAATCTCTTATCTTACACCAAAATTTGACTTGATGATATATTC 1603
 901 rGlyleuSerleu-----TyrlThr----- 907
 1604 TTGGCTTGACCAAGTCTCAACATTTAAATGAGGCTGCATTTCTTCAAGACACACACC 1663
 908 -----ValIleAsnpleuSerAsnIlyPhegluGlyHISle- 920
 1664 TTTCAATGCTTTTGCACAAACAAACTTGCATTCCTGATCTTCAATGTCAT 1723
 921 -----ProSer----- 922
 1724 TGACAAATATATCTTGGGGGATTTTGCACACCTCCATACCTTCAATTTTAAATATGA 1783
 923 -----ValleuGlyAsnpleuIleAlleArgIleleuAsnValS 936
 1784 GTCAACAACATTTATGTTTGGATTCATCCCATTTATACAGCTGTATTTCCCTGACA 1843
 936 eHISAsnAlaIleGlnIlyTyrlleProSerSerleuGlySerleuSerleleuGlnS 956
 1844 CTCTGATTCAGTTTCATTCGACATGACACATCTTAAAGAAATCTGCAATTTTCCA 1903
 956 erleuAsnpleuSerPheAsnGlnleuSer-----GlyGlnleuProG 970
 1904 AGAGCTTAGCC-----TTCTCAATCTTACTTACAAATTCGTT--G 1942
 970 lnglnleuAlaserleuThrPheleuGlnIleuAsnleuSerHISAsnTyrlleuGln 990
 1943 CTGTATATGTAACATCAGAAATTCCTGCAAGTG-- 1977
 990 lYcylleProGlnIlyProGlnPheArgThrPheGlnSerAsnSerTyrlleuGlyAsn 1010
 1978 -----GTCAAGAACAGA 1990
 1010 spgIlyleuArgGlyTyrlProvalSerIlySgIlySvaBrProvalSerGlnIlySva 1030
 1991 AGCAGTTCTTGGATGATGTTGAACAAATGACATGTCACACCTGTAGAGATGATACCT 2050
 1030 snTyrlThrValSerAlaIleuGlnAsnProgln-----GlnSerAsnSerG 1044
 2051 CCTTATGTTGATTTTAAATTAATCTTACCGTTATATGTCAGACAC-----ATCATCA 2104
 1044 lAsnPheAsnAsnPheThrPlySAlaAlaIleuMetGlyTyrlGlySerGlyleuCysIleG 1064
 2105 GTGTGCAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2149
 1064 lYleSerIleIle-----TyrlleuIleuIleSerThrGlyAsnleuAsnGlyTrpleuAlaArgI 1083
 2150 TGAATATACCTTCTTATTTTACCTTATCTTATGCTTATGCTGCTGTAATAAGTACAGCAG 2209
 1083 lIleleuGlnIleuGlnIlySyllyleIleIleMetGlnArg-----ArgIlySylGlnArgG 1101
 2210 GAGAAAGCATCTAT 2223
 1101 lYglnArgAsnTyrl 1105

RESULT 13
 US-09-191-647-2


```

Db      676 ArglyslsArgxllleValThrGlyasnProArgCysGlnIlysProTyPheLeuIysGlu 695
QY      1654 -----GACAAc 1659
Db      696 IleProIleGlnAspValAlaIleGlnAspPheThrCysAsnAspGlyAsnAspAsn 715
QY      1660 ACCCTTTCAAATGCTCTTGGAACAACAACAACCTGATTCCTGGATCC----- 1710
Db      716 SerCysSerProIleHisArgCysProThrGlnCysThrCysLeuAspThrValValArg 735
QY      1711 --TCTAATGTCAATTGGAACAAAATCTTGGGGGGTA----- 1746
Db      736 CysSerAsnIySGlyLeuIlyeValLeuProIlySGlyIleProArgAspValThrGluLeu 755
QY      1747 -----TTTGACACCCCTCAATAGACTT 1767
Db      756 TyrIleuAspGlyAsnGlnPheThrIleuValProIlySGluLeuSerAsnTyIyshiIleu 775
QY      1768 CAATTATTAAATATGAGTCACACAAATCTAATTTGTTGGATTCATCCCATTAATTAACAG 1827
Db      776 ThrIleuIleAspLeuSerAsnshnArgIleSerThrIleuSerAsnGlnSerPheSerAsn 795
QY      1828 CTGATATTCCTTCAGACACTCTTGATTGCAAGTTTCATTCGCATA-----GAG 1872
Db      796 MetThrGlnLeuLeuThrIleuIleuSerTyIyRnaArgLeuArgCysIleProProArg 815
QY      1873 ACATCTAAAGAAATCTGCAACATTTTCCAAAGAGCTTAGCCCTTCAATCTTAATCAAC 1932
Db      816 ThrPheAspGlyLeu-----LysSerIleuArgLeuLeuSerLeuIleGly 830
QY      1933 AATTCCTGTGCT----- 1944
Db      831 AsnAspIleSerValValProGlnGlyAlaPheAsnAspLeuSerAlaIleuSerHisIleu 850
QY      1945 -----TGATATGTGAACATCAGAAATTCCTGACAGTGCT 1980
Db      851 AlaIleGlyAlaAsnProLeuTyCysAsnMetGlnTyIeSerAspTrpVal 870
QY      1981 AAGGAACAG----- 1989
Db      871 LysSerIuTyIySGlnProGlyIleAlaArgCysAlaGlyProGlyGluMetAlaAsp 890
QY      1990 AAGCAGTCTCTTGTCGAAT--GTTCGAACAATGACATGTGCACAACCTGTAGATGAT 2046
Db      891 LysIleuLeuLeuThrThrProSerTyIyshiPheThrCysGlnGlyProValAspValAsn 910
QY      2047 -----ACC 2049
Db      911 IleIleuAlaIyCysAsnProCysIleuSerAsnProCysIyAsnAspGlyThrCysAsn 930
QY      2050 TCCCTTAGTGTTGAATTAATTAATTTCTACCTGT---TATATGTACAAGACAAT----- 2099
Db      931 SerAspProValAspPheTyIyArgCysThrCysProTyIyGlnPheIySGlyGlnAspCys 950
QY      2100 -----CATCAGTGTGTGACAGTGTGAGTGTGATGTGATTCACCTGTAGACTT 2147
Db      951 AspValProIleHisAlaCysIleSerAsnProCysIyshiSGlyGlyThrCysHisIleu 970
QY      2148 TCTGATATACCACTTATTTTTCACCTGATACTTAATGTGCTGCTGAATAAAGTACAGACG 2207
Db      971 LysGlu-----GlyGlnGlnAspGlyPheThr----- 979
QY      2208 AGGAGAAAGCATCTATGATGACTTGT---GATCTACCGGAGTGAGAA 2252
Db      980 -----CysIleCysAlaAspGlyPheGlnGlyGlu 989

```

1. APPLICANT: Kid, Thomas
 2. APPLICANT: Broese, Katja
 3. APPLICANT: Tessier-Lavigne, Marc
 4. TITLE OF INVENTION: Modulating Robo: Lgand Interactions
 5. FILE REFERENCE: B98-031-3
 6. CURRENT APPLICATION NUMBER: US/09/540,245A
 7. CURRENT FILING DATE: 2000-03-31
 8. PRIOR APPLICATION NUMBER: 60/065,544
 9. PRIOR FILING DATE: 1997-11-14
 10. PRIOR APPLICATION NUMBER: 60/081,057
 11. PRIOR FILING DATE: 1998-04-07
 12. NUMBER OF SEQ ID NOS: 20
 13. SOFTWARE: PatentIn Ver. 2.0
 14. SEQ ID NO 2
 15. LENGTH: 1525
 16. TYPE: PRT
 17. ORGANISM: human
 18. US-09-540-245A-2

Alignment Scores:	
Pred. No.:	8, 02e-20
Score:	273.50
Percent Similarity:	31.65%
Best Local Similarity:	19.44%
Query Match:	5,288
DB:	3
Gaps:	32
Length:	1525
Matches:	175
Conservative:	109
Mismatches:	294
Indels:	321
Gaps:	32

US-09-396-985B-46 (1-2951) X US-09-540-245A-2 (1-1525)

QY	160	GAATGCGCATGGTTCTTCAAGAGCGGTCACATGGTTGGAGAAATATGCGAAGATGATCACTCC	219
			:::
Db	214	AbrCysHis---LeuAlaTrp-----	LeuSerAsp 222
QY	220	TGGCTCTGGCTAGGACCTGTGATCAATGCGACSTGTTCTTCTCTGCTGACACCGAGAAC	279
Db	223	TrpLeuAlaGlyAlaGlyProAlaGlyAla---GlyLeuIleuYrTrpGlnCysMetGlyProSerHis	245
QY	280	TTGAA-----	285
Db	242	LeuAlaGlyHisAsnValAlaGluValAlaGlnLysArgGluPheValCysSerAspGlu	261
QY	286	-----CCCTGCATGAG	297
Db	262	GluGlyHisGlnSerPheMetAlaProSerCysSerValLeuHisCysProAlaAlaCys	281
QY	298	GTAAGTCTCAATATTACTTCCATCGATGCAATGCAATGCAAACTGACGAATGCTCGATGAC	357
			:::
Db	282	ThrCysSerAsnAsnIleValAspCysArgGlyValGlyLeuThrGlnIleProAsn	301
QY	358	ATTCTCTTCAACCAAGAACATAGATGAGCTTCAACCCCTGGAAGATCTTAAAAAGC	417
Db	302	LeuProGluThrTrpIleThrGluIleArgLeuGluGlnAsnThrIleLysValIleProPro	321
QY	418	TATAGCTTCCAAATTTTTCAGAACTTCAGTCAAGTGGCTGATTTATCCAGGTGGAATTGA	477
Db	322	GlyAlaPheSerProTyrIleValLysLeuArgArgIleLeuPheLysSerAsnAsnGlnIleSer	341
QY	478	ACAATTGGAAGACAAAGCATGGCATGGCTTACACCACTCTCAAACTTGATCTGACAGGA	537
Db	342	GluLeuAlaProAspAlaPheGlnGlyLeuArgSerLeuAsnSerIleValLeuTyrGly	361
QY	538	AACCCATGACAGATTTTCCCGAGGAAGTTCTCTGGAGCTTAAACAAGTTTAAACAATCTG	597
Db	362	AsnLysIleThrGluLeuProLysSerIleuPheGluGlyLeuPheIleSerGlnLeuLeu	381
QY	598	GTGGCTGTGGAGACAAATGGCTCTCTAGAAACTTCCATATGGACAGCTTATAACC	657
Db	382	-----LeuLeuAsn	384
QY	658	TTTAAAGAACTCAATGTGGCTCACAAATTTTATACATCTCGTAAAGTAACTGCAATATTT	717
Db	385	AlaAsnLysIleAsn-----CysLeuArgValAspAlaPhe	396

QY 718 TCCATCTGCAAGCACTAGATGATGCTTTCTTATTAATACTATTAATACTATTAAT 777
 |||||
Db 397 GluAspLeuHisAsnLeuAsnLeuSerLeuThrAspAsnLysLeuGlnThrIleAla 416
 |||||
QY 778 GTCAACGCACTTAACGATTTTACGTGAATTCACAGTCAATCTCTTTAGACATGCT 837
 |||||
Db 417 LysGluThrPheSerProLeuArgAlaIleGlnThrMetHisLeu-----Ala 432
 |||||
QY 838 TTAAACCCATTTGATCTGATTCACAGCAAGCCCTTGACGGAAATTAAG-----CTCCAT 891
 |||||
Db 433 GluAsnPro-----PheIleCysAspCysHisLeuLysThrLeuAlaAspTyrLeuHis 450
 |||||
QY 892 GAACGTGACTGAAGGTAATTTTAATAGCTCAATATTAATGAAGAACTGCTTCAAAAC 951
 |||||
Db 451 -----ThrAsnProIleGluThrSerGluAlaArgCysThrIleSerProAspArg 466
 |||||
QY 952 CTGGCTGGTTTAACGCTGCATCGGTTGATGCTGGAGAAATTTAAAGATGAAGGAATCTG 1011
 |||||
Db 467 LeuAlaAsnLysArgIle-----GlyGlnIleLysSerLys----- 479
 |||||
QY 1012 GAAATTTTGAACCCCTCATCATGAGAGACTATGTATGTGACCATTTGATGATTCAGG 1071
 |||||
Db 480 -----PheArg 481
 |||||
QY 1072 TTACATATATCAAAATGATTTTTCAGATGATTTGTAAGTTCCATTCCTGGCGAATGTT 1131
 |||||
Db 482 CysSerGlyThrGluAspTyrArgSerLysLeu-----SerGlyAspCysPheIleAspLeu 500
 |||||
QY 1132 TCTGCAATG-----TCTCTGCGACGGTGTATCTATTAATAATCTTA 1170
 |||||
Db 501 AlCysProGluLysCysArgCysGluGlyThrThrValAspCysSerAsnGlnLysLeu 520
 |||||
QY 1171 GAAGATGCTTCCCTCAACATTTTCAATGGCAATCCCTTATCATCATCATTAATGATGCACTAGC 1230
 |||||
Db 521 AsnLysIleProGluHisIleProGlnTyrThrAlaGluLeuArg-----LeuAsnAsnAsn 540
 |||||
QY 1231 AGTTTCCAACTCTGAT-----CTACCCCTTCTTAAAGTTTGA 1269
 |||||
Db 540 IuPheThrValLeuGluAlaThrGlyLysPheLysLysLeuProGlnLeuArgLysIleA 560
 |||||
QY 1270 CTTTAATCTGAACAAAGGCTGTATGATTTTAAAAAGTGGCCCTTCAACAACTCTGACT 1329
 |||||
Db 560 snPheSerAsnAsnLys-----I 566
 |||||
QY 1330 ATCTAGATCTTAGAGAAATGCACTGAGCTTTAGTGGTGCTGTTCTTATTTGATTTGG 1389
 |||||
Db 566 IeThrAspIleGluGlnGlyAlaPheGlnGlyAlaSerGlyValAsnGlnIleLeuLeuT 586
 |||||
QY 1390 GAACAACAGCGCTGAGACACTTAGACCTGAGCTTCATGTGGCCATTTATATGAGTGCCA 1449
 |||||
Db 586 hIserAsnArgLeuGlnAsn-----ValGlnHisLysM 597
 |||||
QY 1450 ATTTCATGGCTTGAAGAAGCTGAGACCTGATTTTTCAGACCTGATCTTATTAAGG 1509
 |||||
Db 597 ePheLysGlyLeuGlnSerLeuLys-----ThrLeuMetLeuArgSerAsnArgIleThrCys 616
 |||||
QY 1510 GTCAACAATTTCTCAGGCTTTATCCCTTGAAGAAAGCTACTTACCTTGACATCTCTAT 1559
 |||||
Db 617 ValGlyAsn-----AspSerPheIleGlyLeuSerSerValArgLeuLeuSerLeuTyrAsp 635
 |||||
QY 1570 ACTAACACCAAAATTTGACTTCGATGATATATTTCTTGCGCTTGACAGCTTCAACACATTA 1629
 |||||
Db 636 AsnGlnIleThrThrValAlaIleProGlyAlaPheAspThrLeuHisSerLeuSerThrLeu 655
 |||||
QY 1630 AAAATGGCTGGCAATTTCTTCAAA----- 1653
 |||||
Db 656 AsnLeuLeuAlaAsnProPheAsnCysAsnCysTyrLeuAlaIleTyrLeuGlyGluTyrLeu 675
 |||||
QY 1653 ----- 1653
 |||||
Db 676 ArgLysLysArgIleValThrGlyAsnProArgCysGlnLysProTyrPheLeuLysGln 695
 |||||
QY 1654 -----GACAAAC 1659
 |||||

Db 696 IleProIleGlnAspValAlaIleGlnAspPheThrCysAspAspGlyAsnAspAspAsn 715
 |||||
QY 1660 ACCCTTTCAAATGCTCTTTGGCAACACAAACAACTTTCAGTCTGATCCT----- 1710
 |||||
Db 716 SerCysSerProLeuSerArgCysProThrGlnCysThrCysLeuAspThrValAlaArg 735
 |||||
QY 1711 ----CTAAATGTCAAATTTGGAACAAATATCTTGGGGGGTA----- 1746
 |||||
Db 736 CysSerAsnLysGlyLeuLysValLeuProLysGlyIleProArgAspValThrGluLeu 755
 |||||
QY 1747 -----TTTGACACCCCTCCATPAGACTT 1767
 |||||
Db 756 TyrLeuAspGlyAsnGlnPheThrLeuValProLysGluLeuSerAsnTyrLysHisLeu 775
 |||||
QY 1768 CAATTATTAATATGATGATGACAAACATCTATTGTTTGGATTCATCCCATTTAAACGAG 1827
 |||||
Db 776 ThrLeuIleAspLeuSerAsnAsnArgIleSerThrLeuSerAsnGlnSerPheSerAsn 795
 |||||
QY 1828 CTGTATTTCCCTCAGACCTCTTGATTCGATTCGATTCGACATA-----GAG 1872
 |||||
Db 796 MetThrGlnLeuLeuThrLeuIleLeuSerTyrAsnArgLeuArgCysIleProProArg 815
 |||||
QY 1873 ACATCTAAAGGAATACTGCAACATTTTCCAAAGAGCTTACCTTTCATCTTAATTAAC 1932
 |||||
Db 816 ThrPheAspGlyLeu-----LysSerLeuArgLeuLeuSerLeuHisGly 830
 |||||
QY 1933 AATTCGTGCT----- 1944
 |||||
Db 831 AsnAspIleSerValAlaProGlnGlyAlaPheAsnAspLeuSerAlaLeuSerHisLeu 850
 |||||
QY 1945 -----TGATATGTGAACATGACAGAAATTCCTGCACTGGGCTC 1980
 |||||
Db 851 AlaIleGlyAlaAsnProLeuTyrCysAspCysAsnMetGlnThrLeuSerAspThrPval 870
 |||||
QY 1981 AAGGAACAG----- 1989
 |||||
Db 871 LysSerGluTyrLysGluProGlyIleAlaArgCysAlaGlyProGlyGluMetAlaAsp 890
 |||||
QY 1990 AAGCAGTTCCTTGATGAT-----GTTGAACAAATGACATGTGCAACACTGTAGAGATGAAT 2046
 |||||
Db 891 LysLeuLeuLeuThrThrProSerLysLysPheThrCysGlnGlyProValAspValAsn 910
 |||||
QY 2047 -----ACC 2049
 |||||
Db 911 IleLeuAlaLysCysAsnProCysLeuSerAsnProCysLysAsnAspGlyThrCysAsn 930
 |||||
QY 2050 TCCTTAGTGTGGATTTTAAATTTTACCTGT-----TATATGACAAAGACAAAT----- 2099
 |||||
Db 931 SerAspProValAspPheTyrArgCysThrCysProTyrGlyPheLysGlyGlnAspCys 950
 |||||
QY 2100 -----CATCAGTGTGACGTGTCAGTGTGATGTGTGATCCACTGATGATTT 2147
 |||||
Db 951 AspValProIleHisAlaCysIleSerAsnProCysLysHisGlyGlyThrCysHisLeu 970
 |||||
QY 2148 TCGATATATACACTTCATTTTACCTGATATTTACCTGATATTTATGCTGGCTGTAAAGTACAGACG 2207
 |||||
Db 971 LysGln-----GlyGlnGlnAspGlyPheThr----- 979
 |||||
QY 2208 AGGAGAAAGCATATGATGATGATTTGT-----GATCTACTGAGTCAAGAA 2252
 |||||
Db 980 -----CysIleCysAlaAspGlyPheGlnGlnGln 989
 |||||

RESULT 15
US-09-540-153-2
Sequence 2, Application US/09540153
Patent No. 6270995
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Teesler-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions

```

: FILE REFERENCE: B98-031-3
:
: CURRENT APPLICATION NUMBER: US/09/540.155
:
: CURRENT FILING DATE: 2000-03-31
:
: PRIOR APPLICATION NUMBER: 09/191,647
:
: PRIOR FILING DATE: 1998-11-13
:
: PRIOR APPLICATION NUMBER: 60/081,057
:
: PRIOR FILING DATE: 1998-04-07
:
: NUMBER OF SEQ ID NOS: 14
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 2
:
: LENGTH: 1525
:
: TYPE: PRT
:
: ORGANISM: human
:
US-09-540-153-2

```

Alignment Scores:	
Pred. No.:	8, 02e-20
Score:	273.50
Percent Similarity:	31.63%
Best Local Similarity:	19.49%
Query Match:	5.28%
DB:	3
Gaps:	
Length:	152
Matches:	175
Conservative:	109
Mismatches:	294
Indels:	32
Gaps:	31

US-09-396-985B-46 (1-2951) X US-09-540-153-2 (1-1525)

[illegible]

QY	778	GTCAACAGCTTACGATTTCTACGAGAAATCCACAAGCATCTCTCTTACAGATGCT	837
Db	417	LyseglYthrPheSerProLeuAlaAlaIleGlnThrMetHisLeu-----Ala	432
QY	838	TTGAACCCAAATTTGACTTCATTCAAGACCAAGCCTTTACAGGAAATTAAG-----CTCCAT	891
Db	433	GlnAsnPro-----PheIleCysAspCysHisIleuLeuStryPheAlaAspTyrLeuHis	450
QY	892	GAAGTGAAGCTTAAGAGGTAATTTTAATAGCTCAAAATTAATGAAGAACTTGCCTTCAAAAC	951
Db	451	-----ThraAsnProIleGluThrSerGlyAlaArgCysThrSerProArgArg	466
QY	952	CTGGCTGGTTTACAGCGTCCATCGGTTGATCTTGGAGAAATTTAAAGATGAAGAAATCTG	1011
Db	467	LeuAlaAsnIlyAsnIlyAspArgIle-----GlyGlnIleIysSerIlyAs-----	479
QY	1012	GAATTTTTTGAACCTCTATCATGAGAGACTATGATGATGACCATTCATGATGATGTCAG	1071
Db	480	-----PheArg	481
QY	1072	TTAACATATACAAATGATTTTTCAGATGATATGTTAAGTTCATGCTGGCCGAATGTT	1131
Db	482	CysSerGlyThrGluAspTyrArgSerIleLeu---SerGlyAspCysPheAlaAspLeu	500
QY	1132	TCCTGCAATG-----TCTTGCGAGGTGATCTATAAAATATCTA	1170
Db	501	AlaCysProGluIlyCysArgCysGluGlyThrThrValAspCysSerAsnGlnIlySerLeu	520
QY	1171	GAAGATGTCCTCAACATTTCAATGGCAATCCCTTATCATCATAGTATGATGCACTAAGC	1230
Db	521	AsnIlyAspProGluHisIleProGlnTyrThrAlaGluLeuArg--LeuAsnAsnAsnG	540
QY	1231	AGTTTCCAACTCGGAT-----CTACCTTTCTTAAAAAGTTTGA	1269
Db	540	IuphethrValLeuGluAlaThrGlyIlePheIlySlyLeuProGlnLeuArgIlyLea	560
QY	1270	CTTTAACTATGACAAAGGCTTATCATGTTTAAAAAAGTGCCCTTACCAAGTCTCAGCT	1329
Db	560	snPheSerAsnAsnIlyS-----I	566
QY	1330	ATCAGATCTTAGTAGAAATGACACTGAGCTTTAGTGAGGCTGTTCTTATTCATGATTTGG	1389
Db	566	IethrAspIleGluGluGlyAlaPheGluGlyAlaSerGlyValAsnGluIleLeuLeuT	586
QY	1390	GAACAAACAGCGCTGAGACACTTAGACCTCAGCTTCATATGGGCATCATATATGAGTCCA	1449
Db	586	hIserAsnAlaArgLeuGluAsn-----ValGlnHisIlySrn	597
QY	1450	ATTTCATGGCTTAGAAGAGCTGACGACCTGATTTTTCAGACTCTACTTATTAAGAG	1509
Db	597	ePheIlySglyIleuGlnSerIleuIlyS--ThrlMetLeuArgSerAsnArgIleThrCys	616
QY	1510	GTCACAGAAATTCAGGCTCTTATCCCTTGAAAAAGTACTTTCATCTTGACATCTCTAT	1569
Db	617	ValGlyAsn--AspSerPheIleGlyLeuSerSerValArgLeuLeuSerLeuTyrAsp	635
QY	1570	ACTAACAACCAAAATTTGACTTCGATGATATATTTCTTGCTTACCACTCATCAACATTA	1629
Db	636	AsnGlnIleThrThrValAlaProGlyAlaPheAspThrLeuHisSerLeuSerThrLeu	655
QY	1630	AAAATGGCTGGCAATTTCTTCAAA-----	1653
Db	656	AsnLeuLeuAlaAsnProPheAsnCysAsnCysTyrIleuAlaTrpLeuGlyGluTrpLeu	675
QY	1653	-----	1653
Db	676	ArgIlyLeuArgIleValThrGlyAsnProArgCysGlnIlySProTyrPheLeuIlySglu	695
QY	1654	-----GACAAAC	1659
Db	696	IleProIleGlnIleAspValAlaIleGlnIleAspPheThrCysAspAspGlyAsnAspAspAsn	715
QY	1660	ACCCTTTCAATGCTCTTGGCAACACAAACAACTGACATCTCTGATCCT-----	1710

Db	716	SetCyserProLeuSerArgCysProThrGluCysLeuThrValValArg	725
		::: ::::	
Qy	1711	---TCTAAATGTCATTTGGAACAATATCTTGGGGGGGA	1746
		::: ::::	
Db	736	CysSerAsnIysGlyLeuValLeuProIysGlyIleProArgValThrGluLeu	755
Qy	1747	-----TTTGACACCCCTGCATAGACTT	1767
Db	756	TyrLeuAspGlyAsnGlnPheThrLeuValProIysGluLeuSerAsnTyrLeuIleu	775
Qy	1768	CAATATATTAATATGAGTCAACAACATATATGTTTGGATGATGCCATTAACACG	1827
		::::	
Db	776	ThrLeuIleAspLeuSerAsnAsnArgIleSerThrLeuSerAsnGlnSerPheSerAsn	795
Qy	1828	CTGTATATCCCTCAGACATCTGATTTGCAGTTGCACATGACATA	1872
		:::	
Db	796	MetThrGlnLeuLeuThrLeuIleLeuSerTyrIleAsnGlyLeuArgCysIleProProArg	815
Qy	1873	ACATCTAAAGAAATACTGCAACATTTTCCAAAGAGCTAGGCTTTCTCATCTTACTACAC	1932
Db	816	ThrPheAspGlyLeu-----LysSerLeuArgLeuLeuSerLeuIleGly	830
Qy	1933	AATCTGTGCT-----	1944
		::::	
Db	831	AsnAspIleSerValProGluGlyAlaPheAsnAspLeuSerAlaLeuSerHisLeu	850
Qy	1945	-----TGATATGTGACATCAGAAATCTTGACAGTGGGTC	1980
Db	851	AlaIleGlyAlaAsnProLeuTyrCysAsnProCysAsnMetGlnTrpLeuSerAspTrpVal	870
Qy	1961	AAGGAACAG-----	1989
		:::	
Db	871	LysSerGluTyrLeuGluProGlyIleAlaArgCysValAspGlyProGluGluMetAlaAsp	890
Qy	1990	AAGCAGTCTTGGTGCAAT---GTTGAACAATATGACATGTGCACACCTGTAGACATGAT	2046
Db	891	LysLeuLeuLeuThrThrProSerTyrLysPheThrCysGlnGlyProValAspValAsn	910
Qy	2047	-----ACC	2049
Db	911	IleLeuAlaLysCysAsnProCysLeuSerAsnProCysLysAsnAspGlyThrCysAsn	930
Qy	2050	TCCTTAGTGGTGGATTTTAATATCTACCTGT---TATATGACAAACAT-----	2099
		::::	
Db	931	SerAspProValAspPheTyrArgCysThrCysProTyrGluPheTyrGlyLAspCys	950
Qy	2100	-----CATCAGTGTGCTAGGTGTAGTATGTGGATGCACCTGATGACATTT	2147
Db	951	AspValProIleHisAlaCysIleSerAsnProCysLysHisGlyThrCysHisLeu	970
Qy	2148	TCTGATATACCACTTCTATTTTGCACSTGATATCTTATGCTGGCTGTAAAAAGTACAGCAG	2207
		::: ::::	
Db	971	LysGlu-----GlyGluGluAspGlyPheTrp-----	979
Qy	2208	AGGAAAGACATCTATGATGCATTTGT---GATCTACTGACGTACGAA	2252
Db	980	-----CysIleCysValAspGlyPheGluGluGlu	989

Search completed: March 29, 2005, 17:39:04
Job time : 79.9256 secs

QY 415 AGCTATAGCTTCTCCAAATTTTTCAGAACTTCAGTGGTGTGATTTATCCAGGTGGAAT 474
 Db 70 AsnThrPheSerAspGluLeuIleAsnLeuThrPheLeuAspLeuThrArgCysGlnIle 89
 QY 475 GAAACATTTGAAACAAGGCGATGGCATGCTTACACCACTTCGAACTTGATGATGCA 534
 Db 90 TyrTrpIleHisGluAspThrPheGlnSerGlnHisArgLeuAspThrLeuValLeuThr 109
 QY 535 GGAACCCCTATCCAGAGTTTCCCCAGGAAGTTTCTGTGAGTAAAGTTTGAACAT 594
 Db 110 AlaAsnProLeuIlePheMetAlaGluThrAlaLeuSerGlyProValAlaLeuHis 129
 QY 595 CTGGTGGCTGTGAGACAAATATGGCTCTGAGAAAGCTTCCTATGAGCAGCTTATA 654
 Db 130 LeuPhePheIleGlnThrGlyIleSerSerIleAspPheIleProLeuHisAsnGlnIys 149
 QY 655 ACCTTAAAGAACTCAATGTGGCTCACAAATTTTATCATCTCTGATGATTCCTGCAAT 714
 Db 150 ThrLeuGlnSerLeuIleGlySerAsnHisIleSerSerIleLeuProIleGly 169
 QY 715 TTTTCCATCTGAGCAACTGATGATGATGATCTTTTATCTATATTCATTAATGAT 774
 Db 170 PheProThr---GluIysLeuIleValLeuAspPheGlnAsnAlaIleHisTyrLeu 188
 QY 775 ACTGTCAACGACTTACAGTCTTCTACGTGAATCCACAACTCACTCTCTTGTAGCAGT 834
 Db 189 SerIysGluAspMetSerSerLeuGlnIle-----AlaThrAsnLeuSerLeuAsnLeu 206
 QY 835 TCTTTGAACCAATGACTTATTCATTCAGACCAAGCTTTCAGGGAATTAAGCTTCAGTAA 894
 Db 207 AsnGlyAsnAspIleAlaGlyIleGluProGlyAlaPheAspSerAlaValPheGlnSer 226
 QY 895 CTGACTCTAAGAGGTATTTTATAGCTCAATATATTAAGAAATCTGCTTCATTAACCTG 954
 Db 227 Leu-----AsnPheGlyGlyThrGlnAsnLeuValIlePheIleGlyLeu 242
 QY 955 GCTGGTTTACAGCTTCATCGGTGATCTTGGAGATTTTAAAGATGAAGAACTGGAA 1014
 Db 243 LysAsnSerThrIleGlnSerLeuThrLeuGlyThrPheGlnAspMetAspAspGluAsp 262
 QY 1015 ATTTTGAACCTCTATCATGGAAGAGATATGTGATGATGATGATGATGATGATGATGAT 1074
 Db 263 Ile---SerProAlaValPheGluGlyLeuCysGlnMetSerValGluSerIleAsnLeu 281
 QY 1075 ACATATACAAATGATTTTTCAGATGATATGTGATGATTCCTGCTGGCAATGTTCT 1134
 Db 282 GlnIysHisIlyrPhePheAsnIleSerSerAsnThrPheIleCysPheSerGlyLeuGln 301
 QY 1135 GCAATGTCTGGCAGGTGTATTAATAATATCTAGAAAGTGTCTTAACATTTTC--- 1191
 Db 302 GluLeuAspLeuThrAlaThr-----HisLeuSerGluLeuProSerGlyLeuVal 318
 QY 1192 -----AAATGGCAATCTTATTCATC 1212
 Db 319 GlyLeuSerThrLeuIleValLeuValLeuSerAlaAsnIleAsnIysPheGluAsnLeu----- 336
 QY 1213 ATTAGATGTCAACTAAGCAG-----TTTCCAACTCTGATCTAACCTTTCTTAAAGT 1265
 Db 337 -----CysGlnIleSerIleSerAsnPheProSerLeuThrHisLeuSerIleLeuSerIly 354
 QY 1266 TTGACTTTTAACTATGACAAAGGGCTATCATGTTTAAATAAAGTGGCCCTTACCAAGTCTC 1325
 Db 355 AsnThrIlyrAspGluGluLeuGlyThrGlyCysLeuGluAsn-----LeuGluAsnLeu 372
 QY 1326 AGTATCTAGATCTTATGAAAGATGACATGAGCTTATGTGGTGGCTGTCTTATATTCGAT 1385
 Db 373 ArgGluLeuAspLeuSerHisAspAspIleGluThrSerAspCysCysAsnLeuGlnLeu 392
 QY 1386 TTGGGAACAAACAGCTGAGACATTAACCTCAGCTTCATGGGCGCATATATGAGT 1445
 Db 393 ArgAsnLeuSerHisIleGlnIleSerLeuAsnLeuSerIlyrAsnGluProLeuSerLeuIys 412
 QY 1446 GCCAAT---TTCATGGGTCTGAAGAGCTGACAGCCTGGAATTTTTCAGACCTGATCTTT 1502

Db 413 ThrGluAlaPheIysGluCysProGlnLeuGluLeuAspLeuAla-PheThrArgLe 432
 QY 1503 AAAAAGGGTACACGAATTCGACGGCTTTATCCCTTGAAAGACTTATTCCTTGACAT 1562
 Db 432 ClysValIysAspAlaGlnSerProPheGlnAsnHisIleLeuIleValLeuAsn 452
 QY 1563 CTCTTATCTATACCAACCAAAATGACCTTCAGTGTATATTTCTTGCTGGCTGACAGTCTCA 1622
 Db 452 uSerHisSerLeuAspIleIleSerSerGluGlnLeuPheAspGlyLeuProAlaLeuG 472
 QY 1623 CACATTTAAATAGCTGGCAATTCCTTCAAAAGCAACACCTT-----TCAATGTCTT 1676
 Db 472 HisIleLeuAsnLeuGlnIlyAsnHisPheProIysGlyAsnIleGlnIlyThrAsnSer 492
 QY 1677 TGCAAACACAAACAACTTGACATCTCTGATCTCTTAAATGTCATTTGCAACAAATATC 1736
 Db 492 uGlnThrLeuGlyArgLeuGluIleLeuValLeuSerPheCysAspLeuSerSerIleAs 512
 QY 1737 TTGGGGGGTATTTTGACACCCCTCATAGACTTCAATATTAATTAATGATGACAAACATCT 1796
 Db 512 pGlnHisAlaPheThrSerLeuIysMetCysAsnHisValAspLeuSerHisAsnArgLe 532
 QY 1797 ATGTGTTTGGAT-----TCATCCCATTAATTAACCACTGTATTCCTCAGACATCT 1847
 Db 532 uThrSerSerSerIleGluAlaLeuSerHisIleuIysGlyIleTyr-----Le 548
 QY 1848 TGATTCGAGTTTCAATTCGCTAGACATCTTAAAGAAATCTGCAACATTTTCCAAAGAG 1907
 Db 548 uAsnLeuAlaSerAsnHisIleSerIleIleLeuProSerLeuLeuProIleuSerG 568
 QY 1908 TCTAGCTTCTCATCTTCACTTCAATTCCTGTGCTGTGATATGTCAGATCAGAAAT 1967
 Db 568 nGlnAspThrIleAsnLeuArgGlnAsnProLeuAspCysThrCysSerAsnIleTyrp 588
 QY 1968 CTTGCACTGGGTGACAGGACAGACAGAGCTTCTGTGATATGTCAGAAATGACATGTGC 2027
 Db 588 eleuGlnTrpIlyrIleGlnIleMetGlnIlyLeuGluAspThrGlnAspThrIleuCysG 608
 QY 2028 AACACCTGTAGAGATGAAT-----ACCTCTTGTGTGTGATTTTAAATATTC 2075
 Db 608 uAsnProProLeuIleuArgGlyValArgLeuSerAspValThrLeuSerCysSerMetAl 628
 QY 2076 TACCTGTATATGACAGACATTCATGATGATGATGATGATGATGATGATGATGATC 2135
 Db 628 alaValGlyIlePhePheLeuIleValIleLeuLeuValPheIleIleLeuLeuIlePh 648
 QY 2136 CACTGTAGCATTTCTGATATACCACTTCAATTTTCACTG 2175
 Db 648 eAlaValIleTyrPheLeuAspArgTrpIlyrGlnHisIle 661
 RESULT 2
 T08664
 Toll protein-like receptor DKFZp54710610.1 - human
 C:Species: Homo sapiens (man)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: T08664
 R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: Z16466
 A:Accession: T08664
 A:Molecule type: mRNA
 A:Residues: 1-786 <POU>
 A:Cross-references: UNIPROT:Q15399; EMBL:AL050262
 A:Experimental source: fetal brain; clone DKFZp54710610
 C:Genetics:
 A>Note: DKFZp54710610.1
 Alignment Scores:
 Pred. No.: 4,81e-25 Length: 786
 Score: 426.50 Matches: 194
 Percent Similarity: 41.32% Conservative: 144
 Best Local Similarity: 23.72% Mismatches: 324

Query Match:	8-248	Indels:	157
DB:	2	Gaps:	31
US-09-396-985B-46 (1-2951) x T08664 (1-786)			
QY 469	GAATTTGAAACATGGAAGACAAAGCATGGAGCTTACACCACTCTCAAACTTGATG		528
DB 24	GlusergluPheIeuValAspArgserIysAsnGlyLeuIleHisVal-----		39
QY 529	CTGACAGAAACCTTATCCAGAGTTTTCCCGAGAAAGTTCTCTGACTACAAAGTTA		588
DB 40	-----ProlysAspLeuSerGlnIleThrThrIle		49
QY 589	GACATCTGGTGGCTGTGAGACAAATATGGCTCTCTAGAAAGCTTCCTATGGACAG		648
DB 50	LeuAsnIle-----SerGlnAsnIylIleSerGlnIleThrThrSerAspIleLeuSer		67
QY 649	CTTATTAACCTTAAGAAATCAATATGGCTGCAATTTTATATCATCTCCGTAGTAACT		708
DB 68	LeuSerIysLeuAspGlyIleLeuIleIleSerHisAsnGlyIleGlnIylLeuAspIleSer		87
QY 709	GCATATTTTCCCATCTGACGAAACCTTACATGTGATCTTTCTTATATCATATTTGAA		768
DB 88	ValPheIysPheAsn---GlnGluIleuGlnIylLeuAspLeuSerHisAsnIysLeuVal		106
QY 769	ACTATTATGTGCACGACTTACAGTTTCTACSTGAATCCAAATGCAAGTAACTCTCT---		825
DB 107	LysIleSerCys-----HisProthValAsnLeuIysHis		118
QY 826	TTAGACATGTCTTTGGAACCCCAATGTACTTTCAGAACCAAGCTTTCAGGGATTAAG		885
DB 119	LeuAspLeuSerPheAsnAlaPheAspAlaLeuProIleCysGlyGlnPheGly---Asn		137
QY 886	CTCCATGACTGACTCTTAAGAGGTATTTTAATAGCTCAATATATATGAAATCTTGCTT		945
DB 138	MetSerGlnLeuIysPheLeuGlyIle---LeuSerThrThrHisIleGlnIylSerSerVal		156
QY 946	CAAAACCGGCTGGTTTACAGTCGATCGG-----TGATCTGGGAGAAATTTAAAGAT		999
DB 157	LeuProIleAlaHisLeuAsnIleSerIylValLeuIleValLeuGlyIleThrIylGly		176
QY 1000	GAAAGAAATCTGGAATTTTGGAAACCTCTTCATGAGAAAGATATGTGATGTGACATT		1058
DB 177	GluIysGln-----AspProIyl-----GlyLeuGlnAspPheAsnThr		189
QY 1060	GATGAGTTCAAGTTTACATAT---ACAATGATTTTTCAGATGATATTGTTAAGTTCCAT		1116
DB 190	GlusIleuHisIleIleValPheProthAsnIys-----GluPheHis		203
QY 1117	TGCTTTGGGAGATGTTTTCGAATGCTCTGGAGAGGTGATGATATATAATATCTGAACAT		1176
DB 204	PheIleLeuAspValSerValIylSerIylValAlaAsnLeuGluLeuSerAsnIleCys		223
QY 1177	GTTCTTCAAACTTTCAAAATGGCAATCCCTTATCAATCAATAGATGTCAATGACAGTT-		1235
DB 224	ValLeuGlnAspSerIylCysSerIylPheLeuSerIleLeuAlaIylLeuGlnIleThrAsn		243
QY 1236	CCAACCTCGGATCTACCTTTCTTAAAGTTTGACTTAACTATGAC-----		1283
DB 244	ProlysLeuSerSerIleuThrIleuAsnAsnIleGlnIylThrIylThrAsnSerPheIleArg		263
QY 1283	-----		1283
DB 264	IleLeuGlnIleuValIylPheIleThrIylValIylPylIylSerIleSerAsnValIylLeu		283
QY 1284	AAAGGCTCATCAGTTTAAAAA-----GTGGCCCTTACCAAGTCTCAGC		1328
DB 284	GlnGlyGlnIleuAspPheArgAspPheAspIylIylSerIylIleuSerIleuAlaIleuSer		303
QY 1329	TATCATGATCTTAAGTAAAGAAATGCACTGACCTTATAGTGGCTGTCTTATTTGATTTG		1388
DB 304	IleHisGlnIleValSerAspValPheGlyIleProGlnSerIylIleIylGlnIlePhe		323

[illegible]

```

Db      663 yme-----glnleCysleuH1eGluArgAnPheValProGlyLysSerIleVa 680
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      2358 TGCCAACATCTCCAGAGAGGCTTCCAGAGCCGAGAGGTTATTTGTGAGTGTCTAG 2417
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      680 lGluAnIlelle---ThrCysileGlySerTylySerIlePheValIleuSerP 699
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      2418 ACACCTTATTCAGACCGTGTGTATCTTGTATGATATGATGATGCTCAACATGCGAGTT 2477
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      699 oAnPheValIInberGutPrCyShiTyGluLeuTyRphenAlaHnIshAnleuPh 719
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      2478 TCTGAGACGCGCTCTGGACATCTTCATTCCTTTCAGAGGTT---GAGAACTCCCT 2534
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      719 eHiegluGlySerAnSerleuIleleuIleLeuLeuGluProIleProGlnTySerI 739
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      2535 GCTAGAGCAGAGGTGAAATGTATCGCTTTCAGAGAAACCTTAACCTGGAATGGA 2594
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      739 eProSerSerTyRhiShiLysLeuLysSerLeuMetAlaArgThrTyLeuGluTyr 759
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      2595 GGACATCTCTGGGAGGACATCTTCTGAGAGAACTTAATAATGCCCTA 2646
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      759 oLysGluLysSerTyShArgGlyLeuPheTrpAlaAnleuArgAlaIle 776

RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C/Accession: A29943
R/Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A>Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, at
A/Reference number: A29943; MUID:88135760; PMID:2449285
A/Molecule type: DNA
A/Residues: 1-1097 <HAS>
A/Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:G158640; PIDD:AAA28941.1;
C/Genetics:
A/Gene: FlyBase:TL
A/Cross-references: FlyBase:FBgn0003717
C/Keywords: transmembrane protein
F/1-17/Domain: signal sequence #status predicted <SIG>
F/18-1097/Product: Toll protein #status predicted <MAT>

Alignment Scores:
Pred. No.: 1-59e-22 Length: 1097
Score: 394.50 Matches: 201
Percent Similarity: 38.15% Conservative: 134
Best Local Similarity: 22.89% Mismatches: 296
Query Match: 7.62% Indels: 248
DB: 2 Gaps: 33

US-09-396-985B-46 (1-2951) x A29943 (1-1097)

```

```

Qy      406 ATCTTAAAAAGTATAGCTTCTCCAAATTTTTCAGAACTTCAGTGGCTGATTTATCGAG 465
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      404 GlyIleSerGlyAspIlePheSerAnleuGlyAnleuValThrleuValMetSerArg 423
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      466 TGTGAATTTGAACAATTTGAAGCAAGGATGGCATGGCTTACACACCTTCGAACTTG 525
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      424 AsnArgleuArgThrIleAspSerArgAlaPheValSerThrAnGlyLeuAnGlyLeu 443
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      526 ATATGACAGGAACCTTACAGAGTTTTCGCCAGAAAGTTTCTGTGAGTAAACAAT 585
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      444 HisleuAspHisAsnAspIleAspLeuGlnPro-----Leu 456
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      586 TTAGACAATCTGGCTGGCTGGAGACAAATTTGACCTCTTGAAGACTTCCTATTGGA 645
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      457 LeuAsp-----IleleuLeuGlnThrGlnIleAsnSer-----ProPheGly 470
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      646 CAGCTTATTAACCTTAAAGAACTCAATGTGGCTCACAT-----TTTATACATTC 656
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      471 TyMetCHisGlyLeuLeuThrleuAnleuValArgAsnAsnSerIleIlePheValTyAsn 490
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      697 TGTAAAGTTACCTGCATATTTTCCCATCTGAGAGAACTGATGATGATCTTTCTAT 756
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      491 -----AspTrpLysAsnThrMetLeuGlnleuArgGlyLeuAspLeuSerTyR 506
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      757 AACTATATTCAACTATTAAGTTCAGAGACTTACAGTTTTCAGTGAATAATCCAGACATC 816
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      507 AsnAsnIleSerleuLeuGlyTyRgluAspLeuAlaPheleuSerGlnAn----- 523
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      817 AATCTCTTTTGAACATGTCTTTGAACCCAAATGACTTCACT-----CAAGACCAAGC 870
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      524 ArgleuHisValAlaMetCThrHisAsnLysAlaArgArgIleAlaLeuProGluAspVal 543
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      871 TTTCAAGGAAATTAAGCTCCATGAACTGACCTCAAGAGTAAATTTATAGCTCAAAATATA 930
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      544 HisleuGlyGluGlyTyRAsnAsnAnleuValHisValAspLeuAsnAspProleu 563
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      931 ATGAAAACCTTGC-----CTTCAAAACCTGGCTGGCTTTCAGCTGCATCGG 975
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      564 ValCysAspCyShThrIleleuTrpPheIleGlnleuValArgIleValHisLysProGln 583
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      976 TTGATCTTGGAGAAATTTAAAGATGAAGAAAT---CTGAAATTTTGAACCTCTATC 1032
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      584 ---TySerArgGlnPheLysLeuArgThrAspArgleuValCysSerGlnProAsnVal 602
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      1033 ATGGAAGACATATGTATGTGACCATGATGATGATGATGATGATATATACATATACAAATGATTT 1092
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      603 LeuGluGlyThrProValArgGlnIleGluProGlnThrleuIleCysProleuAspPhe 622
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      1093 TCAAGATATTTTGTATAGTTCCATTTGCTTGGCAATGTTTCTGCATATGCTCTGGCAGGT 1152
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      623 SerAspAspProArgIleuArgLysCyAspProArgLysCyAsnCyS----- 637
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      1153 GTATCTATTAATAATCTTGAAGAGTGTCTTAAACATTTCAAA---TGGCAATCTTATCA 1209
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      638 -----HisValArgThrTyRAspLysAlaLeu 646
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      1210 ATCATTTAGATGTCAATTAAGAGTTTCCAACTCGATCTTACCTTTCTTAAAGTTGA 1269
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      647 ValIleAsnCyShisSerGlyAsnLeu----- 655
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      1270 CTTTAATATGACAAAGGCTTATCAGTTTAAAAAATGGCCCTTACCAAGTCTCAGCT 1329
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      655 ----- 655
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      1330 ATCTAGATCTTAGTAAGAAATGCACTGAGCTTATGCTGGCTGTTCTTATTTGATTTGG 1389
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      655 ----- 655
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      1390 GAACAAACAGCTTGAAGACATTAAGCTTCAATGTGCGCATTTATGAGTGCA 1449
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      656 -----ThrHisValProArgleuProAnleu----- 664
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

Oy 1450 ATTTCATGGGCTTAGAGAGCTGACGACCTGGATTCTTTCAGCACTCTACTTTAAAGG 1509
Db -----HisLeuAsnMetGlnLeu 670
Oy 1510 GTTCACAGAAATTCAGCGCTTCTTATCCCTTGAAAAGCTACTTACCTGACATCTCTTAT 1569
Db MetGlu-----LeuHisLeuGlnAsnAsnThrLeuLeuAlaArgLeuProSer 685
Oy 1570 ACTAACCAACAAATGACTGATGATATTTCTGGCTTGACCAAGCTGCAACATTA 1629
Db AlaAsnThrPro-----GlyTyrGlnSerValHisSerLeu 697
Oy 1630 AAATGCGTGGCAATCTTCTTCAAGACAACACCTTTCAATGTCTTTGCAAAACAACA 1689
Db HisLeuAlaGlyAsnAsnLeu-----ThrSerIleAspValAspGlnLeuProThr 714
Oy 1690 AACTTGACATCTCTGGATCTCTTAAATGTCAATTGAAACAATATCTTTGGGGGGTATTT 1749
Db AsnLeuThrHisLeuAsp-----IleSerTyr----- 723
Oy 1750 GACACCCCTCAATGCTCAATTAATATATAGATGACACAACATCTATGTTTGGAT 1809
Db -----AsnHisLeuGlnMetLeuAsn----- 730
Oy 1810 TCATCCCATTTATTAACAGCTGTATTCCTTCAGCACTGTGATGAGTTTCAATGCAATA 1869
Db -----AlaThrValIleGlyPheLeuAsnArgThr 740
Oy 1870 GAGACATTAAGAATCTGCAACATTTCCAAAAGCTTAGCCTTCTCAATCTTACT 1929
Db MetLysTyrArgSerVal-----LysLeuSer 749
Oy 1930 AACATTCGTGCTGCTGTATATATGACATCAGAAATTCCTGCACTGGGTCAAGAAAG 1989
Db GlyAsnProTyrMetCysAspCysThrAlaLysProLeuLeuPheThrClnAspAsn 769
Oy 1990 AAGCAGTCTTGGAATGTTGAACAATGACATGCAACACCTGTAGAGATGAATACC 2049
Db PheGlnArgIleGlyAspArgAsnGlnMetCysValAsn--AlaGlnMetProThr 788
Oy 2050 TCCTTAGTGTGGATTTTAATATTTCTACCTGTATATATGACAGAAATC--ATCAGT 2106
Db ArgMetValGlnLeuSerThrAsnAspIleCysProAlaGlnLysGlyValPheIleAla 808
Oy 2107 GGTGAGAGGCTC-----AGTGAATGTGTGATCCAGTGTGACATTTCTGTATATAC 2157
Db LeuAlaValIleAlaLeuThrGlnLeuAlaGlyPheThrAlaLeuTyrTyr 828
Oy 2158 CACTTC-----TATTTTCAC--CTGATACTTATGCTGGC 2190
Db LysPheGlnThrGlnIleLysIleTyrLeuTyrAlaHisAsnLeuLeuThrPheVal 848
Oy 2191 TGTAAAAAGTACAGAGAGAGAAAGCATTTATGATGACATTTGTGATCTACGAGTAC 2250
Db ThrGlnGlnAspLeuAspLysAspLysLysPheAspAlaPheIleSerTyrSerHisLys 868
Oy 2251 AATGAGACTGGGTGAAGAAATAGCTGTGAAGAATTTGAAGAAGAGAGTCCCGCTTT 2310
Db AspGlnSerPheIleGlnLysPyrLeuValProGlnLeuGlnHisGlyProGlnLysPhe 888
Oy 2311 CACCTGCGCTTCATACAGACATTTATCTGGGTGAGCAGTGTGCTGCAACATCTAC 2370
Db GlnLeuCysValHisGlnLysArgAspTyrLeuValGlnGlnHisIleProGlnAsnIleMet 908
Oy 2371 CAGAGAGCTTTCACAAAGACCGAAGGTTATTTGTGTGATGTCTAGACATTTATGAG 2430
Db Arg---SerValAlaAspSerArgArgThrIleIleValLeuSerGlnAsnPheIleLys 927
Oy 2431 AGCCGTGTGTATCTTTGAATATAGATGATGCTCAACATGSCATTTCTGACAGCCGC 2490
Db SerGlnTyrPalaArgLeuGlnIlePheArgAlaAlaHisArgSerAlaLeuAsnGlnIleArg 947
Oy 2491 TCTGCATCATCTTCAATTGTC-----CTTGAGAGGTTGAGAAATGCC 2532

```

```

Db 948 SerArgIleIleValIleIleTyrSerAspIleGlyAspValGlnLysLeuAspGln--- 966
Oy 2533 CTGCTGAGGACGACGAGGTGATTTGATCGCTTCTTGACAGAAACACTACTGGAATGG 2592
Db 967 -----GlnLeuLysAlaTyrLeuLysMetAsnThrTyrLeuLysTyr 980
Oy 2593 GAGGACAACTCTCTGGGAGGACACATCTTCTGAGAAAGACTTAAATGCGCTTA 2646
Db 981 -----GlyAspProTyrPheThrAspLysLeuArgPheAlaLeu 993

RESULT 4
T13852
gene wheeler protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13852
R:Elston, E.; Kooyer, S.; D'avejlyn, D.; Duman, M.; Lawinger, P.; Botos, J.; Bellem, H.
Development 120, 885-899, 1994
A:Title: The Drosophila 18 wheeler is required for morphogenesis and has striking siml.
A:Reference number: Z17796; MUID:95324375; PMID:7600965
A:Accession: T13852
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1389 <END>
A:Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:g415682; PID:g1019104; PIDN:AAA792
A:Gene: wheeler
A:Cross-references: FlyBase:FBgn0004364

Alignment Scores:
Pred. No.: 5,22e-17 Length: 1389
Score: 324.00 Matches: 235
Percent Similarity: 34.29% Conservative: 146
Best Local Similarity: 21.15% Mismatches: 310
Query Match: 6.26% Indels: 422
Gaps: 47

US-09-396-985b-46 (1-2951) x T13852 (1-1389)
Oy 328 GATCAGAAACTCAGCAAAAGTCCCTGATGACATTCCTTCTTCAACCAAGACATGATGTG 387
Db 154 AspAsnAsnIleAspGlnLeuProGlnGlyValTyrCysSerMetProSerLeuGlnLeu 173
Oy 388 AGCTTCAACCCCTTGAAGATCTTAAAGAAGCATAGCTTCTGCAATTTT----- 435
Db 174 LeuAsnLeuThrGlnAsnArgIleArgSerAlaGlnPheLeuGlnPheSerGlnLysLeu 193
Oy 436 -----TCAGAACTTCAG 447
Db 194 CysAlaGlySerAlaLeuSerAsnAlaAsnGlyAlaValSerGlnLysSerGlnLeuGln 213
Oy 448 TGGCTGATTTATCCAGGCTGTAATGAAATTAAGACAAATGAAAGCAATGCGCATGGC-- 504
Db 214 ThrLeuAspValSerPheAsnGlnLeuArgSerLeuProAsp--AlaTyrGlyAlaSer 232
Oy 505 ---TTACACCACTCTCAAACTTGTATCTGACAGAAACCTATCCAGAGTTTCCCA 561
Db 233 ArgLeuArgArgLysGlnThrLeuSerLeuGlnHisAsnAlaIleSerThrLeuAlaPro 252
Oy 562 GGAAGTTCTCTGGAATCAACAGTTTGAACATCTGAGTGGCTGTGAGACAAATGAGCC 621
Db 253 AsnAlaLeuAlaGlyLeuSerSerLeuArgValLeuAsnIleSerTyrAsnHisLeuVal 272
Oy 622 TCTCTAAGAAC----- 633
Db 273 SerLeuProSerGlnAlaPheAlaGlyAsnLysGlnLeuArgGlnLysLeuGlnGly 292
Oy 634 -----TTCCTCATGAGACGTTTAACTTAAAGCTTAAAGCAATGAGT--- 675
Db 293 AsnAspLeuTyrGlnLeuProLysGlyLeuLeuHisArgLeuGlnGlnLeuValLeu 312
Oy 676 -----GTCACAAATTTTATACATTCCTGTAAGTTACCTGCA 711

```

```

Db      313 AspleuSerGlyAsnGlnLeuThrSerHisHisValAspAsnSerThr----- 328
Qy      712 TATTTTCCATCTGAGCAACCTGTACATGTGATCTTTTATCTATATTCAAACT 771
Db      329 ---PheIaGlyLeuIleArgLeuIleValLeuAsnLeuSerAsnAlaLeuSerThrArg 347
Qy      772 ATT-----ACGTGCAACGCTTACGTTTCTAGGTGAAATTCACAAAGTCATCTC 822
Db      348 IleGlySerLysThrPheLysGlnLeuThrPheLeuGln----- 360
Qy      823 TCTTTAGACATGTCTTTGAAACCCAAATTGACTTTCATTCAGAACCAAGCCTTTACAGGAATT 882
Db      361 IleLeuSerMetArgAsnAsnSerIleGlyHisIleGlnGlnGlyAlaPheLeuProLeu 380
Qy      883 ---AAGTCCCATGAACTGACTCTTAAGAGGTATTTTATAGCTCAAAATATATGAAAACT 939
Db      381 TyrAsnLeuHisThrLeu----- 386
Qy      940 TGCCTTCAAAACCTGGCTGGTTTACAGTCCATCGCTTGATCTTGAGGAATTTAAAGAT 999
Db      387 ---AsnLeuAlaGlnAsnArgLeuHisThrLeu-----Asp 397
Qy      1000 GAAAGATCTGGAATTTTGAACCCCTCTATCATGGAAGACTATGTGATGACCAATT 1059
Db      398 AsnArg-----IlePheAsnGlyLeuTyrValLeuThr--- 408
Qy      1060 GATGAGTTCAGGTTAACATATACAAATGATTTTTCAGATGATATTTGTTAGTTCATTCATGC 1119
Db      409 ---LysLeuThrLeuAsnAsnAsnThrPheArgAsnLeuAsnGlnLeuThrGlyLeuArg 424
Qy      1120 TTGGCAATGTTTTCGAATGCTCTGGCAGGTGATCTATATAAATATCTGAAGATGTT 1179
Db      425 PheArgAsnCySerAspLeuLysGlnLeuAspLeuSerSerAsnGlnLeuThrGlnVal 444
Qy      1180 CCTAAACATTTCAAATGGCAAATCCTTATCAATCATATAGATGT----- 1221
Db      445 ProGlnAlaVal-----GlnAspLeuSerMetLeuLysThrLeuAspLeuGlyGlnAsn 462
Qy      1222 CACTACAGCACTTCCAACT----- 1241
Db      463 GlnIleSerGlnPheLysAsnAsnThrPheArgAsnLeuAsnGlnLeuThrGlyLeuArg 482
Qy      1242 --- 1259
Db      483 LeuIleAspAsnArgIleGlyAsnIleThrValGlyMetPheGlnAspLeuProArgLeu 502
Qy      1260 AAAAGTTTGACTTTAACTATGAAACAA---GGGTCTATC-----AGTTTAAAAAA 1307
Db      503 SerValLeuAsnLeuAlaLysAsnArgIleGlnSerIleGlnArgGlyAlaPheAspLys 522
Qy      1307 --- 1307
Db      523 AsnThrGlnIleGlnAlaIleArgLeuAspLysAsnPheLeuThrAspIleAsnGlyIle 542
Qy      1308 ---GTGGCCCTACCAAGTCTCAGTATCTAGATCTTAGAGAAATGACTGAGCTTTAGT 1364
Db      543 PheIaThrLeuAlaSerIleLeuThrPheLeuAsnLeuSerGlnAsnHisLeuValTrp--- 561
Qy      1365 GGTGGCTGTTCTTATCTGATTGATTGGAAACAAACAGCTGAGACACTTAGACCTCAGCTTC 1424
Db      562 ---PheAspTyrAlaPheIleProSerAsn---LeuLysTrpLeuAspIleHisGly 578
Qy      1425 AATGTGTCATCTATTATGAGTCCCAATTCATGGGTCTTAGAAGAG-----CTGCAG 1475
Db      579 Asn---TyrIleGlnAlaLeuGlnLysAsnTyrLysLeuGlnGlnGlnIleArgValThr 597
Qy      1476 CACGTGAGTTTTCGACACTACCTTAAAGGGTCAAGAAATCTCAGAGCTTCTTATC 1535
Db      598 ThrLeuAspAlaSer-HisAsnArgIleThrGlnIleGlyAlaMetSerValProAsnSe 617
Qy      1536 CTTGAAAAAGCTACTTTTACCTTGACATCTCT-----TATACTAACACC-- 1578

```

```

Db      617 rIleGln---LeuLeuPheIleAsnAsnAsnIleIleGlnIleGlnAlaLeuThrPh 636
Qy      1579 -----AAATGACTTCGATGGATATATTTCTTGCTTGACAG 1616
Db      636 eValAspLysThrArgLeuAlaArgValAspLeuTyrAlaAsnValLeuSerLysIleSe 656
Qy      1617 TCTCAACACATTTAAATGAGCT----- 1638
Db      656 rLeuAsnAlaLeuArgValAlaAlaProValSerAlaGlnLysProValProGlnPheTyrLe 676
Qy      1639 ---GGCAATCTTTCAA----- 1652
Db      676 uGlnGlyAsnProPheGlnCyAspCySerMetGlnTrpLeuGlnArgIleAsnAsnIle 696
Qy      1653 ---AGCAACACCCCT-----TTCAAATGCTTGGCAACA 1684
Db      696 uThrThrArgGlnHisProHisValValaAspLeuGlyAsnIleGlnCyLeuMetProHis 716
Qy      1685 CAACAAACCTTGACATTCCTGATCCT----- 1710
Db      716 eSerArg-SerAlaProLeuArgProLeuAlaSerLeuSerAlaSerAspPheValCysL 736
Qy      1711 --- 1726
Db      736 ySTyrGlnSerHisCyAspProThrCyHisCySerGlnTyrGlnGlnCySerGlySerG 756
Qy      1727 AACAAATATCTTGGGGGGTATTTGACACCCCTCCAT----- 1761
Db      756 IuValIleCySProGlnLysCySerCySerPheHisAspAlaThrPalaThrAsnIleV 776
Qy      1761 --- 1761
Db      776 AlaSerCySgIArgGlnAspLeuAlaAlaLeuProAsnArgIleProGlnAspValSerA 796
Qy      1761 --- 1761
Db      796 sPLeuTyrLeuAspGlyAsnAsnMetProGlnLeuGlnValGlnHisLeuThrGlyArgA 816
Qy      1762 --AGACTCAATATTTAAATATAGTACGACAAACATCTATGTTTGGATTCATCCCAT 1819
Db      816 rGAsnLeuArgAlaLeuTyrLeuAsnAlaSerAsnLeuMetThrLeuGlnAsnGlySerL 836
Qy      1820 ATAAACAGCTGTATTCCTCCAGCACTCTTGATGCACTTCAATCGCATGACAGACATCTA 1879
Db      836 euAlaGlnLeuValAsnLeuArgValLeuHisIleGlnIuAsnAsnLysLeuThrAlaLeuG 856
Qy      1880 AAGGA-----ATAC 1888
Db      856 IuGlnThrGlnPheArgSerLeuGlyLeuLeuArgIuLeuTyrLeuHisAsnAsnMetL 876
Qy      1889 TGCAACAT----- 1896
Db      876 euThrHisIleSerAsnAlaThrPheGlnProLeuValIleSerLeuGlnValLeuArgLeuA 896
Qy      1897 -----TTTCCAAAGGTCTAGCCTTTCTTCA 1921
Db      896 sPAsnAsnArgLeuSerSerLeuProHisIleuGlnTyrArgHisIleSerLeuGlnGlyLeuT 916
Qy      1922 ATCTTACTAACATTTCTGTTGCTGTGTATATGTAACAT---CAGAATTTCTCGAGTGGG 1978
Db      916 hTrLeuGlnArgAsnAlaTrpSerCySArgGlnLeuAsnLeuArgGlnLeuAlaGlnPheV 936
Qy      1979 TCAGGAACAGAACAGCTGTTCTGTGATGTTGAAACAAATGACATGT----- 2025
Db      936 AlSerAspAsnAlaMetValValaArgAspAlaHisAspIleTyrCyLeuAspAlaGlyI 956
Qy      2026 --GCACACCTGTAGAGATG-----AATACTCCTTAGTGT 2059
Db      956 IeLysArgGlnLeuGlnLeuIleGlyAsnLeuAlaAsnGlyProAspCySerAspLeuL 976
Qy      2060 TGAATTTATATATCTTACC----- 2079
Db      976 euAspAlaSerAlaSerAsnIleSerSerSerGlnAspLeuAlaGlyAlaIleGlyCyS 996

```

OY 2080 -TGTATATGACAAAGCAATCACTGAGTGTGACGTGAGTGAATGTTGGTA----- 2133
 |||:::|||||:::|||||:::|||||
 Db roCysTTPProAlaValLeuValLeu1IePheLeuValValValLeu1IeLeuPheV 1016
 OY 2134 -----TCCACTGTAGCAATTTCTGAATATACCACTTCTATTTTACCTGTAGTACTTA 2182
 |||:::|||||:::|||||
 Db aLPheArgGLuSerValaIArgMetCTrPheLeuPheAlaH1eTylGlyValaIArgVal----- 1033
 OY 2183 TTGCTGGCTGTAAA---AAGTACAGACAGAGAGAAAGCACTGTATGATGCATTTGTGATCT 2239
 |||:::|||||:::|||||
 Db 1034 -----CysGLuTrPtoArgPheGLuAsePalaGLyLysLeuTyrAspAla1IeLeuH 1051
 OY 2240 ACTGAGTCAGAAATGAGACGTGGGTGAGAAATAGAGCTGTGAAGAAATTTAGAAAGAGAG 2239
 |||:::|||||:::|||||
 Db 1051 IASerGLuLysAspArgTrGLuPheValCysbArgAsn1IeAlaGLuLeuGLuH1eGLyA 1071
 OY 2300 TGCCCGCGTTTCACTCTGTCTCTTCACTACAGAGACTTATTTCTGTGTAGCCATTTGCTG 2359
 |||:::|||||:::|||||
 Db 1071 rGPProPProPheArgLeuYser1IeGLuH1eArgAspLeuPPro-----GlnA 1087
 OY 2360 CCAACATATATCAG-----GAAGCTTCCACAMAGCCGGAGGTTATTGTGTAGTGT 2413
 |||:::|||||:::|||||
 Db 1087 IASerH1eLeuGLuLeuVala1IuGLyAlaArga1ASerArgLys1Ie1IeLeuValLeuT 1107
 OY 2414 CTAGACACTTATTTACAGCGCGGTGTGTATCTTTGATATGAGATTGCTCAACATATGC 2473
 |||:::|||||:::|||||
 Db 1107 hTArgAsnLeuLeuAlaThrGLuTrPAsnArg1IeGLuPheArgAsnAla----- 1123
 OY 2474 AGTTTCTGAGCAGCGCGCTCTGTGCATCATC-----TTCAATTGTCTTGAGAGAG----- 2520
 |||:::|||||:::|||||
 Db 1124 --PheH1eGLuSerLeuArgGLuLeuAlaGLuLysLeuVal1Ie1IeGLuGLuH1eSerV 1143
 OY 2521 -----GTTGGAAGTCCCTCTGTAGGACAGAGGTGGAATTGT 2557
 |||:::|||||:::|||||
 Db 1143 a1SerAlaGLuAlaGLuAspVala1AGluLeuSerProTyrLeuLysSerValPProSerA 1163
 OY 2558 ATCCGCTTCTTACAGCAAGAAACCTTACCTGAAATGAGAGACATCTCTGGGAGAGCAC 2617
 |||:::|||||:::|||||
 Db 1163 snArgLeuLeuThrCysAspArgTyr----- 1171
 OY 2618 TCTTCTGAGAGAGACTTAAATAATGCCCTA 2646
 |||:::|||||:::|||||
 Db 1172 --PheTrpGLuLysLeuArgTyrAla1Ie 1180

RESULT 5
 T13887
 c1r protein - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T13887
 R:Chiang, C.; Beachy, P.A.
 Mech. Dev. 47, 225-239, 1994
 A:Title: Expression of a novel Toll-like gene spans the parasegment boundary and contributes to the formation of the posterior compartment of the wing disc
 A:Reference number: 217805; MUID:95151581; PMID:7848870
 A:Accession: T13887
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1385 <CHI>
 A:Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PIDN:AA333887
 C:Genetics:
 A:Cross-references: FlyBase:FBgn0004364
 A:Note: c1r

Alignment Scores:
 Pred. No.: 7.47e-17 Length: 1385
 Score: 322.00 Matches: 229
 Percent Similarity: 34.45% Conservative: 151
 Best Local Similarity: 20.76% Mismatches: 159
 Query Match: 6.22% Indels: 406
 DB: 2 Gaps: 44

US-09-396-985B-46 (1-2951) x T13887 (1-1385)

QY	328	GATCAGAAACTCAGGAAGTCCCGATGACACTTCCTCTTCAACCAAGACATGATGCTG	387
Db	154	AaphanaenilearglnleuproglnuylvaltrpCysSerMetProSerleuInleu	173
QY	388	AGCTTCAACCCCTTGAGAGATCTTAAAAAGCTATAGCTTCCTCAATTTT	435
Db	174	LeuDenleuThrGlnAenArgIleArgSerAlaGluPheLeuGlyPheSerGluIlyleu	193
QY	436	-----TCAGAACTTCAG	447
Db	194	CysAlaGlySerAlaLeuSerAsnAlaAsnGlyAlaValSerGlyGlySerGluIn	213
QY	448	TGGCTGGATTATTCAGAGTGTGAAATGAAACAATTGAACAGACGGCATGGCATGC	504
Db	214	ThrLeuSerValSerPheAsnGluIleuArgSerLeuProSer--AlatrGlyAlaSer	232
QY	505	---TTACACCACTTCCTCAAACTTGATGACTGACAGGAACCCATPCACAGTTTTTCCCA	561
Db	233	ArgLeuArgArgLeuGlnThrLeuSerleuGlnIleAsnAsnIleSerThrleuAlaPro	252
QY	562	GAAGATTCTCTGGACATCAACAGTTTATGACAACTGTGTGGCTGTGTGACACAAATGGCC	621
Db	253	AsnAlaLeuAlaGlyLeuSerSerleuArgValLeuAsnIleSerTyAlaAsnIleVal	272
QY	622	TCTCTAGAACCTTCCTATTGACACGCTTAATACCTTAAAGAAATCAATGTGGCTAC	681
Db	273	SerleuProSerGlnAlaPheAlaGlyAsnIlySerGluLeuArgGluIleuGlnGly	292
QY	682	AATTTTATACACTTCCTGTAACTTACCT	708
Db	293	AsnAspLeuTy-----GluLeuProIlySerGlyLeuLeuIleValArgLeuGlnleuLeu	310
QY	709	-----GCATATTTTCC	720
Db	311	ValleuAspLeuSerGlyAsnGlnleuThrAspIleShiValaAspAsnSerThrPheAla	330
QY	721	AATCTGACGAACCTAGTACATGTGGATCTTCTTATTAATCTATATTCAAACTAT	774
Db	331	GlyleuIleArgleuIleValleuAsnleuSerAsnAsnIleleuThrArgIleGlySer	350
QY	775	---ACTGCACACGACTACAGTTTCTACGTGAAAATGCACAAAGTCAATCTCTTTAAC	831
Db	351	LysThrThrPheIlySerGluLeuTyPheLeuGln-----IleLeuAsp	363
QY	832	ATGCTTTGAAACCCCAATGACTTCAATTCACAAAGCAAGCTTTACAGGGAAT	888
Db	364	MetArgAsnAsnSerIleGlyIleIleGluGlnGlyAlaPheLeuProleuTyArgleu	383
QY	889	CATGAACCTGACTTAAGAGGTATTTTATAGTCAATAATATATGAACCTGCCTTCA	948
Db	384	HisThrIleu-----	386
QY	949	AACCTGGCTGTTTACACGTCATCGGTGATCTTTGGAGATTTAAAGATGAAGCAAT	1008
Db	387	AsnleuAlaGluAsnArgleuIleThrleu-----AspAsnArg--	399
QY	1009	CTGGAATTTTGAACCTCATCATGAGAAAGCAATGTATGTGAGCCATGTGAGAGTTC	1068
Db	400	-----IlePheAsnIlyleuTyValleuThr-----	408
QY	1069	AGGTTAACATATACAAATGATTTTTCAGATGATATTTGTTAATTCATTCCTGGCCGAT	1128
Db	409	LysleuThrIleuAsnAsnleuVal---SerIleValIleuSerGlnAlaPheArgAsn	427
QY	1129	GTTTGTGCATGTCTCTGGCAGGTGTATCTATAAATATCTAGAAGATGTTCTTAACAT	1188
Db	428	CysSerAspLeuIlySerGluLeuAspLeuSerSerAsnGlnleuThrGlnValaProGln--	446
QY	1189	TTCAAAATGGCAATCCTTATCAATCATTAAGAT-----CAACTAGC	1230
Db	447	---AlaAlaGlnAspLeuSerMetleuSerIlyThrleuAspLeuGlyGluAsnGlnIleSer	465

QY 1231 AGTTCGAACCT----- 1241
|||:
Db 466 GluPheLysAsnAsnThrPheArgAsnLeuAsnGlnLeuThrGlyLeuArgLeuIleAsp 485
QY 1242 -----CTGATCTACCCCTTTCTTAAAGTTG 1268
486 AsnArgIleGlyAsnIleThrValGlyMetPheGlnAspLeuProArgLeuSerValLeu 505
QY 1269 ACTTAACTAAGAACAA--GGGTCTATC-----AGTTTAAAAA----- 1307
|||:
Db 506 AsnLeuAlaLysAsnArgIleGlnSerIleGlnArgGlyAlaPheAspLysAsnThrGlu 525
QY 1308 -----GTGACC 1313
Db 526 IleGlnAlaIleArgLeuAspLysLysPheLeuThrAspIleAsnGlyIlePheAlaThr 545
QY 1314 CTACCAAGTCTACGCTATCTAGATCTTAGAAATGCACTGAGCTTTAGTGCGCTGT 1373
|||:
Db 546 LeuIleSerLeuLeuThrLeuAsnLeuSerGlnAsnIleValTyr-----Phe 562
QY 1374 TCTTATTCTGATTTGGGAACAAACAGCTGAGACACTTACCTCAGCTTCATGCGCC 1433
|||:
Db 563 AspTyrAlaPheIleProSerAsn--LeuLysThrLeuAspIleHisGlyAsn--Tyr 580
QY 1434 ATCATTTATGAGTGCATTTTCATGGGTCTAGAGAG-----CTGCAGACCTGGAT 1484
|||:
Db 581 IleGlnAlaLeuGlyAsnTyrTyrLysLeuGlnGlnGlnIleArgValThrThrLeuAsp 600
QY 1485 TTTTCAGACCTCTACTTTAAAGGGTGCAGAAATTCACGCGTTCTTATCCCTGAAA 1544
|||:
Db 601 AlaSer-HisAsnArgIleThrGlnIleGlyAlaMetSerValProAsnSerIleGlu- 619
QY 1545 GCTACTTACTCTGACATCTCT-----TATCTAACCC----- 1578
|||:
Db 620 -LeuLeuPheIleAsnAsnIleIleGlyGlnIleGlnAlaAsnThrPheValAspLys 639
QY 1579 -----AAATTTGACTTCGATGTATATTTCTGGCTTGACAGCTCTCAACAC 1625
|||:
Db 639 sThrArgLeuAlaArgValAspLeuTyrAlaAsnValLeuSerLysIleSerLeuAsnAl 659
QY 1626 ATTAAATATGCT-----GGCAA 1643
|||:
Db 659 AlaLeuArgValAlaProValSerAlaGlnLysProValProGlnPheTyrLeuGlyLys 679
QY 1644 TTTCTTTCAA-----AG 1654
|||:
Db 679 nProPheGlnCysAspCysSerMetGluTyrLeuGlnArgIleAsnAsnLeuThrThrAr 699
QY 1655 ACAACACCCCT-----TTCAATGTCTTTGGCAACACAAACAACT 1693
|||:
Db 699 GlnHisProHisValValAspLeuGlyAsnIleGlnCysLeuMetProHisSerArg-S 719
QY 1694 TGACATTTCTGGATCT----- 1710
|||:
Db 719 eraIaProLeuArgProLeuAlaSerLeuSerAlaSerAspPheValCysLysTyrGlnS 739
QY 1711 -----TCTAAATGTCAATTTGGAACAAATAT 1735
|||:
Db 739 erHisCysProProThrCysHisCysCysGlyTyrGlnGlnCysGlnValIleC 759
QY 1736 CTGGGGGGGATTTTGACACCCCTCAT----- 1761
|||:
Db 759 ysrProGlyAsnCysSerCysPheHisAspAlaThrTyrAlaThrAsnIleValAspCysG 779
QY 1761 ----- 1761
Db 779 LysArgGlnAspLeuAlaIleuProAsnArgIleProGlnAspValSerAspLeuTyrL 799
QY 1762 -----AGACTTC 1768
|||:
Db 799 euAspGlyLysAsnMetProGlnLeuGlnValGlyHisLeuThrGlyLysArgAsnLeu 819
QY 1769 AATTATTAAATATGATGTCACAAATCTATTGTTTGGATTCATCCCATTAATAACAGC 1828

Db 819 rglAlaLeuTyrLeuAsnAlaSerAsnLeuMetThrLeuGlnAsnGlySerLeuAlaGlnL 839
QY 1829 TGTATTCCTTGACACACTCTTGATTTGACATTTCAATGCGATAGACATCTTAAAGCA----- 1884
|||:
Db 839 euValAsnLeuArgValLeuHisLeuGlnLysAsnLysLeuThrAlaLeuGlnGlyThrG 859
QY 1885 -----ATATGCAACAT- 1896
|||:
Db 859 IuPheArgSerLeuGlyLeuLeuArgGlyLeuTyrLeuHisAsnAsnMetLeuThrHisI 879
QY 1896 ----- 1896
Db 879 IeSerAsnAlaThrPheGluProLeuValSerLeuGlnValLeuArgLeuAspAsnAsn 899
QY 1897 -----TTTCCAAAGTCTACGCTTCTTCAATCTTAACTA 1930
|||:
Db 899 rglLeuSerSerLeuProHisLeuGlnTyrArgHisSerLeuGlnGlyLeuThrLeuGlyA 919
QY 1931 ACAATTCTGTGCTGTATATGTGAACAT--CAGAAATTCCTGCAGTGGGTCAAGGAC 1987
|||:
Db 919 rghAsnAlaTyrPserCysArgCysGlnGlnLeuArgGlnLeuAlaGlnPheValSerAspA 939
QY 1988 AGAAGCAGTTCCTGTGATGTGAACAAATGACATGT-----GCAACAC 2032
|||:
Db 939 snAlaMetValAlaArgAspAlaHisAspIleTyrCysLeuAspAlaGlyIleLysArgG 959
QY 2033 CTGTAGACATG-----AATACCTCTTAAGTGTGGATTTTA 2068
|||:
Db 959 IuLeuGlnLeuIleGlyAsnLeuAlaAsnGlyProAspCysSsrAspLeuAspAlaS 979
QY 2069 ATATTTACTCTGTATATG-----TCAAGACAAATCATCAGTG 2107
|||:
Db 979 eraIaSerAsnIleSerSerSerGlnAspLeuAlaGlyGlyTyrArgLeuProLeuAs 999
QY 2108 TGTCAAGTGTCAAGTGTATGTGTATCTCACTGTACGATTTCTGATATACACTTC----- 2163
|||:
Db 999 IalAlaValLeuValLeuIlePheLeuAspValValLeuIleIleValPheValPheArgG 1019
QY 2164 -----TATTTTCACTGTACTTATGCTGCTGCTGTAAAAAGTACA 2203
|||:
Db 1019 IuSerValArgMetTyrLeuPheAlaHisTyrGlyLysArgValCysGlnProArgPheG 1039
QY 2204 GCAGAGAGAAAGACATGTATGATGATGTGATGTCTACGAGTCAAGATGAGAGAGCGG 2263
|||:
Db 1039 IuAspAlaGlyLysLeuTyrAspAlaIleIleLeuHisSerSerGlnLysAspTyrGlnPheV 1059
QY 2264 TGAGAAATGAGCTGTAAAGATTTAGAAAGAGAGAGCGCCGCTTCACTGTGCTTC 2323
|||:
Db 1059 alCysArgAsnIleAlaIleGlnLeuGlnHisGlyArgProProPheArgLeuCysIleG 1079
QY 2324 ACTACAGAGACTTATTTCTGTGTGTACCATGTGCTGCCAATCATCATCAG-----GAAG 2377
|||:
Db 1079 IuGlnIuArgAspLeuProPro-----GlnAlaSerHisLeuGlnIleValAlaGlnG 1095
QY 2378 GCTTCCAAAGAGCGGAGGTTATGTGTAGTGTGTACACACTTATTCAGAGCCGTT 2437
|||:
Db 1095 IyAlaArgAlaSerArgLysIleIleLeuValLeuThrArgAsnLeuAlaThrGluT 1115
QY 2438 GGTGTATCTTTGAATATGATTTGCTCAACATGCGATTTCTGAGCAGCGCTGTGCA 2497
|||:
Db 1115 rPheAsnArgIleGlnPheArgAsnAla-----PheHisGlnSerLeuArgGlyL 1131
QY 2498 TCATCT-----TTCATGTCTCTTGAGAG-----G 2521
|||:
Db 1131 euAlaGlnLysLeuValIleIleGlnGlnLysSerValSerAlaGlnAlaGlnAspValA 1151
QY 2522 TTGAGAGTCCCTGCTGAGCAGAGCTGGAATTTGTATGCGCTTCTTACGAGAAACGCT 2581
|||:
Db 1151 IagIuLeuSerProTyrLeuLysSerValProSerAsnAspGlyLeuThrCysAspArgT 1171
QY 2582 ACCTGGAATGGAGAGCAATCTCTGGGAGGAGCAGATCTTCTGGAGAAAGACTTAAATG 2641
|||:
|||:
|||:

```

Db      1171  Yr-----PhetrgpluylsleuarkgTYRA 1179
QY      2642  CCCTA 2646
Db      1179  laile 1180
RESULT 6
A29944
chaoptin precursor - fruit fly (Drosophila melanogaster)
N/Alternate names: photoreceptor cell-specific membrane protein
C/Species: Drosophila melanogaster
C/Date: 15-Dec-1968 #sequence_revision 15-Dec-1968 #text_change 09-Jul-2004
C/Accession: A29944; A21123
R:Reinke, R.; Krantz, D.E.; Yen, D.; Zipursky, S.L.
Cell 52, 291-301, 1988
A>Title: Chaoptin, a cell surface glycoprotein required for Drosophila photoreceptor cell
A:Reference number: A29944; MUID:88135762; PMID:3124963
A:Accession: A29944
A:Molecule type: DNA
A:Residues: 1-1134 <REI>
A:Cross-references: UNIPROT:P12024; GB:M19008; GB:M19009; GB:M19011; GB:M19017
R:Zipursky, S.L.; Venkatesh, T.R.; Teplov, D.B.; Benzer, S.
Cell 36, 15-26, 1984
A>Title: Neuronal development in the Drosophila retina: monoclonal antibodies as molecular
A:Reference number: A21123; MUID:84106810; PMID:6420071
A:Accession: A21123
A:Molecule type: Protein
A:Residues: 31-43,'HX','46-49','H' <ZIP>
C/Genetics:
A:Gene: FLYBase:chp
A:Cross-references: FLYBase:FBgn0000313
A:Introns: 1/3 80/3; 318/3; 377/2 422/2; 702/1 745/3; 831/2; 998/2
C/Superfamily: chaoptin; leucine-rich alpha-2-glycoprotein repeat homology
C/Keywords: cell adhesion; glycoprotein; membrane protein
F:1-29/Domain: signal sequence #status predicted <MAY>
F:30-1134/Product: chaoptin #status predicted <MAY>
F:80-102/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LRR2>
F:103-126/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:128-151/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:152-175/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:177-200/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F:202-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F:226-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F:250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F:279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F:303-335/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F:326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F:351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F:375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F:401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F:428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F:453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F:477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F:502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
F:527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>
F:551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR20>
F:577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR21>
F:601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR22>
F:625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR23>
F:649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR24>
F:673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR25>
F:708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR26>
F:733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR27>
F:757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR28>
F:781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR29>
F:805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR30>
F:828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR31>
F:854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR32>
F:879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR33>
F:903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR34>
F:928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR35>
F:949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR36>
F:973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR37>

```

Accession	Protein	Score	Length	Matches	Conservative	Mismatches	Indels	Gaps
F.996-10109/Domain	leucine-rich alpha-2-glycoprotein repeat	1.72e-14	1134	117	137	121	278	248
F.1021-1044/Domain	leucine-rich alpha-2-glycoprotein repeat	1.72e-14	1134	117	137	121	278	248
F.1056-1080/Domain	leucine-rich alpha-2-glycoprotein repeat	1.72e-14	1134	117	137	121	278	248
US-09-396-985B-46 (1-2951) x A29944 (1-1134)								
QY	309 TATTACCTTACCAATGATGATCAGAAATCTGACAAAGTCCCTGATGAC-----	357						
DB	105 TyrnlgueulvylleSerglYAsnHis-LeuthrculileProbaerAlaPhehTcgl	124						
QY	358 -----	365						
DB	124 YleuglnArSerleuTrpGluLeuileLeuProGlnAsnArleuValGluileProSe	144						
QY	366 TTCAAC-----	404						
DB	144 TlySerleuArGlnlyleuGlnlyVleuArGlnHileuAspIeuGlyYrAsnHisIleTh	164						
QY	405 GATCTTAAAAAGCTATAGCTTCTCCAAATTTTTCAGAA-----CTTGAGTGGCTGATTTATC	461						
DB	164 rHisIleGlnHIsArSerPheArGslYleuGlnArSerleuGlnTrleuIleleuAr	184						
QY	462 CAGGTGGAAATTGAACAATTGAAGACAGACGATGGCATGGCTTACACCACTGTCAA	521						
DB	184 gGluAsnCysIleSerGlnleuMetSerHisSerPheSerGlyleuLeuileleuGlnTh	204						
QY	522 CTGTATCTGACAGAGAAACCTATCCAGAGTTTTCCCAAGAAATTTC---TGTGACT	578						
DB	204 rLeuAspIeuSerGlyAsnArleuPheGlnIleAspTrGsAlPheValAspGlyMe	224						
QY	579 AACAAATTGACAAATCTGTGTGGCTGTGGACACAAATGGCTCTTACAAAGCTTCC	638						
DB	224 tProArGlnleuThrArGlnleuLeuLeuThrAspArAlleuSerGluileProTyArAspAl	244						
QY	639 TATTGACAGCTTATTAACCTTTAAAGAAATCAATATGGCTCAAAATTTTATATTCCTG	698						
DB	244 AleuGlyProleuYSerleuArGlnTrleuAspIleSerHisAsnValIleTrpSerle	264						
QY	699 TAACTTACCTGCATATTTT-----TCCAAATGACGAAACCTAGACATGTGGA	746						
DB	264 uSerGlyAsnGlnuThrYrGluileYrAlaSerThrlyleuAsnIeuAspArAlleuH	284						
QY	747 TCTTTCTTATATCATATATTCAAATATTAATCTGTCAACGACTTATACAGTTTCTACGTA	806						
DB	284 sIeuGlnuThrAsnHisIleGlnValleuProTrGsArSerPheleYrPhe-----	301						
QY	807 TCACAAATCATCTCTTTGACATGCTTTGAAACCCAAATGATTCATTCAGAACCA	866						
DB	302 -AspTrValAsnArGlnrPhe---PheAspGlyAsnProIleHisThrleuArGluAs	320						
QY	867 AGCTTTACAGGAATTAAGCTCCATGAATGACTCTAAGA-----	906						
DB	320 rAlaPheYrProAlaArGlnIleArGlnIleYrMetArGlyrCysGlyleuThrAsnI	340						
QY	907 -----GGTATTTTATATAGCTCAAAATTAATGAAAATTCGCTTCA	947						
DB	340 eSerProValAlaPheArSerleuValAsnSerleuGlnIleleuAspIeuSerGlyAs	360						
QY	948 AAACCTGCTGTTTACACGTCATCGTATGATC-----TTGGG	986						
DB	360 nAsnleuThrlyleuHis---HisYrleuPheAsnArPheArValleuArGValI	379						
QY	987 AGAATTTAAAGATCAAAAGAAATCTGGAATTTTGAACCTCTATCATGGAAGACATATG	1046						
DB	379 eSerMetArAspArAsnlyS---IleYrIleGlnlyrProTrGlnuThrPheAsnAlaVa	398						

QY 1047 TGATGACCATTTGATGATTCAGGTTAAACATATACAAATGATTTTCAGATGATATTCG 1106
 DB 398 IHIgTyrThrLeu-----LeuLysLeuAerLeuSerGlyAsp--ArgAsnAspProth 415
 QY 1107 TAAAGTTCATTCGTTGGGGAATGTTCCTGCAAATG---TCCTCGCAGAGTTCATATATAA 1163
 DB 415 rAsnLeuGlnThrLeuArgAsnMetThrArgMetArgAsnMetArgSerLeuSerIleSe 435
 QY 1164 ATATCTGAGAGATGTT-----CTTAAACATTTCAA-----TGGCA 1199
 DB 435 rArgLeuGlySerSerSerValGlyProGluAspPheLysAspPheGlyValGlyLeuG 455
 QY 1200 ATCTTATTCATCTATTCATGATGATCAAGTTCAGAGTTTCCAGTTCAGATCCCTTT--- 1256
 DB 455 uAspLeuGlnIleThrArgAlaSerLeuSerGlyTylIeGlnSerHlalaPheLysHlva 475
 QY 1257 -----CTTAAAGTTTGAATTCATATGATGAC----- 1283
 DB 475 lArgGlyLeuLysArgLeuAerPheSerSerGluAsnGlyLysLeuSerIleGluAsnAspAl 495
 QY 1284 -----AAAGGCTCTATCAGTTTAAAGAAAGT 1309
 DB 495 aPheHlAsgluIleGlyHlSerLeuLysSerLeuLysMetSerHlAsgluTyrSerGlySe 515
 QY 1310 GGCCCTACCA-----AGTCTCAGCTATCTAGATCTTAGTAG 1345
 DB 515 rAlaLeuProAlaGluProLeuArgHlAyleuThrSerLeuGlnGluLeuAerPheSerA 535
 QY 1346 AAATGCACTGAGCTTATAGTGGCTGTCTTATTCGATTTG----- 1388
 DB 535 nAsnHlAslSerSerMetSerAerThrSerPheHlAsgluLysAsnLeuArgLeuLe 555
 QY 1389 -----GGAACA----- 1394
 DB 555 uGluLeuHlAsAspAsnArgIleGluGlnValLeuLysGlyThrPheGlnGluAerIleH 575
 QY 1395 -AACAGCCTGAGACCTTACAGCTCAGCTTCAAGTGTCCATCATTAATGATGCGCAAT-- 1451
 DB 575 sSerLysLeuGlnGluLysLeuArgPheAsnHlAyleuThrSerIleSerGlnHlAsH 595
 QY 1451 ----- 1451
 DB 595 rPhePheAspLeuGluAlaLeuArgLysLeuHlAyleuAspAsnLysIleAspLysI 615
 QY 1452 -----TTCATGGCTTAAAGAGCTGCAGACCTG----- 1481
 DB 615 eGluArgArgAlaPheMetAsnLeuAspGluLeuGlnLysLysLeuSerLeuArgGlyAsnL 635
 QY 1481 ----- 1481
 DB 635 sIleAsnAsnLeuAlaAspGluSerPheGlnAsnLeuProLysLeuGlnIleLeuAerP 655
 QY 1482 -----GATTTTTCAGACCTTATTAAGAGCTGCAGAAATTC 1522
 DB 655 cAlaPheAsnGlnLeuProAsnPheAsnPheAspArgPhe-AspGlnAlaGlyHlAs 675
 QY 1523 CA-----GCGTTCTTATCCCTTAAAGCTTATAC----- 1554
 DB 675 eTAsnLeuAsnValAsnValSerHlAsAsnGlnIleArgGlnLeuMetLysArgSerSer 695
 QY 1555 -----CTTGACATCT 1564
 DB 695 rPserGlyArgAsnGlnHlAsgluLysMetLysHlSerAsnLleLysIleLeuAspLys 715
 QY 1565 CTTATCTAACACCAAAATTCATTCGATGATATTTCTT---GCTTGCACAGTCTCA 1621
 DB 715 eHlAsAsnAsnLysSerIleIleHlAsProGlyTyrPheArgProAlaGluLysSerLeu 735
 QY 1622 AACATTTAAATGCTGACATTCCTTCAAGACACACCTTTCAATGCTTTTGCA 1681
 DB 735 hHlAslAsnHlAyleuGlyTyrAsnSerLeuMet---AsnThrThrArgAspValPheGly 754

QY 1682 AACAAACAACTTGACATTCCTGATTCCTTAAATGATTCGAACAAATATCTTGGG 1741
 DB 754 smetProHlAsLeuGlnThrLeuAspLeuSerLysArgHlAsgluLeuAerPheA 774
 QY 1742 GGGTATTTGACACCTCCATAGACCTTCATATTAATATATAGATCAACAAATCTATTCG 1801
 DB 774 sPAlaPheLysAsnThrLysGlnLeuGlnLeuValPhePheGlyHlAsAsnLysLeuSerA 794
 QY 1802 TTTTGATTCATCCCATTAATACACAGCTGATTCCTCCAGACATCTTGATTCGATTTCA 1861
 DB 794 sPleProGlnAspIlePheLysProValGlnGlyLeuArgIleValAspPheSerHlAs 814
 QY 1862 AT-----CGCATAGACA 1873
 DB 814 smHlAsLeuArgGlyLeuProAspAsnLeuPheLysArgHlAsgluLysMetGluLysLeuAsp 834
 QY 1874 CATCTAAAGAAATACAGCAACATTTCCAAAGAT----- 1908
 DB 834 aLserHlAsAsnMetLeuLysIleProSerSerLeuSerSerLeuAlaAlaLeuT 854
 QY 1909 --CTAGCTTCTTCATCTTACATCAATTCGTGCTGTATATGAA-----C 1957
 DB 854 hLysLeuCysGluLeuHlSerSerAsnAsnHlSerThrIleHlSerMetAspLeuS 874
 QY 1958 ATCAGAAATC-----CTCAGTGGGTCAAGACAGAAAGCAATTCCTTGATATGAA-- 2011
 DB 874 eTAsnLysPheAspArgSerLeuArgTyrLeuAspIleSerLysArgHlAsgluLeuArgIleA 894
 QY 2012 AACAAATGACATGTCACACCTGTAGAGATGAATACCTTCCTAGTGTGATTTAATA 2071
 DB 894 sPAspAlaValPheAlaThr-----MetProLysLeuAlaValLeuAspLeuSerH 911
 QY 2072 ATTCT 2076
 DB 911 lAsn 912
 RESULT 7
 T15864
 hypothetical protein C56B6.6 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T15864
 R/Pulson, L.
 submitted to the EMBL Data Library, November 1995
 A/Description: The sequence of C. elegans cosmid C56B6.
 A/Reference number: S69019
 A/Accession: T15864
 A/Status: preliminary; translated from GB/EMBL/DDBV
 A/Molecule type: DNA
 A/Residues: 1-1066 <FULL>
 A/Cross-references: UNIPROT:Q18902; EMBL:U039996; NID:91055114; PID:91055120; PIDN:AAA81
 A/Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3;
 Alignment Scores:
 Pred. No.: 4,58e-14 Length: 1066
 Score: 286.00 Matches: 186
 Percent Similarity: 35.35% Conservative: 136
 Best Local Similarity: 20.42% Mismatches: 234
 Query Match: 5.52% Indels: 356
 DB: 2 Gaps: 35
 US-09-396-985B-46 (1-2951) x T15864 (1-1066)
 QY 261 CTGCTGACACAGGAAGTTGATCCCTCAGATAGAGTAGTTCCTAATATTAACCA 320
 DB 116 LeuAsnAspLeuLysThrLeuGlnSerIleAspLeuGluGlyAsn-AsnIleThrHlAs-- 134
 QY 321 ATGATGATGATGAAATCTCAGCAAGAGTCCCTGATGACATTCCTTCAACCAAGAAAT 380
 DB 135 -----LeuMetAspThrAsnGlnValThrPheGluSerGluMetLysVal 149

OY	381	AGATGTCGAGCTTCAACCCCTTGAAAGATGTTAAAGCTATGAGCTTCCATATTTTTCAGA	440
Db	149		169
OY	441	ACTTCAGTGGCTGGAATTTATCCAGGTGTGMAATTGMAACAATTTGAGAACAAGCATGGCA	500
Db	169		189
OY	501	TGGCTTACACCACTCTCAAC-	522
Db	189		209
OY	522	-----	522
Db	209	gGlyMetLeuLysAsnPheAlaLeuThrLeuLysThrLeuLysLeuAlaGlnAsnMetI	229
OY	522	-----	522
Db	229	eHisAlaThrProGluAlaLeuArgAspLeuArgAsnLeuThrHisLeuAsnLeuAsnG	249
OY	522	-----	522
Db	249	yAsnLysLeuAsnArgIleAspGlyAspValLeuLysGlyCysThrAspThrLeuValG	269
OY	523	-TTGATACTGACAGGAACCCCTATCCAGAGTTTCCCAGAGATTTCTGTGACTAC	581
Db	269		289
OY	582	AAGTTTACACATCTGAGTGGCTGTGGAGACAATAATGGCTCTCTAGAA-	630
Db	289		309
OY	631	-----AGTTCCTCTATTTGACAGACTTATTAACCTTAAAGAACTCAATGTGGCTCA	683
Db	309		329
OY	684	TTTATATATCTCTGAATTAAGTTTATTTTCCATCTGACGAACCTATGATCATGT	743
Db	329		349
OY	744	GGATCTTCTATTAACCTATTTCAACACTTAACT-	785
Db	349		369
OY	786	CTTACAG- TTTACGTGAAT-	816
Db	369		389
OY	817	-----AATCTCTCTTTAGACATGCTTTGAACCCAAATTTGACTTCAATTCAGA	863
Db	389		407
OY	864	CCAGGCCCTTGAGGAAT- AGCTCCAGATCACTGACTATAGAGGTAAT-	912
Db	407		427
OY	913	-----TTTAATAGCTCAAAATTAATGAAGAACTTGCTTCAAAACCT	953
Db	427		447
OY	954	GGCTGGTTTACACCTCCATCGGTGATCTTGAGAGATTTAAAGATGAAGAAATCTGGA	1013
Db	447		467
OY	1014	AATTTTGAACCCCTATACAGGAAGACATATGATGTGACATATGATGAGTTT	1073
Db	467		471
OY	1074	AACATATCAAAATGATTTTTCAGATGATATTGTTAAGTTCCATGCTTGAGGAAATGTTTC	1133
Db	471		480
OY	1134	TGCAATGTCTCTGAGAGGTGA- TCTATATAAATATCTAGAGATGTTCTCTAAACATTT	1190

```

Db      460 rsermetlrpheserlaenleuaglaenulrgylleu---aspleuserhlaasn-- 498
Qy      1191 CAAATGGCAATCTTATCAATCATATGATGCAATAG-CAGTTTCCAACTGGATCT 1245
Db      499 -----ArgllellelyslleuProSerAlaLeuTrglnleuProAlaLeuAspVa 516
Qy      1250 A-----CC 1257
Db      516 lleuHlsleuaprhlaenleuAenGlu1laapraRgaapAlaPheargSerPheSe 536
Qy      1253 CTTTCTTAAAGTTTGACTTTAAGTCATGAACA-- 1286
Db      536 raspleuIndserleuLysleuSerHlaasnAlaPheargRgPheSerCysGluPheLe 556
Qy      1287 -GGGCTATCAAGTTTAAAAAGTGCCCTTCAAGCTCAGTATCAGATCTTATGATAG 1345
Db      556 uGlySerlleSer-----GlnValHlsGlnleuAapleuSerSe 569
Qy      1346 AAATGCACTGAGC-----TTTAGTGCGGCTGTTCTTATTCGATTT 1387
Db      569 rasIndlnlleasnGlnleuAapllePheCys1laalargGly1leargLysleuSerle 589
Qy      1388 GGGAAACAACGC-----CTGAG 1405
Db      589 uAlaserasnSerValGluLys1leasnArgLysleuGlnleuAlaTrhGluLeuTh 609
Qy      1406 ACACTTAACCTGCACTTCATGAGGCGCATC---ATTATGATGCGCAATTCATGGAGCT 1462
Db      609 rSerlleaprlleSerHlaasnGlylle1laapValaapSerapAlaPheCysGluCy 629
Qy      1463 AGAAGAGCTGACGACCTGATTTTTCGACACTCTACTTAA-- 1506
Db      629 sargLysleuSerHlsleLysleuSer-HlaasnTrylleargAsnleuTrpLysGlyT 649
Qy      1507 -----AGGTCACAGAAATTCGACGTTTATTC-- 1536
Db      649 hrArgValCys1leProTrp1leSerHlsleuTrhPheCysPheThrlYsgluH 669
Qy      1537 --CTTGAACCTACTTACCTTACCTTAC-- 1560
Db      669 lsleuGluArgTrh1leSerPheSerTrylle1leValaapSerSerGlnleuHrSerP 689
Qy      1561 -----ATCTTATATCTAACACCAAAATGACTTC-----GATGGTA 1597
Db      689 heGlyAsnleuSer1leuSerPheAlaasnAnLysValaapSer1leGluAapGlyA 709
Qy      1598 TATTTCTTGCGTTGACCGCTGTCAACACATTAAAAATGGCTGGCAAT----- 1644
Db      709 laPheGluAsnleuSerleuLys1leleuAapleuSerAsnAsnProValThrSerT 729
Qy      1645 -----TCTTTCAAAAGC-----AACACCCCTTCAAAAGTC---TTTGCAAACA 1684
Db      729 rpSerProThralaPhehRgaapleuSerHlsSer1leSer1leAsnMetAlaasnT 749
Qy      1685 CA----- 1686
Db      749 hrGlyleuPheSerMetProLysPheSerHlaargSer1leGlnSerleuasn1leSerC 769
Qy      1687 -----ACAAACTTGACATTC 1702
Db      769 ysaAnLys1leTrglnleuSerGluYsaPleuAlaProleuThrlYsaVala1a1a1 789
Qy      1703 TGGATCCCTTAAATGTCATTTGGAAACAATCTGGGGGGTATTTGACACCCGTCATA 1762
Db      789 euAaprlleSerHlaasnAnleuLysGln1leSerSerMetAlaPheIndProleu1leH 809
Qy      1763 GACTTCATATTATAATGATGACAAACAATCATATTGTTTGGATTCATCCCATATA 1822
Db      809 lsleuLysGlnleuAsnValSerHlaasnPro1leTrhHlsleuThraasnHls1leG 829
Qy      1823 ACCAGCTTATTCCTC----- 1839

```

Db 829 lnglnleuTyrlYleuTyraSnllleProabMetAlaArgProTyGlnlleSerSerI 849
QY 1840 -----AGCACTCTGT 1849
Db 849 leleuSerAbnleuProProleuHiSthrlYrValaBpIlleYgluSerAlaLeuA 869
QY 1850 ATTGCAGTTTCAATCGATAGACATCTTAAGAACTAGTCAACATTTTCCAAAGAGTC 1909
Db 869 sPaYglnPheTy-rThAlaBpHrArg-----LeuLeuAArgHleu-----ValV 885
QY 1910 TAGCTTCTTCAATCTTACTTACAACTTCTGTCTGTATATGTGAACATCAGAAATTC 1969
Db 885 AlaAlaGlyArgAbnleuThrlYsIlleGluValGlyAlaPheAlaThrlleArgGlyPhe 904
QY 1970 TGCAGTGGGTCAAGAAACAGAAAGAGTTCTTGTAATGTTGAACAATGACATGTGCA 2029
Db 905 -----ArgV 906
QY 2030 CACCTTGAGATGAATACCTCTTAGTGTGATTTTAATATCTTACCTGTATATGT 2089
Db 906 AlaGylleGlnllleHlaBnSerSerIlleGlnlupheProSerArg-----lleP 923
QY 2090 ACAAGACATCATCATGCTGTCACTGTGTCACTGTGATTTGCTA----- 2133
Db 923 heaPThrleuThrlYleSerIlleuSerleuSerleuThraPAbnlyleuThrt 943
QY 2134 -----TTCACCTGTAGCA 2145
Db 943 hrPheAbnProPheGlnSerThrlValAla 952

RESULT 8

JC5239
Insulin-like growth factor acid-labile chain - baboon
C:Species: Papio sp. (baboon)
C:Date: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
C:Accession: JC5239
R:Delhanty, P.; Baxter, R.C.
Biochem. Biophys. Res. Commun. 227, 897-902, 1996
A:Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
A:Reference number: JC5239; MUID:97040714; PMID:8886027
A:Contents: liver
A:Accession: JC5239
A:Molecule type: mRNA
A:Residues: 1-605
C:Comment: This factor is structurally related to proinsulin and have insulin-like meta

Alignment Scores:

Pred. NO.: 4.55e-14 Length: 605
Score: 285.50 Matches: 144
Percent Similarity: 36.06% Conservative: 94
Best Local Similarity: 21.82% Mismatches: 240
Query Match: 5.51% Indels: 183
DB: 2 Gaps: 17

US-09-396-985B-46 (1-2951) x JC5239 (1-605)

QY 301 GTTCTATATATTACTACCAATGCATGCATGAGAACTCAGAAAGTCCGTATGACATT 360
Db 53 ValaBnglnleuSerValPheCySerSerArgAbnleuThrlYgluPheProaBpGlylle 72
QY 361 CCTTCTTCAACCAAGACATAGATCTGAGTTCAACCCCTTGAAGATCTTAAAAAGCTAT 420
Db 73 ProGlnGlyThrlGlnAlaLeuThrlleuBpSerAbnleuSerIlleProProAla 92
QY 421 AGTTTCTTCAATTTTTCAGAACTTCAAGTGTGATTTATCCAGGTGAAATGAAACA 480
Db 93 AlaPheArgAbnleuSerSerleuAlaPheleuBnleuGlnGlnGlyGlnleuGlySer 112
QY 481 ATTGAAGCAAGGATGGCATGGCTTACACACCTCTTAACTTGAATCTGACAGAAAC 540
Db 113 leuGlnPProGlnAlaLeuGlnleuGlnleuBnleuCyShleuHleuGlnleuArgBn 132
QY 541 CCTATCCAGAGTTTTCCTCCAGAAAGTTTCTGTGACATAACAAGTTTGAACATCTGGTG 600

Db 133 GlnleuArgSerleuAlaValGlyThrlPheAlaTy-rThrProAlaLeuAlaLeuGly 152
QY 601 GCTGTGAGACAAATTTGGCCTCTCTAGAAAGGTTCCCTATTGGACAGCTTATACCTTA 660
Db 153 leuSerAbnAbnArgleuSerArgleuGlnleuAer----- 163
QY 661 AAGAAATCAATGTGGTCAAAATTTATATCATCTCTGTAAAGTTACCTGCATATTTTCC 720
Db 164 -----GlyleuPheGln 167
QY 721 AATCTGACGAACCTTATGATGTGATCTTTCTTATTAATCTTAAACTATTAATCTGTG 780
Db 168 GlyleuGlyAbnleuThrlPheleuBnleuGlyThrlAbnSerleuAlaVal----- 184
QY 781 AACGACTTACAGTTTCTACGTGAAATCCCAAGTCAATCTCTTTAGACATGTCTTGG 840
Db 184 ----- 184
QY 841 AACCCATTTGACTTATTCAGACCAAGCCTTTCAGGAAT--AAGCTCAGTAAGCTG 897
Db 185 -----leuProAbnAlaAlaPheArgGlyleuGlyGlnleuArgGlnleu 199
QY 898 ACTCTAAGAGTAATTTTAATGACTCAATATATATGAAAATTGCTCTCAAAACCTGGCT 957
Db 200 ValleuAlaGlyAbn----- 204
QY 958 GGTTTACAGCTCCATCGGTGTGATCTTGGAGAAATTTAAAGATGAAGAAATCTGAAT 1017
Db 205 -----ArgleuAlaTyR 208
QY 1018 TTGAACCTCTATCATGTGAAGACATATGATGTGACCATGTGAGATTCAAGTTTAA 1077
Db 209 leuGlnProAlaLeuPheSerGlyleuAlaGlnleuArg----- 221
QY 1078 TATACAAATGATTTTCAGATGATATTTGAATTCATTTGCTGGCGAATGTTTCTGCA 1137
Db 222 -----GlyleuAbnleuSerArg 227
QY 1138 ATGTCTGTGGCAGGTGATCTATTAATAATCTGAAGATGTCTTAAACATTTCAATGG 1197
Db 228 AsnAlaLeuAlaGlnAlaIleuValaBnValPheAlaGlnleuPro-----Argleu 244
QY 1198 CAATCTTATCAATCATTAATGATGTCACTAAGCAGTTTCCAACT-----CTGAT 1247
Db 245 GlnlyleuTyrlYleuBpArgleuBpArgleuBnleuAlaValAlaProGlyAlaPheleuGly 264
QY 1248 CTACCTTTCTTAAAGTTTGAATTTACTTATGAACAA-----GGGTCTATCAGTTT 1301
Db 265 leuTyvalaLeuArgTrleuBpArgleuBnleuSerHlaBnArgValaGlyleuGlnleuBp 284
QY 1302 AAAAATGTGGCCCTACCAAGTCTCAGCTATCTGATGTAGTAAGTGAAGTGAAGCTT 1361
Db 285 ThrPheProGlyleuGlnleuGlyValleuArgValleuArgleuSerHlaBnAlaIleuAlaSer 304
QY 1362 AGTGTGGCTGTCTTATTTCTGAT-----TTGGGAACAAC 1397
Db 305 leuArgProArgThrlPheGlnleuBpArgleuBnleuPheleuGlnleuGlnleuGlnleuBn 324
QY 1398 AGCTGAGACATTTTAACTCAGCTTCAATGGTGCCATCTTATGAGTCCCAATTTGATG 1457
Db 325 ArgIleArgGlnleu-----AlaGlnArgSerPheGln 335
QY 1458 GGTTAAGAAAGCTGACGACACCTGGATTTTTCAGACCTTACTTATTAAGGCTCAGACA 1517
Db 336 GlyleuGlyGlnleuGlnleuValleu-ThrlleuBpHlaBnGlnleuGlnleuGlnleuVal--Ly 354
QY 1518 ATTCTGACGCTTCTTATCCCTTGAAGACTTACTTATCTGACATCTTATATACTAACAC 1577
Db 354 sValGlyAlaPheleuGlyleuThrlBnValaValaMetAbnleuSerGlyleuGlyBle 374
QY 1578 CAATATTTGACTGTGATATATTTCTTGGCTTGAACAGTCTCAACATTAATAATGGC 1637
Db 1578 ----- 1637

Db 374 uArgAsnLeuProGluGlnValPheArgGlyLeuGlyLeuLeuHisSerLeuHisLeuG 394
 1638 TGGCAATTC-----1647
 Db 394 uGlySerCysLeuGlyArgGlyLeaArgProHisThrPheHisGlyLeuSerGlyLeuArg 414
 1648 -----TTCAAGACGACACCCCTTCAAAAGTCCTTGCAAAACA-----AC 1688
 Db 414 gLeuPheLeuLysAspAsnGlyLeuValGlyIleGluGlnSerLeuTrpGlyLeuA 434
 1689 AAACCTTGACATTCCTCGATCCCTCTCTAAATATGCATTTGGACAAATATCTGGGGGATAT 1748
 Db 434 aGluLeuLeuGlnLeuLeuAspLeuThrSerAsnGlnLeuThrHisLeuProHisGlnLeuP 454
 1749 TGACACCTCCATAGACTTCATATTTAAATATGATGACACACATCTATTTGTTGA 1808
 Db 454 eGlnGlyLeuGlyLysLeuGlnGlyTrpLeuLeuLeuSerHisAsnArgLeuHisGlnLeuP 474
 1809 TTCAATCCCATATATAACGACGCTGATTTCCCTGACACCTTGATTTGACGTTTCATCCCAT 1868
 Db 474 cAlaAspAlaLeuGlyProLeuGlnArgAlaPheTrpLeuAspAlaSerHisAsnArgLe 494
 1869 AGAGACATCTTAAAGGAATATCTGCAACATTTCCAAAGAGTCTTACCTCTTCATCTTAC 1928
 Db 494 uGlnAlaLeuProGlySerLeuLeuAlaSerLeuGlyArgLeuArgGlyTrpLeuAsnLeu 514
 1929 TAAACATTCGTGCTGCTGTATATATGTGAACATCAGAAATTCCTGCAG-----TGGGTCAA 1982
 Db 514 gAsnHisSerLeuArgTrpPheThrProGlnProProGlyLeuGlnArgLeuTrpLeuG 534
 1983 GGAACAGAGAGAGTTCTTGCGAATGTTGAACAAATGACATGTGCAACACCTGTAGAG-- 2040
 Db 534 uGly-----AsnProTrpAspCysSerCysProLeuLysAl 546
 2041 -----ATGAATACCTCCTTAGTGTGTGATTTTAATATTTACCTG 2081
 Db 546 aLeuArgAspPheAlaLeuGlnAsnProSerAlaValProArgPheValGlnAlaIleCy 566
 2082 T-----TATATGTACAGACATCATCATGATGTGCA 2112
 Db 566 sGluGlyAspAspCysGlnProProValTrpThrTyrAsnAsnIleThrCysAlaSer 585

RESULT 9
 Jc6128
 Insulin-like growth factor binding complex acid labile chain - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
 C/Accession: Jc6128
 R/BotSciair, Y.R.; Seto, D.; Hsieh, S.; Hurst, K.R.; Ooi, G.T.
 Proc. Natl. Acad. Sci. U.S.A. 93, 10028-10033, 1996
 A/Title: Organization and chromosomal localization of the gene encoding the mouse acid 1
 A/Reference number: Jc6128; MUID:96413591; PMID:8816745
 A/Accession: Jc6128
 A/Molecule type: DNA
 A/Residues: 1-603 <BOT>
 A/Cross-references: UNIPROT:P70389; GB:U66900; NID:g1621612; PIDN:AA17270.1; PID:g1621612
 C/Comment: This protein is a serum protein and it is of the ternary complex in the phys
 C/Genetics:
 A/Gene: als
 A/Map position: 17

Alignment Scores:
 Pred. NO.:
 Score: 7.79e-14 Length: 603
 Percent Similarity: 282.50 Matches: 153
 Best Local Similarity: 35.29% Conservative: 82
 Query Match: 22.97% Mismatches: 228
 DB: 5.46% Indels: 203
 Gaps: 23

US-09-396-985B-46 (1-2951) x Jc6128 (1-603)
 322 TGcATGATcTGAAAGcTcAGAAAGcTcCGATGATcATcTcTcTTTGACcAGAAcATA 381
 |||
 ::: |||:::||||| ||||| |||||::: |||

D	60	CysSerSerSerArgAsnLeuThrGlnLeuProAspGlyLeuProValSerThrArgAlaLeu	79
Q	382	GATGTGAAGCTTCAACCCCTTGAGAGCTTTAAAGAACTATAGCTTCCAAATTTTTCAGA	441
D	80	TrpLeuArgGlyAsnAsnLeuSerSerLeuProSerLeuAlaIlePheGlnAsnLeuSerSer	99
Q	442	CTTCAGTGGCTGGATTATGCAAGGTGGAAATTGAACAATTGAAGAACAAGGCATGGCAT	501
D	100	LeuAspPheLeuAsnLeuGlnGlySerThrLeuArgSerLeuGlyProGlnIleLeuLeu	119
Q	502	GGCTTACACACCCCTCAAACTTATGATGTGCACAGAAACCCCTATACCAAGCTTTTCCCA	561
D	120	GlyLeuGlnAsnLeuGlyTrpHisLeuHisValLeuGlnLysArgAsnLeuLeuArgSerLeuAlaIa	139
Q	562	GGAAGTTTCTCTGGACTTAACAGATTATGACAACTATGCTGGTGGCTGGAGACAAATTGGCC	621
D	140	GlyLeuPheArgHisThrProSerLeuAlaSerLeuSerLeuGlyAsnAsnLeuLeuGly	159
Q	622	TTCTCTAAAGACTCCCTATTTGACACCTTATTAACCTTAAGAAACCTAAATGGCTGCAC	681
D	160	ArgLeuGlnGlnGlyLeuPheArgGlyLeuSerHisValLeuTrpAspLeuAsnLeuGlyTrp	179
Q	682	AATTTT-----ATACATTCCTGT	699
D	180	AsnSerLeuValValLeuProArgThrValPheGlnGlyLeuGlyAsnLeuHisGlnLeuLeu	199
Q	700	AAGTTA-----CTTGCAATATTTTCCAACTGTGACGAC	732
D	200	ValLeuAlaGlyAsnLysLeuThrThrTyLeuGlnIleProAlaLeuLeuGlyGlyGly	219
Q	733	CTAGTACATGGGATCTTTCTTATTAACATAATTCAAACTATTAAGCTGCACAGCTTACAG	792
D	220	LeuArgGlyLeuAspLeuSerArgAsnAlaLeuArgSerValLysAlaAsn-----Val	237
Q	793	TTTCTAGGTGAATAATCACAAGCTCAACTCTCTTATGACATGCTTTGAAACCAATGAC	852
D	238	PheIleHisValLeuProArgLeuGlnLysLeuGlyLeuAspArgAsnLeu-----IleThr	255
Q	853	TTCAATTCAAGACCAAGCCCTTCAAGGAAATTAAAG--CTCCATGAAGTACACTTAAGAGT	909
D	256	AlaValAlaProArgAlaPheLeuGlnLysMetLysAlaLeuArgTrpLeuAspLeuSerHis	275
Q	910	AATTTATTAAGCTCAATATATATGAATACTTGCTTCAAAACCTGGCTGGTTTACAGCTC	969
D	276	Asn---ArgValAlaGlyLeuGlnAspThrPheProGlyLeuLeuGlyLeuHisVal	294
Q	970	CATCGGTTGATCTTGGGA-----GAATTAAAGTGAAGAAG	1009
D	295	LeuThrLeuAlaHisValAsnAlaIleThrSerLeuArgProArgThrPheLysAspLeuHis	314
Q	1006	AATCTGGAATTTTGTGA-----CCCTCATCATG	1035
D	315	PheLeuGlnGlnLeuGlnLeuGlnLysAsnArgLysArgGlnLeuGlnLysThrPhe	334
Q	1036	GAAAGACTATGTGATGTGCACATGATGAGCTTCAAGGTTACATATACAAATGATTTTCA	1099
D	335	GlnGlyLeu-----GlyGlnLeuGlyValLeuThrLeuAsnAspAsnGln	349
Q	1096	GATGATATGTTTAAAG-----TTCCATTCCTTGGGAAATGTTTGCAGATCTCTGG	1144
D	350	IleHisGlnValLysValGlyAlaPhePheGlnGlyLeuPheAsnValAlaValMetAsnLeu	369
Q	1147	GCAGGTGTATCTTAATAATATCTAGAAGATGTTCTTAAACATTTTCAATAGGCAATCTTAA	1206
D	370	SecGly-----AsnGlyLeuArgSerLeuProGlnHisVal---PheGlnGlyLeu	385
Q	1207	TCAATCATTAAGATGTCAATACAGATTTCCAACTCTGGATCTTACCTTTCTTAAAGTT	1266
D	386	Gly-----ArgLeuHisSerLeuHisVal-----	393
Q	1267	TGACCTTAACTATGACAAAGGCTCATGATTTTAAAAAAGTGGCCCTACCAAGTCTCA	1326
D	393	-----	393

QY 1327 GCTATCTAGATCTTAGTAGAAGAAATGACTGAGCTTTAGTGAGCTGTTCTTATCTGATT 1386
Db 393 ----- 393
QY 1387 TGGGAACAACAGCGCTGAGACATTAGACCTCAGCTTCAATGTCATCATTTATGAGTG 1446
Db 393 ----- 393
QY 1447 CCAATTTACATGGCTGAGAGAGCTGACACCTGATTTTTCAGACCTGACTTTAAA 1506
Db 394 ----- 394
QY 1507 AGGCTACAGAAATCTCAGCGTCTTATCCCTGAAAAAGCTATTACCTTGACATCTCT 1566
Db 400 ArgTLeuArgLeuHisThr----- 405
QY 1567 TATATCTAACACCAAAATTTGACTGATGATATTTCTTGCTTGACCACTGTCACACA 1626
Db 406 ----- PheAlaGlyLeuSerGlyLeuArg 414
QY 1627 TTTAAATATGGCTGCAATTTCTTTAAAGACACACCTTCAATGTC----- 1674
Db 415 LeuPheLeu-----ArgAspAsnSerIleSerIleGlyGlyGlnSer 429
QY 1675 TTTGCAACACACAACTTGACATTCCTGATCCTTCAATATGTCATTTGGAACAATA 1734
Db 430 LeuAlaGlyLeuSerGlyLeuLeuGlnLeuSerLeuThrAlaAsnGlnLeuThrHisLeu 449
QY 1735 TCTTGGGGGCTATTGACACCCCTTCATAGACTTCAATTTAAATATGAGTCACACAAAT 1794
Db 450 ProArgGlnLeuPheGlnGlyLeuGlyGlnLeuGlnLeuLeuSerAsnAsnGln 469
QY 1795 CTATGTTTGGATTCATCCCATTAATACAGAGCTGATTCCTCAGACCTTGATTC 1854
Db 470 LeuThrMetLeuSerGlyAspValLeuGlyProLeuGlnArgAlaPheTrpLeuAspLeu 489
QY 1855 AGTTTCATGCTAGACAGACA---TCTAAAGAAATACGCAACATTTCCAAAGAGTCTA 1911
Db 490 SerIleAsnArgLeuGlnThrProAlaGlnGlyLeuPheSerLeuGlyArg---Leu 508
QY 1912 GCCTTCTTCATCTTACTAACAAATCTGTGCTGTATATGTAACATCAGAAATTCCTG 1971
Db 509 ArgGlyLeuLeuLeuArgAsnAsnSerLeu-----GlnThrPheVal 522
QY 1972 CAGTGGGTCAAGACAGACAGAGCTCTTGCTGATGTGAACAATGACATGTCACACA 2031
Db 523 ProGlnProGlyLeuGlnArgLeuTrpLeu---AspAlaAsnProTrpAspCysSerCys 541
QY 2032 CCTGTAGAG-----ATGAATACCTCCTTAGTGTGATTTTAT 2070
Db 542 ProLeuGlyAlaLeuArgAspPheAlaLeuGlnAsnProGlyValValProArgPheVal 561
QY 2071 AATTTACTCTGT-----TATATGTAACAAGACATCATCAGT 2106
Db 562 GlnThrValCysGlnGlyAspAspCysGlnProValTyrThrTyrAsnAsnIleThrCys 581
QY 2107 GTTCAGAGGTCACTGAG 2124
Db 582 AlaGlyProAlaAsnVal 587
RESULT 10
JC1282
insulin-like growth factor-binding protein acid labile chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JC1282
R/Dat: J.; Baker: R.C.
Biochem: Biophys. Res. Commun. 188, 304-309, 1992
A/Title: Molecular cloning of the acid-labile subunit of the rat insulin-like growth fac
A/Reference number: JC1282; MUID:93038676; PMID:1384485
A/Accession: JC1282
A/Molecule type: mRNA

A/Residue: 1-603 <DAI>
A/Cross-references: UNIPROT:P35859; GB:546785; NID:9258002; PIDN:AA23770.2; PID:957059
A/Experimental source: liver
A/Note: the authors translated the codon AAG for residue 63 as Arg, AAA for residue 205
F/1-27/Domain: signal sequence #status predicted <Sig>
F/28-603/Product: insulin-like growth factor binding protein, acid labile chain #status
F/267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR>
Alignment Scores:
Pred. No.: 1 22e-13 Length: 603
Score: 280.00 Matches: 163
Percent Similarity: 38.12% Conservative: 81
Best Local Similarity: 25.47% Mismatches: 221
Query Match: 5.41% Indels: 176
DB: 2 Gaps: 26
US-09-396-985b-46 (1-2951) x JC1282 (1-603)
QY 322 TGCATGGATCAGAAACTCAGCAAAAGTCCCTGATGACATTCCTTTCACCAAGAACATA 381
Db 60 CysSerSerIysAsnLeuThrHisLeuProAspAspIleProValSerThrArgAlaLeu 79
QY 382 GATCTGAGCTTCAACCCCTTGAAGATCTTAAAAAGCTATAGCTTTCCTCAATTTTTCGAA 441
Db 80 TrpLeuAspGlyAsnAsnLeuSerSerIleProSerAlaAlaPheGlnAsnLeuSerSer 99
QY 442 CTTCAGAGGTGGATTTATCCAGGTGCGAATTTGAATGAACATTTGACAGCAGCGCAT 501
Db 100 LeuAspPheLeuAsnLeuGlnGlySerTrpLeuArgSerLeuGlnProGlnAlaLeuLeu 119
QY 502 GCGTTACACACCTTCAAACTTGATATGACAGAAACCTTATCCAGACTTTTCCCA 561
Db 120 GlyLeuGlnAsnLeuTyrTyrLeuHisLeuGlnArgAsnArgLeuArgAsnLeuAlaVal 139
QY 562 GGAAGTTCTCTGAGCTTAACAAGTTTATGACAAATCTGTGCTGTGGAGACAAATTTGCC 621
Db 140 GlyLeuPheThrHisThrProSerLeuAlaSerLeuSerLeuSerAsnLeuGly 159
QY 622 TCTGTAGAAAGCTTCCCTATATGACAGCTTATTAACCTTAAAGAACTCATGTGGCTCAC 681
Db 160 ArgLeuGlnGlnGlyLeuPheGlnGlyLeuSerHisLeuTrpAspLeuAsnLeuGlyTrp 179
QY 682 AATTTT-----ATACATTCCTGT 699
Db 180 AsnSerLeuValValLeuProAspThrValPheGlnGlyLeuGlyAsnLeuHisLeuLeu 199
QY 700 AAGTTA-----CTGCATATTTTTCATTCGACAGAC 732
Db 200 ValLeuAlaGlyAsnGlyLeuThrTyrLeuGlnProAlaLeuPheCysGlyLeuGlyGlu 219
QY 732 CTAGTACATGAGATCTTCTTAACTATATTAATTAATTAATTAATTAATTAATTAATTAAT 792
Db 220 LeuArgGlyLeuAspLeuSerArgAsnAlaLeuArgSerValIlyAlaAsnValPheVal 239
QY 793 TTTCTACGTGAATAACCAAGTC---AATCTCTTTTACAGATGCTTGAACCCCAATT 849
Db 240 HisLeu-----ProArgLeuGlnGlyLeuTyrLeuSerArgAsnLeu-----Ile 254
QY 850 GACTTCAATTCAGACCAAGCCTTTCAGGGAATTAG---CTCCATGACATGACTCTAGA 906
Db 255 ThrAlaValAlaProGlyAlaPheLeuGlyMetLeuAlaLeuArgTrpLeuAspLeuSer 274
QY 907 GGTAAATTTTAATGCTCAAAATATATATGAATACTGCTGAAAACCTGGCTGGTTTACAC 966
Db 275 HisAsn---ArgValAlaGlyLeuMetGlnAspThrPheProGlyLeuGlyLeuHis 293
QY 967 GTCCATCGGTGATCTTTGGA-----GAATTTAAAGATGAA 1002
Db 294 ValLeuArgLeuAlaHisAsnAlaIleAlaSerLeuArgProArgThrPheIlyAspLeu 313
QY 1003 AGCAATCTGGAATTTTGA-----CCCTCATC 1032
Db 314 HisPheLeuGlnGlyLeuGlnLeuGlyHisAsnArgIleArgGlnLeuGlyGluArgThr 333

Qy	597	GGTGGCTGTGAGACAAAAATTTGGCTCTCTTAGAAAGCTTCCCTATTGGACAGCTTAATAC	656
Db	508	uAsnLeuValAsnAsnGlnLeuSerGlySerIleProGlnGluIleGlyIleuAspGlySe	528
Qy	657	CTTAAAGAACTCAATGTGCTCCACAAATTTATACATCTCCGTAAAGTATACCGATATTT	716
Db	528	rLeuAsnValLeuAspLeuSerGlnValAsnAlaLeuAsnGly---SerIleProAlaSerph	547
Qy	717	TTCCAATTCAGCAAGACCTAGTACATGTGGATCTTTCTTAATACATATATCAAACTATAC	776
Db	547	eGlyAsnLeuAsnLeuSerAspArgLeuAsnLeuValAsnAsnGlnLeuSerGlySerIle	567
Qy	777	TGTCAAGACACTTACAGTTCTTACGTGAAATCCACAGTCAATCTCT	825
Db	567	eProGlnGluIleGlyIleuArgSerLeuAsnAspLeuGlyLeuSerGlnValAsnAla	587
Qy	826	-----TTAACAATG-----	834
Db	587	uAsnGlySerIleProAlaSerLeuGlyAsnLeuAsnAsnLeuSerMetLeuIleuTy	607
Qy	834	-----	834
Db	607	rAsnAsnGlnLeuSerGlySerIleProGlnGluIleGlyIleuSerSerLeuThrTy	627
Qy	835	-----TCTTGAC-----CCAATTGACTTCAATCAAGACA	866
Db	627	rLeuSerLeuGlyAsnAsnSerLeuAsnGlyLeuIleProAlaSerPheGlyAsnMetArg	647
Qy	867	AGCCTTACAGGAATTATAGCTCCATGAACTGACTCTAAGAGTAAATTTATATAGCTCA--	924
Db	647	gAsnLeuGlnAlaLeuIleLeuAsnAspAsnAsnLeuIleGlyGluIleProSerSerVal	667
Qy	925	-----ATAATAATGAAA-----	936
Db	667	LCysAsnLeuThrSerLeuGluValAlaLeuTyMetProArgAsnAsnLeuGlyGlyVal	687
Qy	937	----ACTTGCTTCAAAAACCTGGCTGTTTACAGCTCCATGCTGTTGATCTTGGAGAATT	992
Db	687	lProGlnGlyLeuGlyAsnIleSerAsnLeuGlnValLeuSerMetSerSerAsnSerPh	707
Qy	993	TAAAGATGAAGAAGAACTCGAAATTTTGAACCCCTATCAATGGAAGACATATGATGT	1052
Db	707	eSerGlyGluLeu-----ProSerSerIleSerMetLeuThrSerIle	721
Qy	1053	GACCATTTGATGAGTTCAGGTTAACAATATACAAATGATTTTTCAGATGATTTGTAATGTT	1112
Db	721	uGlnIleLeuAspPheGly-----ArgAsnAsnLeuGlnGlyAlaIleProGln-	737
Qy	1113	CCATTGCTTGGCGAATGTTTCTTCGACATGTCCTG-	1146
Db	738	---CysPheGlyAsnIleSerSerLeuGlnValPheAspMetGlnAsnAsnGlyLeuSe	756
Qy	1147	-----GCAAGGTATATCTAATAAATATCA-----	1170
Db	756	rGlyThrLeuProThrAsnPheSerIleGlyCysSerLeuIleSerLeuAsnLeuHiLeG	776
Qy	1171	-----GAAGATGTTCCATACATTTT-----AATGGCAATCCTT	1205
Db	776	YAsnGlnLeuGlnuAspGlnIleProArgSerLeuAspAsnGlyValGlyIleGlnValLe	796
Qy	1206	ATCAATCATTAAGATGCAACTAAGC--AGTTTCCAACCTTGAT-----CTAACCTT	1255
Db	796	uAspLeuGlyAspAsnGlnLeuAsnAspThrPheProMetTrpLeuGlyThrLeuProG	816
Qy	1256	TCTTAAAAAGTTGACTTTTATACATGAACAA-----GGGTCTATC-----AGTTTAA	1303
Db	816	uLeuArgValLeuAspLeuThrSerAsnGlyLeuHiLeGlyProIleArgSerSerArgAl	836
Qy	1304	AAAATGGCCCTACCAAGCTCAGCTATCATAGATCTTATGTAAGAAATGACAGCTTAA	1363
Db	836	agIuIleMetPheProAspLeuArgIleIleAspLeuSerArgAsnAlaPheSer-----	854
Qy	1364	TGGTGGCTGTTCTTATCTGATTTTGGAAACAACAGCTGAGACCTTAGACCTTCAAGCTT	1423

Db	855	-----				-----	855		
Qy	1424	CAATGGTC	CAATTTATAGTGC	CAATTTCA	TGGGCTTAGAAG	AGCTGCAGCACTGGA	1483		
Db	866	-LysGlyMet	ArgThrValAsp	SerThrMet	GluGluPro	SerTyrGluSerTyrTrpAs	885		
Qy	1484	TTTTTCAG	CACTCTACTTTAAAA	GGGTGCACAG	AAATTC	TCAAGCTTTATCCCTTGAAA	1543		
Db	885	PAAPSer	ValValValThr	LeuGln	-----	LeuGlnLeuValA	901		
Qy	1544	AGCACTT	ACTTGACATCTCTAT	ACTTAACACAA	AAATTA	CTTGAGTGTATATTC	1603		
Db	901	rglleuSer	Leu-----	TyrThr	-----	-----	907		
Qy	1604	TTGGCTG	CAACAGTCTCAAC	ATTAATAAA	TGGCTGC	CAATTTTCAAGACAA	1663		
Db	908	-----	-----	ValIle	AspLeuSerSer	AsnLysPheGluGlyHisIle	920		
Qy	1664	TTTCAAT	TGCTTGCAAA	CAACAA	CTTGAC	ATTCCTGATCCTTCTTAATGTCAAT	1723		
Db	921	-----	-----	ProSer	-----	-----	922		
Qy	1724	TGGAACA	AAATCTTTGGGGG	GTATTTGAC	ACCTCCAT	PAGCTTCATTTAATATGA	1783		
Db	923	-----	-----	Valleu	GlyAspLeuIleAlaIleArg	SylleuAsnValS	936		
Qy	1784	GTCAACA	CAATCTATGTTT	TGGATTCATCC	CAATTAA	CCAGCTGTATTCCTCAGCA	1843		
Db	936	erHis	AsnAlaIleuGlnGly	TyrIlePro	SerSerLeuGlySer	LeuSerIleLeuGlnS	956		
Qy	1844	CTCTTGAT	TGCAGTTTCAT	TGCATPAG	ACATCTAA	AGAAATCTGCACATTTTCCA	1903		
Db	956	erIleu	AspLeuSerPhe	AsnGlnLeuSer	-----	GlyGluIleProG	970		
Qy	1904	AGAGCT	TAAGC-----	TTCTCA	TCTTACTA	CAATCTGTGTT--G	1942		
Db	970	I	ngI	nLeuAlaSer	LeuThrPhe	LeuGluPheLeuAsnLeuSerHis	AsnTyrLeuGlnG	990	
Qy	1943	CTTGAT	ATGTGCAAC	TAGAAATTC	TCTGCAG	TGG-----	1977		
Db	990	LyCy	SileProGlnGly	ProGln	He	ArgThrPheGluSer	AsnSerTyrGluGlyAsnA	1010	
Qy	1978	-----	-----	-----	-----	-----	-----	1978	
Db	1010	spGly	LeuArgGlyTyr	ProValSer	LeuSylCySgly	AspProValSer	IleLysAs	1030	
Qy	1991	AGCACT	TTTGTAATCTTGA	ATCTTGA	CAAAATG	ATGACATGCA	CCGTGAGATGAATCACT	2050	
Db	1030	snTyr	ThrValSer	AlaLeuGln	AspGln-----	-----	GluSer	AsnSerG	1044
Qy	2051	CCTTAG	TGTGTGATTTAT	TATATCTAC	CTGTATATG	ACAAACAATCAATCACTG	ATGTGT	2110	
Db	1044	Iu	phePheAsn	AspPheTrp	LysAlaAla	LeuMetGlyTyrGly	SerGlyLeu	CysIleG	1064
Qy	2111	CAGTGC	TAGTGTG-----	ATTGTG	TATCACT-----	-----	GTAC	CAATTTCTGA	2152
Db	1064	LyIle	SerMetIleTyr	IleLeuIle	SerThrGly	AsnLeuArgTyr	Pro	AlaArgIleI	1084
Qy	2153	TATACCA	CTTCTATTTTCA	CTGATCTT	ATATTCG	TGCGGTG	TGTA	AAAAAGTACAGCAGAGAG	2212
Db	1084	I	euGly	LeuGln	HisIle	SylleuMetGlnArg-----	ArgLys	LeuSylGlnArgGlyG	1102
Qy	2213	AAAGCA	CTTAT	2223	-----	-----	-----	-----	-----
Db	1102	I	Arg	AsnTyr	1105	-----	-----	-----	-----

C:Accession: T42218
 R:Nakajima, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
 Genomics 51, 27-34, 1998
 A:Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
 A:Reference number: Z14126; MUID:98360089; PMID:9693030
 A:Accession: T42218
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1531 <NAK>
 A:Cross-references: UNIPROT:O88279; EMBL:AB011530; NID:93449289; PIDD:BA32460.1; PID:93
 A:Experimental source: strain Sprague-Dawley; brain
 C:Gene: MEGF4
 C:Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Alignment Scores:

Pred. No.:	5,5e-13	Length:	1531
Score:	272.50	Matches:	169
Percent Similarity:	33.58%	Conservative:	98
Best Local Similarity:	21.26%	Mismatches:	260
Query Match:	2	Indels:	268
DB:		Gaps:	28

US-09-396-985B-46 (1-2951) x T42218 (1-1531)

```

QY 160 GATCGTCATGTCCTCATGCGCTCCACTGTTGCAGAAATGCGAGATGATGCTCC 219
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 220 AspCysHisLeuAlaTrp-----LeuSerGln 228

QY 220 TGGCTCTGGCTAGAGACTTGATCATGCGACTGTTCTTCTGCTGACACAGAAAGC 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 229 TripleArgGlnArgProThrIle---GlyLeuPheThrGlnCysSerGlyProAlaSer 247

QY 280 TTGAT----- 285
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 248 LeuArgGlyLeuAsnValAlaGlnValGlnYserGlnPheSerCysSerGlyGlnGly 267

QY 286 -----CCCGCATAGAGGA 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 268 GlnAlaAlaGlnValProAlaCysThrLeuSerSerGlySerCysProAlaMetCysSer 287

QY 301 GTTCTCAATATTACCTACCATGATGATGATGATGATGATGATGATGATGATGATGAT 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 288 CysSerAsnGlyIleValAspCysArgGlyGlyGlyLeuThrAlaIleProAlaAsnLeu 307

QY 361 CCTTTTCAACCAAGAACATGATCTGAGCTTCAACCCCTTGAAGATCTTAAAGCTAT 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 308 ProGlnThrMetThrGlnIleArgLeuGlnLeuAsnGlyIleYserIleProProGly 327

QY 421 AGCTTCTCCAACTTTTTCAGAACTTCAGTGGCTGATTTATCCAGGTGGAATTGAACA 480
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 328 AlaPheSerProArgArgLeuArgLeuArgIleAlaPheLeuSerAsnAsnGlnIleAlaGlu 347

QY 481 ATTGAAGACAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 348 IleAlaProAlaPheGlnGlyLeuArgSerIleLeuAsnSerIleValLeuTyrGlyAsn 367

QY 541 CCTATCCAGAGTTTTCCTCCAGAAAGTTTCTGATGATGATGATGATGATGATGATGAT 600
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 368 LysIleThrAspLeuProArgGlyValPheGlyGlyLeuTyrThrLeuGlnLeuLeu--- 386

QY 601 GCTGTGGAGACAAATTTGGCTCTCTAGAAAGCTTCCTATTTGGACACTTATAACCTTA 660
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 387 -----LeuLeuAsnAla 390

QY 661 AAGAACTCAATGCTGCTCACAATTTTATACATTCCTGTAAGTACCTGCAATATTTTCC 720
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 391 AsnLysIleAsn-----CysIleArgProAlaPheGln 402

QY 721 AATTCAGGAACCTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 403 AspLeuGlnAsnLeuSerLeuSerLeuTyrAspAsnLysIleGlnSerLeuAlaLys 422
  
```

```

QY 781 AAGCACTTACAGTTTCTACGTGAAATCCAGAACTCAATCTCTTGAAGATGCTTTG 840
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 423 GlyThrPheThrSerLeuArg-----AlaIleGlnThrLeuHisLeuAlaGln 438

QY 841 AACCAATGATCTTCAATCAAGACCAAGCCCTTTCAGGAAATTAAGCTCCAGTAAGTACT 900
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 439 AsnPro-----PheIleCysAsp-----CysAsnLeuLys 448

QY 901 CTAAAGGTAATTTTAATAGCTCAAAATATATGAAGAACT-----TGCCCT--- 945
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 449 TripleAlaAspPheLeuArgThrAsnProIleGlnThrGlnGlyAlaArgCysAlaSer 468

QY 946 ---CAAACTGCTGCTGTTTACACGTCATGCGGTGATCTTGGGCAATTTAAATGAA 1002
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 469 ProArgArgLeuAlaAsnLysArgIleGlyGlnIleLysSerLysPheArgCysSer 488

QY 1003 AGGAATTCGAAATTTTGAACCTCTATCATGGAAGACTATGATGATGATGATGATGAT 1062
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 489 AlaLysGlnGlnTyrPheIleProGly-----ThrGln 499

QY 1063 GAGTTCAGGTTTAACATATACAAATGATTTTCAAGATGATTTGTT-----AAGTTC 1113
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 500 AspTyrHisLeu-----AsnSerGlnCysThrSerAspValAlaCysProHisLysCys 517

QY 1114 CATTCCTGGCGAATGTTTCTGCAATGCTCTGCGAGGCTGATCTATTAATATCTAGAA 1173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 518 ArgCysGlnAlaSerVal-ValGlnCys-SerGlyLeuLysSerLysIleProGln 537

QY 1174 GATGTTCTTAAACATTTTCAAAATGCGAATCTTATCATGATGATGATGATGATGATGAT 1233
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 537 rgIlePro-----GlnSerThrThrGln- 544

QY 1224 TTCCAACCTCGATCTACCTTTCTTAAAGTTGACTTATACATGATGAAAGGCTCTA 1293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 545 -----LeuArgLeuAsnAsnAsnGlnI 552

QY 1294 TCAGT-----TTTAAAAAAGTGCCCTCCCAAGCTCGAGCTATC 1332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 552 IeSerIleLeuGlnAlaThrGlyLeuPheLysLys-----LeuSerHisLeuLysLysI 570

QY 1333 TAGATCTTATGAGAATGCACTGAGC-----TTTAGTGCTGCTGTT 1374
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 570 LeuAsnSerAsnAsnLysValSerGlnIleGlnAspGlyThrPheGlnGlyAlaThrS 590

QY 1375 CTATATTCGAT-----TTGGAAACAAACAGCCTGAGACACTTGAAGCTCAAGCTTCAATG 1428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 590 erValSerGlnLeuHisIleuThrAlaAsnGlnLeuGlnSer----- 603

QY 1429 GTGCCATCATATGAGTCCCAATTTTCATGGGTCTAGAAAGCTGCGACCTGATTTT 1488
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 604 -----ValArgSerGlyMetPheArgGlyLeuAspGlyLeuArg-ThrLeuMetLeu 620

QY 1489 CAGCACTCTACTTTTAAAAAAGGCTCAGAAATTCACAGGTCCTTATCCCTTGAAGAGCTA 1548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 621 ArgAsnAsnArgIleSerCysIleHisAsn---AspSerPheThrGlnLeuArgAsnVal 639

QY 1549 CTTACCTTGAACATCTCTTATATCAACACCAAAATGACTTCGATGATGATGATGATGAT 1608
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 640 ArgLeuLeuSerLeuTyrAspAsnHisIleThrThrIleSerProGlyAlaPheAspThr 659

QY 1609 TTGACCAAGTCTCAACACATTTTAAATAGGCTGGCAATCTTCAAGAACAC----- 1659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 660 LeuGlnAlaLeuSerThrLeuAsnLeuLeuAlaAsnProPheAsnCysAsnCysGlnLeu 679

QY 1659 ----- 1659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 680 AlaThrLeuGlnAspThrPheLeuArgLysIleValIleThrGlnAsnProArgCysGln 699

QY 1659 ----- 1659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 700 AsnProAspPheLeuArgGlnIleProLeuGlnAspValAlaPheProAspPheArgCys 719

QY 1659 ----- 1659
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
```

Db 720 GluIuGlugluGluGluValGlyCysLeuProArProGInGysProGInGluCysAla 739
 QY 1660 -----ACCTTTCAAT-----GTC 1674
 Db 740 CysLeuArpThrValValArgCysSerAsnLysHisLeuGlnAlaLeuProLysGlyIle 759
 QY 1675 TTTGCAACACAACTTGACATTCCTGGATCCTCTAAATGTCATTTGGAACAATA 1734
 Db 760 ProLysAsnValThrGluLeu---TyrLeuAspLysAsnGlnPheThrLeuValPro--- 777
 QY 1735 TCTTGGGGGTATTGACACCCCTGCATAGACTTATTAATATGATGACACAACT 1794
 Db 778 -----GlyGlnLeuSerThrPheLysTyrLeuGlnLeuValAspLeuSerAsnAsnLys 795
 QY 1795 CTAATGTTTGGATTCATCCCATTAATACAGCTGATTCCTCAGACCTTTGATTC 1854
 Db 796 IleSerLeuSerLeuSerSerPheThrAsnMetSerGlnLeuThrThrIleLeu 815
 QY 1855 AGTTCAATCGCATAGACATCTAAAGGATACGCAACTTTCCAAAGACTAGCC 1914
 Db 816 SerTyrAsnAlaLeuGlnCysIleProProLeuAlaPheGlnGlyLeuArgSerLeuArg 835
 QY 1915 TTCTTCATCTTACTTAACAATTCGTGCT----- 1944
 Db 836 LeuLeuSerLeuHisGlyAsnAspValSerThrLeuGlnGluGlyIlePheAlaAspVal 855
 QY 1945 -----TGTATATGTGAACATCAG 1962
 Db 856 ThrSerLeuSerHisLeuAlaIleGlyAlaAsnProLeuTyrCysAspCysHisLeuAsnArg 875
 QY 1963 AAATTCCTGCAGTGGGTCAAGAAACAGAGAGTTCCTGGATGTTGGAACAATGCA 2022
 Db 876 TrpLeuSerSerThrValValThrGlyTyrLys-----GluProGlyIleAlaArg 892
 QY 2023 TGTGCAACACCTGTAGAGATGAATACCTCTTAGGTG 2061
 Db 893 CysAlaGlyProProGluMetGluGlyLysLeuLeuLeu 905
 RESULT 13
 A41915
 Insulin-like growth factor-binding complex acid-labile chain precursor - human
 N:Alternate names: Acid-labile Subunit (ALS)
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A41915
 R:Leong, S.R.; Baxter, R.C.; Camerato, T.; Dai, J.; Wood, W.I.
 Mol. Endocrinol. 6, 870-876, 1992
 A:Title: Structure and functional expression of the acid-labile subunit of the insulin-1
 A:Reference number: A41915; MUID:92357025; PMID:1379671
 A:Accession: A41915
 A:Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 1-605 <LRO>
 A:Cross-references: UNIPROT:P35858; GB:M6826; NID:G184807; PIDN:AAA36047.1; PID:G184808
 A:Experimental source: liver
 A>Note: sequence extracted from NCBI backbone (NCBI:110171)
 F:75-98/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>
 F:99-122/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>
 F:123-146/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>
 F:147-170/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR4>
 F:171-194/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR5>
 F:195-218/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
 F:219-242/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
 F:243-266/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
 F:267-290/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
 F:291-314/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
 F:315-338/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
 F:339-362/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
 F:363-386/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
 F:387-410/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
 F:411-434/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
 F:435-458/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>

F:459-482/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
 F:483-506/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
 F:507-529/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
 Alignment Scores:
 Pred. No.: 3,09e-12 Length: 605
 Score: 262.00 Matches: 145
 Percent Similarity: 36.59% Conservative: 95
 Best Local Similarity: 22.10% Mismatches: 239
 Query Match: 5.06% Indels: 177
 DB: 2 Gaps: 18
 US-09-396-985b-46 (1-2951) x A41915 (1-605)
 QY 322 TGCATGATCGAAGAACTGACGAAGTCCGATGACATTCCTTCAACGAACAATA 361
 Db 60 CysSerSerArgAsnLeuThrArgLeuProAspGlyValProGlyGlyThrGlnAlaLeu 79
 QY 382 GATCTGAGCTTCAACCCCTTGAAGATCTTAAAGCTATAGCTTCCCAATTTTTCAGA 441
 Db 80 TrpLeuAspLysAsnLeuSerSerValProProAlaAlaPheGlnAsnLeuSerSer 99
 QY 442 CTTCAGTGGCTGATTTATTCAGGTGTAATGAAATGAAACAATTGAACAAGCATGGCAT 501
 Db 100 LeuGlyPheLeuAsnLeuGlnGlyGlyGlnLeuGlySerLeuGluProGlnAlaLeuLeu 119
 QY 502 GCGTTACACCAACCTCTCAACTGATCTGACAGAAACCTTACAGAGTTTTCGCCA 561
 Db 120 GlyLeuGluAsnLeuCysHisLeuHisLeuGlnArgAsnGlnLeuArgSerLeuAlaLeu 139
 QY 562 GAAATTTCTCTGACTCAACAGTTTGAACATCTGTGCTGTGAGACAAATTGGCC 621
 Db 140 GlyThrPheAlaHisThrProAlaLeuAlaSerLeuGlyLeuSerAsnAsnArgLeuSer 159
 QY 622 TCTCTAGAAAGCTTCCCTATTGACACGCTTAACCTTAAGAAACTCAATGTGGCTCAC 681
 Db 160 ArgLeuGluAsp----- 163
 QY 682 AATTTATACATTCCTGTAGTTACCTGCATATTTTCCATCTGACGAACCTAGTACAT 741
 Db 164 -----GlyLeuPheGluGlyLeuGlySerLeuTrpAsp 174
 QY 742 GTGATCTTCTTATACCTATTAATCAACATTAATCTGCAACGATTCAGTTTCTACGT 801
 Db 175 LeuAsnLeuGlyTrpAsnSerLeuAlaVal----- 184
 QY 802 GAAATCCACAGTCAATCTCTCTTAGACATGCTTGAACCCCAATTGACTTCATTCAA 861
 Db 185 -----LeuPro 186
 QY 862 GACCAAGCTTTCAGGGAATT---AGCTCATGAACTGACTTGAAGGATATTTAAT 918
 Db 187 AspAlaAlaPheArgGlyLeuGlySerLeuArgGlyLeuValAlaGlyAsn----- 204
 QY 919 AGCTCAATATTAATGAAGAACTTGCTTCAAAACCTGGCTGTTACACGTTCATCGGTG 978
 Db 204 ----- 204
 QY 979 ATCTTGGAGAAATTAAGATGAAGAAATCTGAAATTTTGAACCTCTATCATGAA 1038
 Db 205 -----ArgLeuAlaTyrLeuGlnProAlaLeuPheSer 215
 QY 1039 GGAATATGATGATGACCATTTGATGACTTACAGTTACATATACAAATGATTTTCGAT 1098
 Db 216 GlyLeuAlaGlyLeuArg-----GluLeuAspLeuSerArg 227
 QY 1099 GATATGTTGTAAGTCAATGCTTGGCGAATGTTCTGCAATGCTCTGACAGGTATCT 1158
 Db 228 Asn-AlaLeuArgAlaIleLysAlaAsnValPheValGln-----Le 241
 QY 1159 ATAAATATATCAAGAGATGTTCTTAAACATTTCAATGGAACATCTTATCATCATTTAGA 1218
 Db 241 UPProArgLeuGlnLysLeuTyrLeu-----AspArgAsn-LeuIle-----A 255

QY 283 -----AATCCGTGATAGAGTAGTTCCTAATATTACC 315
 Db GluCyeglValaglAuaenseCyProHisProcys--ArgCybAlaaspGlylLeval 306
 QY 316 TACCAATGCATGCATCAGAAATCAGCAAAAGTCCCTGATGCATTCCTTCTTCAACAAG 375
 Db -----ArgCybaArgGluLySerLeuThrSerValProValThrLeuProAspPThrThr 325
 QY 376 AACATAGATCTGACCTTCAACCCCTTGAAAGCTTAAAAAGCTATAGCTTCCAAATTTT 435
 Db -----AspValArgLeuGluGlnAsnPhelIethrGluLeuProProLySerPheSerPhe 345
 QY 326 AspValArgLeuGluGlnAsnPhelIethrGluLeuProProLySerPheSerPhe 345
 Db -----TCAGAACTTCAGTGGCTGATTTATCCAGGTGTAATGAACAATTGAAGACAGCA 495
 QY 436 TCAGAACTTCAGTGGCTGATTTATCCAGGTGTAATGAACAATTGAAGACAGCA 495
 Db -----ArgArgLeuArgArgIleAspLeuSerAsnAsnIleSerArgIleAlaHisAspAla 365
 QY 496 TGGCATGGCTTACACACCTCTCAAACTGTGATGACAGAGAAACCTATCCAGAGTTT 555
 Db -----LeuSerGlyLeuLySerGlnLeuThrThrLeuValLeuYrGlyAsnLyIleLyAspLeu 385
 QY 556 TCCCGAGGAAGTTTCTGTGACTTAACAAGTTTAGCAATCTGGGGCTGGAGACAAA 615
 Db -----ProserGlyValPheLySerGlyLeuGlySerLeuArgLeuLeuLeuAsnAlaAsnGln 405
 QY 386 ProserGlyValPheLySerGlyLeuGlySerLeuArgLeuLeuLeuAsnAlaAsnGln 405
 QY 616 TTGGCTCTCTAGAAAGCTTCCATTTGACAGCTTATACCTTAAAGAACTGAAATGTG 675
 Db -----IleSerCybIleArgLyAspAlaPheArgAspLeuHisSerLeuSerLeuSerLeu 425
 QY 676 GCTCAAAATTTTATATACATCTCTGTAAAGTACCTGATATTTTCCAACTGACACAACTA 735
 Db -----TyrAspAsnAsnIleGlnSerLeu--AlaAsnGlyThrPheAspAlaMetLySerMet 444
 QY 426 TyrAspAsnAsnIleGlnSerLeu--AlaAsnGlyThrPheAspAlaMetLySerMet 444
 QY 736 GTACATGCATCTTCTTATTAAC--TATATCAAACTATTACTGACAGCACTTA-- 789
 Db -----LysThrValHisLeuAlaIleAsnProPheIleCybAspCybAsnLeuArgTrpLeuAla 464
 QY 445 LysThrValHisLeuAlaIleAsnProPheIleCybAspCybAsnLeuArgTrpLeuAla 464
 QY 790 CAGTTTCTACGTGAAATTCACAAGTCAATCTCTTTAGACATGCTTTGAACCCAAAT 849
 Db -----AspYrLeuHisLyAsnPro-----IleGlnThrSer-GlyAlaArgCy 479
 QY 850 GACTTCATTCAGAACCAAGCTTTCAGGGAATTAAAGCTCCATGAACCTGACTTAAGAGT 909
 Db -----GlnGluLySerPheLyCy----- 500
 QY 910 AATTTAATAGCTCAAAATATATAGAAATTCGCTTCAAAACCTGGCTGTTTACAGTTC 969
 Db -----CATCGTTGATCTTGGAGAAATTAAAGATGAAGAATCTGAAATTTTGAACCTCT 1029
 QY 970 CATCGTTGATCTTGGAGAAATTAAAGATGAAGAATCTGAAATTTTGAACCTCT 1029
 Db -----SerTrpGlyLeuArgMetLy----- 508
 QY 501 -----SerTrpGlyLeuArgMetLy----- 508
 QY 1030 ATCATGGAAGACTATGTGATGTGACCATTTATGATGATTGACGTTAATATACAAATGAT 1089
 Db ----- 508
 QY 508 ----- 508
 QY 1090 TTTTCAGATGATATTGTTAAGTTCATTCCTGGGGAATG-- 1130
 Db -----LeuSer-GlyGluCybArgMetAspSerAspCyb 520
 QY 509 -----LeuSer-GlyGluCybArgMetAspSerAspCyb 520
 QY 1131 -----TTTCGAATGTCTCTGGAGGTGATCTTAAATATCTAGAAAGATGTTCTTAA 1185
 Db -----roAlaMetCybHisCybGluGlyThrThrValAspCybThrGlyArgArg----- 536
 QY 520 roAlaMetCybHisCybGluGlyThrThrValAspCybThrGlyArgArg----- 536
 QY 1186 CATTCAAAATGGCAATCTTATCAATCATTTAGATGTAACCTAAGCAGTTTCCAACTCTGG 1245
 Db -----LeuLySerGlnIleProArg--A 543
 QY 537 -----LeuLySerGlnIleProArg--A 543
 QY 1246 ATTCACCTTTCTTAAAGTTTGACTTATATAGAACAA--GGGCTTCA 1296
 Db -----543 splice--LeuHisThrThrGluLeuLeuLeuAspAsnGluLeuGlyArgIle 562
 QY 543 splice--LeuHisThrThrGluLeuLeuLeuAspAsnGluLeuGlyArgIle 562
 QY 1297 GTTTTAAAAAGTG-----GCCCTACCAAGTCTCAGCTATCTAGATCTTATAGTGAATG 1350

Db 562 -----erSerAspGlyLeuPheGlyArgLeuProHisIleuValLySerGluLeuLyArgAsn 582
 QY 1351 CACTGAGCTTTAGTGGGTGGTGTCTTATTCGATTCGATTTGGGAACAACAGCTGAGACT 1410
 Db -----Ileu-----ThrGlyIleGluProAsnAla----- 590
 QY 582 Ileu-----ThrGlyIleGluProAsnAla----- 590
 QY 1411 TAGACCTCAGCTCAATGTGTCATCATTTATGATGTCCAATTCATGGGCTCTAGAGAGC 1470
 Db ----- 591
 QY 591 ----- 591
 QY 1471 TGCAGACCTGGAATTTTTCAGCACTCTATTAAAAAGGCTCACAGATTTCTAGCGTTC 1530
 Db -----IeGlnGluLeuGlnLeuGly-GluAsnLyIleLySerGlnIleSerAsn--LysMetPhe 615
 QY 597 IeGlnGluLeuGlnLeuGly-GluAsnLyIleLySerGlnIleSerAsn--LysMetPhe 615
 QY 1531 TTATCCCTTGAAGAAAGCTACTTACCTTGACATCTCTTATCTAACCACCAAAATTAAGTTC 1590
 Db ----- 616
 QY 616 LeuGlyLeuHisGlnIleuLyThrLeuAsnLeuYrAspAsnGlnIleSerCybValMet 635
 QY 1591 GATGTATATTTCTGGCTTGACCAAGCTGTCACACATTAATAAAGCTGGCAATTTCTTC 1650
 Db -----ProGlySerPheGlnHisLeuAsnSerLeuThrSerLeuAsnLeuAlaSerAsnProPhe 655
 QY 636 ProGlySerPheGlnHisLeuAsnSerLeuThrSerLeuAsnLeuAlaSerAsnProPhe 655
 QY 1651 AAAGACACACACCTTTCAAATGTCCTTTCGAACAACAACAACATTCATTCCTGAT-- 1707
 Db -----AsnCysAsnCysHisIleuAlaTrpPheAlaGluCybValArgLybSerLeuAsnGly 675
 QY 656 AsnCysAsnCysHisIleuAlaTrpPheAlaGluCybValArgLybSerLeuAsnGly 675
 QY 1708 -----CCTTCTTAA-- 1716
 QY 676 GlyAlaAlaArgCybGlyAlaProSerLybValArgAspValGlnIleLyAspLeuPro 695
 Db ----- 1716
 QY 1716 ----- 1716
 QY 696 HisSerGluPheLybCybSerSerGluAsnSerGlnGlyCybLeuGlyAspGlyYrCyb 715
 Db ----- 1717
 QY 1717 -----TGT----- 1719
 QY 716 ProProSerCybThrCybThrGlyThrValValAlaCybSerArgAsnGlnLeuLyGln 735
 Db ----- 1720
 QY 1720 -----CAATGGAA 1728
 QY 736 IleProArgGlyIleProAlaGluThrSerGlnLeuYrLeuGlnSerAsnGlnIleGln 755
 QY 1729 CAATATCTTGGGGGATTTTGACACCTCTCATAGACTCTCAATTTATTAATAGAGCAC 1788
 Db -----GlnIleHisYrGlnArgIleArgHisLeuArgSerLeuThrArgLeuAspLeuSerAsn 775
 QY 756 GlnIleHisYrGlnArgIleArgHisLeuArgSerLeuThrArgLeuAspLeuSerAsn 775
 QY 1789 AACATCTATTTGTTTGGATTCATCCATTAATTAACAGCTGATTCCTCAGCACTCTT 1848
 Db -----AsnGlnIleThrIleLeuSerAsnYrThrPheAlaAsnLeuThrLybLeuSerThrLeu 795
 QY 776 AsnGlnIleThrIleLeuSerAsnYrThrPheAlaAsnLeuThrLybLeuSerThrLeu 795
 QY 1849 GATTGCAAGTTCAATGCATAGAG-----ACATCTAAAGAAAT-- 1887
 Db ----- 796
 QY 796 IleIleSerYrAsnLybLeuGlnCybLeuGlnArgHisAlaLeuSerGlyLeuAsnAsn 815
 QY 1888 -----CTGCAACATTTTCCA----- 1902
 Db ----- 816
 QY 816 LeuArgValAlaSerLeuHisGlyAsnArgIleSerMetLeuProGlnGlySerPheGln 835
 QY 1903 -----AAGAGTTAGCTTCTTCAATCTTACTAACAATTCGTGCTGTATATGTGAA 1956
 Db -----AspLeuLySerLeuThrHisIleAlaLeuGlySerAsnProLeuYrCybAspCybGly 855
 QY 836 AspLeuLySerLeuThrHisIleAlaLeuGlySerAsnProLeuYrCybAspCybGly 855
 QY 1957 CATCAAGAAATTCCTGCAAGTGGGTCAGCAAGAACAGACAGCTTCTTGGAATCTTGAACA 2016
 Db -----LeuLySerPheSerAspTrpIleLyb-----LeuAspYrValGluPro 870
 QY 856 LeuLySerPheSerAspTrpIleLyb-----LeuAspYrValGluPro 870
 QY 2017 -----ATGACATGTGCAACACCTGTAGAGATGATATACCTCTTAAGTGTGAAATTTAAT 2070
 Db -----871 GlyIleAlaArgCybAlaGluProGlnGlnMetLybAspLybLeuIleLeuSerThrPro 890
 QY 871 GlyIleAlaArgCybAlaGluProGlnGlnMetLybAspLybLeuIleLeuSerThrPro 890
 QY 2071 AATTTCAAC----- 2079

Db 891 SerSerSerPheValCysArgGlyValArgValArgAsnProIleLeuAlaLysCysAsnAla 910
 QY 2080 TGTATAT-----GTACAGACATCATCATGTGTGAGT-----GGT 2117
 Db 911 CysPheGlnGlnProCysGlnAsnGlnAlaGlnCysValAlaLeuProGlnArgGlyTyr 930
 QY 2118 CAGTGTGATTGT-----GGTATCAGCTGT 2141
 Db 931 GlnCysLeuCysGlnProGlyTyrHisGlyLysHisCys 943

RESULT 15

slit protein 1 precursor - fruit fly (Drosophila melanogaster)
 CDate: 30-Apr-1991 #sequence revision 30-Apr-1991 #text change 02-Aug-2002
 CAccession: A36665; A31640; S13523
 R.Rochberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
 Genes Dev. 4, 2169-2187, 1990
 A>Title: slit: an extracellular protein necessary for development of midline glia and co
 A.Reference number: A36665; MUID:9109665; PMID:2176636
 A.Accession: A36665
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 1-1480 <ROT>
 A.Cross-references: GB:X53959; NID:98614; PIDN:CAA37910.1; PID:98615
 R.Rochberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
 Cell 55, 1047-1059, 1988
 A>Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
 A.Reference number: A31640; MUID:89077533; PMID:3144436
 A.Accession: A31640
 A.Molecule type: DNA
 A.Residues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YNA', <RO2>
 A.Cross-references: GB:M23543; NID:9340939; PID:9514357
 C.Genetics:
 A.Gene: FlyBase:slit
 A.Cross-references: FlyBase:FBgn0003425
 A.Introns: 1351/3
 CSuperfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein x
 F/66-91/Domain: proteoglycan amino-terminal homology <PAH1>
 C/Keywords: alternative splicing; growth factor
 F/101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F/125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F/149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F/173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F/197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F/228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
 F/288-313/Domain: proteoglycan amino-terminal homology <PAH2>
 F/323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F/347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F/371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
 F/395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
 F/419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
 F/450-484/Domain: proteoglycan carboxyl-terminal homology <PCS2>
 F/512-557/Domain: proteoglycan amino-terminal homology <PAH3>
 F/547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
 F/572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
 F/596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
 F/620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
 F/651-685/Domain: proteoglycan carboxyl-terminal homology <PCS3>
 F/708-723/Domain: proteoglycan amino-terminal homology <PAH4>
 F/743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
 F/767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
 F/791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
 F/815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
 F/846-880/Domain: proteoglycan carboxyl-terminal homology <PCS4>
 F/1028-1061/Domain: EGF homology <EGF>
 F/1068-1099/Domain: EGF homology <EGF2>
 F/1115-1148/Domain: EGF homology <EGF1>

Alignment Scores:

Pred. No.: 5.64e-12 Length: 1480
 Score: 259.50 Matches: 183
 Percent Similarity: 32.05% Conservative: 91

Beet Local Similarity: 21.40% Mismatches: 273
 Query Match: 5.01% Indels: 309
 DB: 2 Gaps: 33
 US-09-396-985B-46 (1-2951) x A36665 (1-1480)
 QY 115 GGAGAGGAGGAGTGTCCCGAGACTGTGCGGTGACGAGTTACAGATGTCATGTTCTC 174
 Db 220 G1AAG1eA1aG1aLeuA1aArgLeuSerAsnProPheAlaCysAspCysHis---Leu 238
 QY 175 TCATGCGCTCCAGCTGGTTGACAGAAATCCAGATGATGCTCCGTGCTGCTGAGT 234
 Db 239 SerTyrLeuSerArgPheLeuArgSerAlaThrArgLeuAlaPro----- 253
 QY 235 ACTGTGATCATGAGCACTGTTCTTCCTCGCTGACACAGAGAGTTG----- 282
 Db 254 -----TyrThrArgCysGlnSerProSerGlnLeuArgGlyGlnAsn 267
 QY 282 ----- 282
 Db 268 ValAlaAspLeuHisAspGlnGluPheLysCysSerGlyLeuThrGlnHisAlaProMet 287
 QY 283 -----AATCCCTGCATAGAGAGTTCCTAATATATAC 315
 Db 288 GluCysGlyAlaGluAsnSerCysProHisProCys---ArgCysAlaAspGlyLeuAl 306
 QY 316 TACCAATGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 375
 Db 307 ---AspCysArgGlyLysSerLeuThrSerValProValThrLeuProAspAspThrThr 325
 QY 376 AACATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 435
 Db 326 AspValAlaGluGluGlnAsnPheLeuThrGluLeuProProLysSerPheSerSerhe 345
 QY 436 TCAGAACTTCAGTGGCTGATTTATCCAGGTGATGAAATGGAACATGGAAGACAGCA 495
 Db 346 ArgArgLeuArgArgGlyLeuAspLeuSerAsnAsnHisSerArgIleAlaHisAspAla 365
 QY 496 TGGATGCTTACACACACCTCTCAACTGTATGATGACAGAAACCTATTCACAGTTT 555
 Db 366 LeuSerGlyLeuLysGlnLeuThrThrLeuValLeuLysGlyAsnLysIleLysAspLeu 385
 QY 556 TCCCGAGAGATTTCTCTGACATAACAAGTTTACACATCTGGTGGTGGAGCAAA 615
 Db 386 ProSerGlyValPheLysGlyLeuGlySerLeuArgLeuLeuLeuAlaAsnGlu 405
 QY 616 TTGACCTCTCAGAAACCTCTCTATTTGACAGCTTATTAACCTTAAAGAACTCAATGTG 675
 Db 406 IleSerCysIleArgLysAspAlaPheArgAspLeuHisSerLeuSerLeuSerLeu 425
 QY 676 GCTCACAATTTATATACATTCCTGTAAAGTACCTGATATTTTCCATCTGACAGACCTA 735
 Db 426 TyrAspAsnAsnIleGlnSerLeu---AlaAsnGlyThrPheAspAlaMetLysSerMet 444
 QY 736 GTACATGTGATCTTTCTTTTAC---TATATCAACATAATTACTCAACAGACTTA--- 789
 Db 445 LysThrValHisLeuAlaLysAsnProPheIleCysAspCysAsnLeuAlaGlyTyrLeuAla 464
 QY 790 CAGTTTCTAGCGTGAATTCACAGTCAATCTCTTTAGACAGTCTTTGAAACCAATT 849
 Db 465 AspTyrLeuHisLysLysAsnPro-----IleGluThrSer-GlyAlaArgCys 479
 QY 850 GACTTCTTGAAGACCAAGCTTTCAGGGAATTAAGCTTCATGACATGACTTGAAGGT 909
 Db 479 sGluSerProLysArgMetHisArgArgArgIleGluSerLeuArg----- 494
 QY 910 AATTTTATAGCTCAATATATATATGAAATCTGCTTCAAAACCTGGCTGTATACAGTGC 969
 Db 495 -----GluGlyLysPheLysCys----- 500
 QY 970 CATCGTTGATCTTGGAGAAATTTAAAGATGAAAGAAATCTGAAATTTTGAACCTCT 1029
 Db 501 -----SerTyrGlyGluLeuArgMetLys----- 508

```

Qy 1030 ATCATGAAGGACATGATGATGACCATTTGATGATTCAGTTAACAATATACAATATGAT 1089
Db 508 -----
Qy 1090 TTTTCAGATGATATGTTTAAGTCCATTGCTGGCCGAATGT----- 1130
Db 509 -----
Qy 1131 -----TTTCGAATGTCCTGGCAGGATATCTATTAATAATCTAGAAAGATGTTCCATAA 1185
Db 520 roAlaMetCysHIScysgluGlyThrValAspCysThrGlyArgArg----- 536
Qy 1186 CATTTCAAAATGGCAATCCTTATCAATCATGATGATCAATGATGATTCAGATTTCAACTCTGG 1245
Db 537 -----LeuLysGluIleProArg---A 543
Qy 1246 ATCTACCTCTTTCTTAAAGTTTGACTTTAATCATGAACAA-----GGGTCTATCA 1296
Db 543 spIlePro--LeuHISThrThrGluLeuLeuAsnAspAsnGluLeuGlyArgIleS 562
Qy 1297 GTTTTAAAAAGTG-----GCCCTACCAAGTCTCAGCTATCTAGATCTTGTAGTAATG 1350
Db 562 eISerAspGlyLeuPheGlyValArgLeuProHISLeuValLysLeuGluLeuLysArgAsnG 582
Qy 1351 CACTGAGCTTTAGTGGTGGCTGTTCTTATCTGATTTGGGAAACAACAGCTGAGACACT 1410
Db 582 InLeu-----ThrGlyIleGluProAsnAla----- 590
Qy 1411 TAGACCTCAGCTCAATGGTGCATCATTTATGAGTGCACATTTGATGGGTCTAGAGAGC 1470
Db 591 -----PheGluGlyIleSerHIS 597
Qy 1471 TGCAGCACTGGATTTTTCAGCACTCTACTTAAAGGTCACAGAAATTCAGCGTTC 1530
Db 597 IeGluGluLeuGluLeuGly--GluAsnLysIleLysGluIleSerAsn--LysMetPhe 615
Qy 1531 TTATCCCTTGAAGAGTACTTACCTTGACATCTCTTATCTAACAACCAAAATTGACTTC 1590
Db 616 LeuGlyLeuHISGluLeuLysThrLeuAsnLeuTyrrAspAsnGluIleSerCysValMet 635
Qy 1591 GATGGTATATTTCTGGCTTGACAGCTCAACACATTTAAATAGCTGGCAATTCCTTTC 1650
Db 636 ProGlySerPheGluHISLeuAsnSerLeuThrSerLeuAsnLeuAlaSerAsnProPhe 655
Qy 1651 AAAAGCAACACCTTCAATGTCCTTGCAACACACAACTTGACATTCCTGAT--- 1707
Db 656 AsnCysAsnCysHISLeuAlaTrrPheAlaGluCysValArgLysLysSerLeuAsnGly 675
Qy 1708 -----CCTTCTPAA----- 1716
Db 676 GluAlaAlaArgCysGlyAlaProSerLysValArgAspValGlnIleLysAspLeuPro 695
Qy 1716 ----- 1716
Db 696 HISserGluPheLysCysSerSerGluAsnSerGluGlyCysLeuGlyAspGlyTyrrCys 715
Qy 1717 -----TGT----- 1719
Db 716 ProProSerCysThrCysThrGlyThrValValaLacCysSerArgAsnGlnLeuLysGlu 735
Qy 1720 -----CAATGGGA 1728
Db 736 IleProArgGlyIleProAlaGluThrSerGluLeuTyrrLeuGluSerAsnGlnIleGlu 755
Qy 1729 CAAATATCTTGGGGGATTTTGACACCTCCATAGACTTCATTTAATATATAGATCAC 1788
Db 756 GlnIleHISLysTyrrGluArgIleArgHISLeuArgSerLeuThrArgLeuAspLeuSerAsn 775
Qy 1789 AACATATCATTTGTTTGGATTCATCCATTAATAACAGCTGTATTCCTCCAGACCTCTT 1848
Db 776 AsnGlnIleThrIleLeuSerAsnTyrrThrPheAlaAsnLeuThrLysLeuSerThrLeu 795

```

```

Qy 1849 GATTGCAGTTTCAATGCAATGAG-----ACATCTAAAGGAATA----- 1887
Db 796 IleIleSerTyrrAsnLysLeuGlnCysLeuGluArgHISAlaLeuSerGlyLeuAsnAsn 815
Qy 1888 -----CTGCACATTTTCCA----- 1902
Db 816 LeuArgValaLysLeuHISGlyAsnArgIleSerMetLeuProGluGlySerPheGlu 835
Qy 1903 -----AAGAGTCAAGCTTCTTCAATCTTACTAACAATCTGTGCTGTATATGCGAA 1956
Db 836 AspLeuLysSerLeuThrHISIleAlaLeuGlySerAsnProLeuTyrrCysAspCysGly 855
Qy 1957 CATCAGAAATTCCTGACAGTGGTCAAGGAACAGAACGATTCCTGTGTAATGTTGAACA 2016
Db 856 LeuLysTrrPheSerAspTrrIleLys-----LeuAspTyrrValGluPro 870
Qy 2017 -----ATGACATGTCGAACACCTGTGAGAGATGAATACCTCTTGTAGTTGAAATTTAAT 2070
Db 871 GlyIleAlaArgCysAlaGluProGluGlnMetLysAspLysLeuIleLeuSerThrPro 890
Qy 2071 AATTCTAC----- 2079
Db 891 SerSerSerPheValCysArgGlyArgValArgAsnAspIleLeuAlaLysCysAsnAla 910
Qy 2080 TGTATAT-----GTACAGACAAATCATCACTGTGTCTCACT-----GGT 2117
Db 911 CysPheGluGlnProCysGlnAsnGlnAlaGlnCysValaLacLeuProGlnArgGluTyrr 930
Qy 2118 CAGTGTGATTTGT-----GGTATCACTGT 2141
Db 931 GlnCysLeuCysGlnProGluTyrrHISGlyLysHISLys 943

```

Search completed: March 29, 2005, 17:35:41
 Job time : 89.7375 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:30:23 ; Search time 159.482 Seconds

(without alignments)
18950.714 Million cell updates/sec

Title: US-09-396-985B-46

Perfect score: 5177
Sequence: 1 cctcctgcgaagcgaagcagat.....ccttaatcgaagagaag 2951

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+np2.model -DEV-xlh
-Q=/cgn2.1/USPTO_epool/US09396985/runat_28032005.155743.21146/app.query.fasta-1.85098
-DB=UniProt_03 -QEXT=faetan -SUFFIX=rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09396985 @CGN 1.1 5213 @runat_28032005.155743.21146 -NCPu=6 -ICPU=3
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_03:*

1: uniprot_sprot:*\n2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4283	82.7	835	1	TLR4_MOUSE
2	4264	82.4	835	2	Q8K2T5
3	3683	75.1	835	1	TLR4_RAT
4	3371.5	65.1	838	1	TLR4_CRICR
5	2792	53.9	839	1	TLR4_HUMAN
6	2792	53.9	839	1	TLR4_HUMAN
7	2791	53.9	843	1	TLR4_HORSE
8	2783	53.8	826	1	TLR4_PAPAN
9	2762.5	53.4	833	1	TLR4_FELCA
10	2753	53.2	837	2	Q8SPB8
11	2751	53.1	828	1	TLR4_PONPY
12	2737	52.9	841	1	TLR4_POVIN
13	2734	52.8	841	2	Q8SQ55
14	2732	52.8	841	2	Q6WCDS
15	2730	52.7	841	2	Q6WCDS
16	2656	51.3	841	1	TLR4_PIG

17	2573.5	49.7	839	2	Q8MIQ2	Q8miq2 oryctolagus
18	1902.5	36.7	836	2	Q8SOH3	Q8soh3 canis famli
19	1705.5	32.9	843	2	Q7ZTG5	Q7ztg5 gallus galli
20	1183	22.9	819	2	Q6TSA1	Q6tsa1 brachydanio
21	1163	22.5	817	2	Q6NV08	Q6nv08 brachydanio
22	743	14.4	258	2	Q70EX4	Q70ex4 sus scrofa
23	681	13.2	991	2	Q6R5N8	Q6r5n8 mus musculus
24	664.5	12.8	940	2	Q8T753	Q8t753 brachyosco
25	631	12.2	945	2	Q801P9	Q801p9 carassius a
26	611.5	11.8	973	2	Q6KCC7	Q6kcc7 oncorhynch
27	607.5	11.7	961	2	Q76CT9	Q76ct9 paralichthy
28	598.5	11.6	961	2	Q76CT7	Q76ct7 paralichthy
29	579.5	11.2	661	1	C180_HUMAN	Q99467 homo sapien
30	569.5	11.0	661	2	Q8C251	Q8c251 mus musculus
31	567.5	11.0	661	2	C180_MOUSE	Q62192 mus musculus
32	559	10.8	1032	1	TLR8_MOUSE	P56682 mus musculus
33	541	10.5	1041	2	Q6UX16	Q6ux16 homo sapien
34	539	10.4	1041	1	TLR8_HUMAN	Q9ntr97 homo sapien
35	531	10.3	1028	2	Q865R7	Q865r7 sus scrofa
36	530.5	10.2	661	2	Q7YRL4	Q7yrl4 sus scrofa
37	519.5	10.0	784	2	Q6YGU2	Q6ygu2 rattus norv
38	514	9.9	785	2	Q6TN21	Q6tn21 sus scrofa
39	514	9.9	785	2	Q76L24	Q76l24 sus scrofa
40	513.5	9.9	784	1	TLR2_MOUSE	Q9gun7 mus musculus
41	513	9.9	1050	1	TLR7_MOUSE	P56681 mus musculus
42	512	9.9	104	2	Q7YSE1	Q7yse1 sus scrofa
43	510.5	9.9	784	2	Q8K3D9	Q8k3d9 mus musculus
44	506.5	9.8	784	2	Q811T5	Q811t5 mus musculus
45	506	9.8	1049	1	TLR7_HUMAN	Q9nyk1 homo sapien

ALIGNMENTS

RESULT 1
ID TLR4_MOUSE STANDARD; Q92203; PRT; 835 AA.
AC Q90UK6; Q9D691; Q9Q2F5; Q9Z203;
AD 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-1-like receptor 4 precursor.
GN Name=TLR4; Synonyms=Lps;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ;
RX MEDLINE=99187984; PubMed=10087992; DOI=10.1006/bcmd.1998.0201;
RA Poltorak A., Smirnova I., He X., Liu M.-Y., Van Huffel C., Chan E.K.L.,
RA Birdwell D., Alejos E., Silva M., Du X., Thompson P., Chan E.K.L.,
RA Ledesma J., Roe B., Clifton S., Vogel S.N., Beutler B.,
RT "Genetic and physical mapping of the Lps locus: identification of the
RT Toll-4 receptor as a candidate gene in the critical region.";
RL Blood Cells Mol. Dis. 24:340-355(1998).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT LPS-TOLERANT HIS-712.
RC STRAIN=C3H/HeJ;
RX MEDLINE=99069627; PubMed=9851930; DOI=10.1126/science.282.5396.2085;
RA Poltorak A., He X., Smirnova I., Liu M.-Y., Van Huffel C., Du X.,
RA Birdwell D., Alejos E., Silva M., Galanos C., Freudenberg M.,
RA Ricciardi-Castagnoli P., Layton B., Beutler B.,
RT "Defective LPS signaling in C3H/HeJ and C57BL/10ScCr mice: mutations
RT in Tlr4 gene.";
RL Science 282:2085-2088(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT LPS-TOLERANT HIS-712.
RC STRAIN=C57BL/6J;
RX MEDLINE=99145502; PubMed=9989976;
RA Qureshi S.T., Lathiviere L., Leveque G., Clermont S., Moore K.J.,
RA Gros P., Malo D.,
RT "Endotoxin-tolerant mice have mutations in Toll-like receptor 4

RT (TIR4).";

RL J. Exp. Med. 189:615-625(1999).

RL [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Macrophage;

RX MEDLINE=20014145; PubMed=10548109; DOI=10.1038/44605;

RA Underhill D.M., Ozinsky A., Hajjar A.M., Stevens A., Wilson C.B.,

RA Baerentzen M., Ademar A.;

RT "The Toll-like receptor 2 is recruited to macrophage phagosomes and

RT discriminates between pathogens.";

RL Nature 401:811-815(1999).

RL [5]

RP SEQUENCE FROM N.A., AND VARIANTS ASN-94; ILE-209; GLY-219; ILE-254;

RP ILE-423; SER-477; ALA-516; ASP-593; ILE-600; VAL-607; ILE-637; HIS-761

RP AND IYS-811.

RC STRAIN=Various strains;

RX MEDLINE=20558910; PubMed=11104518;

RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;

RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4

RT locus (TLR4).";

RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).

RL [6]

RP SEQUENCE OF 1-154 FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nishikido I., Otsu N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackebush J.,

RA Schirral L.M., Kanapin A., Matuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Busic V., Chochia C., Corbani L.E., Cousins S.,

RA Dalla E.A., Dregan T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaesteland T., Gariboldi M., Giasi C., Godzik A., Gough J.,

RA Grimmond S., Gustinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.W., King B.L.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lehnart B., Lyons P.A.,

RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pettea G., Pesole G.,

RA Petrovsky N., Pilla J., Pontius J.U., Qi D., Ramchandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sadelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carrincci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RL [7]

RP FUNCTION.

RX MEDLINE=20507837; PubMed=10952994; DOI=10.1074/jbc.M007386200;

RP Rhue S.H., Hwang D.;

RT "Murine Toll-like receptor 4 confers lipopolysaccharide responsiveness

RT as determined by activation of NF kappa B and expression of the

RT inducible cyclooxygenase.";

RL J. Biol. Chem. 275:34035-34040(2000).

RL [8]

RP FUNCTION: Cooperates with LY96 and CD14 to mediate the innate

RP immune response to bacterial lipopolysaccharide (LPS). Acts via

RP MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine

RP secretion and the inflammatory response (By similarity).

CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a

CC multi-protein complex containing at least CD14, LY96 and TIR4.

CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via

CC their respective TIR domains.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -1- TISSUE SPECIFICITY: Highly expressed in heart, spleen, lung and

CC muscle. Lower levels are found in liver and kidney.

CC -1- POLYMORPHISM: Interstrain analysis reveals that TLR4 is a

CC polymorphic protein and that the extracellular domain is far more

CC variable than the cytoplasmic domain, which is variable at the C-

CC terminal.

CC -1- DISEASE: The protein is encoded by the Lps locus, an important

CC susceptibility locus, influencing the propensity to develop a

CC disseminated Gram-negative infection.

CC -1- SIMILARITY: Belongs to the Toll-like receptor family.

CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.

CC -1- SIMILARITY: Contains 1 TIR domain.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>

CC or send an email to license@1sb-sib.ch).

CC -----

DR EMBL: AF095353; AAC9411.1; -;

DR EMBL: AF185285; AAF04278.1; -;

DR EMBL: AF110133; AAD29272.1; -;

DR EMBL: AF177767; AAF05317.1; -;

DR EMBL: AK014533; -; NOT_ANNOTATED_CDS.

DR HSSP: Q15399; 1FVY.

DR MGP: MGI.96824; TLR4.

DR GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.

DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.

DR GO: GO:0004888; F:transmembrane receptor activity; ISS.

DR GO: GO:0007250; P:activation of NF-kappaB-inducing kinase; NAS.

DR GO: GO:0016046; P:detection of fungi; ISS.

DR GO: GO:0009598; P:detection of pathogenic bacteria; ISS.

DR GO: GO:0042116; P:macrophage activation; ISS.

DR GO: GO:0045576; P:mast cell activation; NAS.

DR GO: GO:0045671; P:negative regulation of osteoclast different. . .; ISS.

DR GO: GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; NAS.

DR GO: GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.

DR GO: GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; NAS.

DR GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; NAS.

DR GO: GO:0042088; P:T-helper 1 type immune response; ISS.

DR InterPro: IPR001611; LRR.

DR InterPro: IPR000483; LRR_Cterm.

DR InterPro: IPR00157; TIR.

DR Pfam: PF00560; LRR; 10.

DR Pfam: PF00582; TIR; 1.

DR PRINTS: PR00019; LEURICRPT.

DR SMART: SM00082; LRRCT; 1.

DR SMART: SM00255; TIR; 1.

DR PROSITE: PS50104; TIR; 1.

KW Disease mutation; Glycoprotein; Immune response;

KW Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;

KW Repeat; Signal; Transmembrane

FT SIGNAL 1 25 Potential.

FT CHAIN 26 835 Toll-like receptor 4.

FT DOMAIN 26 638 Extracellular (Potential).

FT TRANSMEM 639 659 Potential.

FT DOMAIN 660 835 Cytoplasmic (Potential).

FT REPEAT 29 52 LRR 1.

FT REPEAT 53 75 LRR 2.

FT REPEAT 76 99 LRR 3.

FT REPEAT 100 123 LRR 4.

FT REPEAT 127 148 LRR 5.

FT REPEAT 149 172 LRR 6.

FT REPEAT 173 196 LRR 7.

FT REPEAT 201 224 LRR 8.

FT REPEAT 227 251 LRR 9.

FT REPEAT 305 330 LRR 10.

FT REPEAT 348 370 LRR 11.

FT REPEAT 371 393 LRR 12.

FT REPEAT 396 419 LRR 13.

FT REPEAT 420 443 LRR 14.

FT REPEAT 468 492 LRR 15.

FT REPEAT 494 516 LRR 16.

FT REPEAT 517 540 LRR 17.
 FT REPEAT 542 563 LRR 18.
 FT REPEAT 565 589 LRR 19.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 34 34 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 75 75 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 172 172 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 204 204 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 237 237 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 307 307 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 492 492 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 524 524 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 572 572 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 613 613 N-linked (GlcNAc . . .) (Potential).

Alignment Scores:
 Pred. No.: 0 Length: 835
 Score: 4283.00 Matches: 831
 Percent Similarity: 99.52% Conservative: 1
 Best Local Similarity: 99.40% Mismatches: 3
 Query Match: 82.73% Indels: 2
 DB: 1 Gaps: 0

US-09-396-985b-46 (1-2951) x TLR4_MOUSE (1-835)

QY 208 ATGATGCTCCCTGGCTCCCTGCTAGACCTGATCATGAGCATGTTCTTCTGCTGCTG 267
 Db 1 MetheProProthProleuLeuAlaArgThreuleMetAlaLeuPheSerCysLeu 20
 QY 268 ACACCAAGAACTGTAATCCCTGCTAGAGGTAGTCTTAATATTACTTACCAATGACATG 327
 Db 21 ThrProIlySerLeuAenProCysIleGluValValProAenIleThrTyGlnCysMet 40
 QY 328 GATCAGAACTCAGCAAAAGTCCCTGATGACATTCCTTCTTCAACCAAGACATGATCTG 387
 Db 41 AspIlnIlySerLeuSerValProAspAspIleProSerSerThrIlyAsnIleAspLeu 60
 QY 388 AGCTTCAACCCCTTGAAGATCTTAAAGCTATAGCTTCTTCATTTTTCAGAACTTCAG 447
 Db 61 SerPheAsnProleuIlyIleLeuIlySerTySerPheSerAenPheSerGluLeuGln 80
 QY 448 TGCGTGATTTATCAGAGTGTGAATGAATGAACATTTGAAGCAAGGACATGGCATGGCTTA 507
 Db 81 TrpLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspIlySalatrpHisGlyLeu 100
 QY 508 CACCACTCTCAACTGATTACTGACAGAAACCTATCCAGAGTTTTCGCCAGAGAT 567
 Db 101 HisHisLeuSerAenLeuIleLeuThrGlyAsnProIleGlnSerPheSerProGlySer 120
 QY 568 TTCTCTGGACTACAGATTAGACATCTGGTGGCTGGAGACAAATTGGCTCTCTTA 627
 Db 121 PheSerIlyLeuThrSerLeuGluAsnLeuValAlaValGluThrIlySleuAlaSerLeu 140
 QY 628 GAAAGCTTCCTTATGACAGCTTATACCTTAAAGAACTCAATGGGCTCCCAATTTT 687
 Db 141 GluSerPheProIleGlyGlnLeuIleThrLeuIlySlyLeuAenValAlaHisAsnPhe 160
 QY 688 ATACATTCCTGTAGTTACCTGATATTTTTCANCTGACGAACCTAGTACATGTGGAT 747
 Db 161 IleHisSerCysIlyLeuProIleTyPheSerAsnLeuThrAsnLeuValHisValAsp 180
 QY 748 CTTTCTTATATATATTAATCAACTATAGTGTCAAGCATTAAGTTTCTTACGTGAAT 807
 Db 181 LeuSerTyAsnTyIleGlnThrIleThrValAsnAspLeuGlnPheLeuArgGluAsn 200
 QY 808 CCAAGATGATCTCTTATAGACATGCTTTGAACCAATTTGATCTTATTAAGACCA 867
 Db 201 ProGlnAlaAsnLeuSerLeuAspMetSerLeuAsnProIleAspPheIleGlnAspGln 220
 QY 868 GCCTTTCAGGGAATTAAGTTCATGAACTGATCTTAAGAGTAAATTTTAATAGCTCAAT 927

Db 221 AlaPheGlnGlyIlyLeuSleuHisGluLeuThrLeuArgIlyAsnPheAsnSerSerAsn 240
 QY 928 ATATAGAAACCTGCTTCAAAACCTGGCTGTTTATACCTGCATCGGCTTATGTTGGGA 987
 Db 241 IleMetTySerTySlyLeuGlnAenLeuAlaGlyLeuHisValHisArgLeuIleLeuGly 260
 QY 988 GAATTTAAAGATGAAAGAACTGGAATTTTGAACCCCTCATCATGAAAGACTATGT 1047
 Db 261 GluPheIlyAspGluAsnLeuGlnIlePheGluProSerIleMetGluGlyLeuCys 280
 QY 1048 GATGTGACCAATGATGAGTTCAAGTTTAACATATACAAATGATTTTTCAGATGATTTGTT 1107
 Db 281 AspValThrIleAspGluPheArgLeuThrTyThrAsnAspPheSerAspIleVal 300
 QY 1108 AAGTTCATGCTTGGGGAATGTTTCTGCAATGCTTCTGGCAGGTGATATATTAATAT 1167
 Db 301 LysPheHisCysSlyLeuAlaAenValSerAlaMetSerLeuAlaGlyValSerIleTySer 320
 QY 1168 CTAGAAAGATGCTTCTTAAACATTTCAAAATGGCAATCCTTATCAATCATTAAGATCAACT- 1226
 Db 321 LeuGlnAspValAlProIlyHisPheIlySerTyGlnSerLeuSerIleIleArgCysGlnLeu 340
 QY 1227 AAGCAGTTTCCAACTGTGATCTACCTTTCTTAAAGTTGACTTTAACTATGACAA 1286
 Db 341 LysGlnPheProThrLeuAspLeuProPheLeuIlySerLeuThrLeuThrMetAsnIly 360
 QY 1287 GGGTCTATCACTTTTAAAGAGGCGCTTCCAAAGTCTCAGCTATCTAGATCTTATGATGA 1346
 Db 361 GlySerIleSerPheIlySlyValAlaLeuProSerLeuSerTyIlyLeuAspLeuSerArg 380
 QY 1347 AATGCACTGAGCTTTAGTGTGCTGTTCTTATTTCTGATTTTGGAGCAACAAACAGCTGAG 1406
 Db 381 AsnAlaLeuSerPheSerArgIlyCysTySerTySerAspLeuIlyThrAsnSerLeuArg 400
 QY 1407 CACTTACAGCTCAGCTTCAATGGTGCATCATTAATGATGCCAATTTGATGGCTAGAA 1466
 Db 401 HisLeuAspLeuSerPheAsnGlyAlaIleIleMetSerAlaAsnPheMetGlyLeuGln 420
 QY 1467 GAGCTGACAGCACTGATTTTTCAGACCTTACTTTAAAGGGTCAACAGATTTCTCAGC 1526
 Db 421 GluLeuGlnHisLeuAsp-PheGlnHisSerThrLeuIlyArgValThrGluPheSerAl 440
 QY 1527 GTCTTATCCCTTGAAGGCTTACTTACCTTGAATCTTCTTATACCTTAAACCAAAATTTGA 1586
 Db 440 AsnLeuSerLeuGlnIlySlyLeuLeuTyIlyLeuAspIleSerTyThrAsnThrIlySleAs 460
 QY 1587 CTTGATGTATATTTCTTGGCTTGAACAGCTTCAACACATTAATAATGGCTGGCAATTC 1646
 Db 460 PheAspGlyIlePheLeuGlyLeuThrSerLeuAenThrLeuIlyMetAlaGlyAsnSe 480
 QY 1647 TTTCAAGACACACACCTTCAAAATGCTTTTGCAACACAACTTGACATTTCTGGA 1706
 Db 480 rPheIlyAspAsnThrLeuSerAsnValPheAlaAsnThrThrAsnLeuThrPheLeuAs 500
 QY 1707 TCCTTCAAAATGTCAATTTGGAACAAATATTTGGGGGGATTGGAACACCTGCATAGACT 1766
 Db 500 PheuserTySlyGlnLeuGlnIleGlnIleSerTrpGlyValAlaPheAspThrLeuHisArg 520
 QY 1767 TCAATTTAATATATGATGACAAACATCATATTGTTTGGATGATCCCATTAATACCA 1826
 Db 520 uGlnLeuLeuAsnMetSerHisAsnAsnLeuLeuPheLeuAspSerSerHisTyArgAsnG 540
 QY 1827 GCTGTATTCCTTCAAGCACTTGTATTTGACATTCGATAGACATCTTAAGGAAT 1886
 Db 540 nLeuTySerLeuSerThrLeuAspCysSerPheAsnArgIleGluThrSerIlyGlyI 560
 QY 1887 ACTGCAACATTTTCCAAAGAGTGTAGCTTCTTCAATCTTACCAATCTGTGCTG 1946
 Db 560 eIleuGlnHisPheProIlySerLeuAlaPhePheAsnLeuThrAsnAsnSerValAlaCys 580
 QY 1947 TATATGTGAACATCAGAAATTCCTGCAAGTGGGTCAAGGAACAGACAGTTCTTGGTGA 2006
 Db 580 sIleCysGlnHisGlnIlyPheLeuGlnTrpValIlyGlnGlnIlyGlnPheLeuValAs 600

Oy		2007	IGTTGAACAATGACATGTGGACAACCCCTGTAGAGA TGAATACCTCCTTAGTGGATT	2068
Db		600	nvaIgluInmetcNrysalattnrPrvvalGlueetnsnhtSerleuValleaBph	620
Oy		2067	TAAATAATCTPACTGTGTATATGTCANACACATCATCAGTGCTGCAGGTCACTGTGAT	2126
Db		620	easnhbsnerhrcysrlymeclryllyThnllelseerValseervalValserValI	640
Oy		2127	TGTGTATATCCACTGTAGCATTTCTGATADACCACTTCTAATTTTCACTGTATCTTAATGC	2186
Db		640	evalValserhnrValalaphneullelryrhIspherhPhenhsleulleulleal	660
Oy		2187	TGGCGTGTAAAAGTACACGACGAGGAGAAAGCATCATGATCCATTGTGATCTCTCGAG	2246
Db		660	aGIYcsylsyshsrlySerArsglgJlnserllelryrsplabPevalIIeIrySerSe	680
Oy		2247	TCAGATGAGGACTGGGTGAGAAATAGACTGGTAAAGAAATTAGAGAGAGAGGCCCG	2306
Db		680	rGlmsndlnubprtpValArGaengJluDeuVallysmsneuGlugllyValProAr	700
Oy		2307	CTTTCACTCTGCGCTTCACTACAGAGACTTATTTCTGGTGTAGCCATTTGCTGCCAACAT	2366
Db		700	gphenlsleucysleuhlstryArGsApheIlpeoolValalatlalaaIasnll	720
Oy		2367	CATCCAGAGAGGCTTCCACAAGAGCGGAGAGTTATGTGGTAGTGTAGACCTTAT	2426
Db		720	eIlleglnuqllyphenlslysserArsllyValIIelvalValalsesrAghlsapheIl	740
Oy		2427	TCAGAGCCGTTGGTGTATCTTTGAAATATAGATTGCTTCAAACATGCGAGTTTCTGAGCAG	2486
Db		740	eGlaserArgrtprCyrllepheglutryGlnllelaelnhrtrpglnPhleuseerSe	760
Oy		2487	CCGCTCTGGCATCATCTTCAATTTGTCTTGAGAAAGGTGAGAAATGCTGCTGAGGCACGA	2546
Db		760	rArserstlyllellepheilleValleugJluylsValGlulysserleueurArsglngl	780
Oy		2547	GGTGGAATTGTATGCGCTTCTTAGCAGAAACACCTACCTGGAAATGGGAGAGCAATCCCT	2606
Db		780	nValgluLeutyrrArgleuleuseerArghsnthrTyrlenuqlutrpgluabpahnProIe	800
Oy		2607	GGGAGGACACATCTTCTGAGAGACCTTAAAAATGCCCCATTGTGATGGAGAAAGCCTCGAA	2666
Db		800	uGlYArghstllepheNrprArGArgleuLyAsnblaleuueuBpglyslaserAs	820
Oy		2667	TTCCTGAGAGAAACAGACAGAGAGAAACAAGAAACGGCACCTTGAGACC	2712
Db		820	nProgluInthrAlagluInguInguInguInguInthrAlathrtyPrthr	835
RESULT 2				
O8K2T5 PRELIMINARY; PRT; 835 AA.				
ID	O8K2T5			
AC	O8K2T5			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Toil-like receptor 4.			
GN	Name=tlr4;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CZCH II; TISSUE=Mammary tumor;			
RX	MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Klausner R.D., Collins F.S., Wagner L., Shennem C.M., Schuler G.D.,			
RA	Aleschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,			
RA	Ditchenko L., Marustina K., Farmer A.A., Rudin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavini T.P., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Yoshimi S., Carlinici P., Prange C.,			

RA	Bohak S.A.,	Loggellano N.A.,	Peters G.J.,	Abrahamson R.D.,	Mullaly S.J.,
RA	Richard S.A.,	McEwan P.J.,	McEwan K.J.,	Malek J.A.,	Gunaratne P.H.,
RA	Richard S.,	Worley K.C.,	Hale S.,	Garcia A.M.,	Gay L.J.,
RA	Villalón D.R.,	Muzny D.M.,	Sodergren B.J.,	Lu X.,	Gibbs R.A.,
RA	Faley J.,	Helton E.,	Ketteman M.,	Madan A.,	Rodrigues S.,
RA	Whiting M.,	Madan A.,	Young A.C.,	Shevchenko Y.,	Bouffard G.G.,
RA	Blakeley R.W.,	Touchman J.W.,	Green E.D.,	Dickson M.C.,	
RA	Rodriguez A.C.,	Grimwood J.,	Schmutz J.,	Wiers R.M.,	Butterfield Y.S.,
RA	Krzywinski M.I.,	Skalska U.,	Smalins D.E.,	Schmerch A.,	Schein J.E.,
RA	Jones S.J.,	Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human				
RT	and mouse cDNA sequences."				
RT	Proc. Natl. Acad. Sci. U.S.A.	99:16899-16903	(2002).		
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C2CH II; TISSUE=Mammary tumor;				
RA	Strausberg R.;				
RL	Submitted (MAY-2002) to the EMBL/genbank/DBJ databases.				
DR	EMBL; BC029856; AAR29856.1; -.				
DR	HSSP; 060603; 1077.				
DR	MGD; MGI:96824; TIR4.				
DR	GO; GO:0005615; C:extracellular space; TAS.				
DR	GO; GO:0016021; C:integral to membrane; TAS.				
DR	GO; GO:0004872; F:receptor activity; IDA.				
DR	GO; GO:0007249; P-1-kappaB kinase/NF-kappaB cascade; IDA.				
DR	InterPro; IPRO00863; P-Toll signaling pathway; IDA.				
DR	InterPro; IPRO00887; Aldlase_KDPG_KHG.				
DR	InterPro; IPRO01611; LRR.				
DR	InterPro; IPRO00483; LRR_Cterm.				
DR	InterPro; IPRO00157; TIR.				
DR	Pfam; PF00560; LRR_1; 10.				
DR	Pfam; PF01582; TIR_1.				
DR	PRINTS; PRO0019; LEURCHRP.				
DR	SMART; SM00082; LRCT; 1.				
DR	SMART; SM00255; TIR; 1.				
DR	PROSITE; PS00159; ALDOLASE_KDPG_KHG_1; UNKNOWN_1.				
DR	PROSITE; PSS0104; TIR; 1.				
KW	Receptor.				
SC	SEQUENCE 835 AA; 95488 MW; A103C3997A59CF5B CRC64;				
Alignment Scores:					
	Pred. No.:	0	Length:	835	
	Score:	4264.00	Matches:	826	
	Percent Similarity:	99.40%	Conservative:	5	
	Best Local Similarity:	98.80%	Mismatches:	4	
	Query Match:	82.36%	Indels:	2	
	DB:	2	Gaps:	0	
US-09-396-985B-46 (1-2951) x Q8K2T5 (1-835)					
QY	208	ATGATGCTCCCTGAGCTCTGCTGCTAGCACTGATCATGAGCACTGTTCTTCTCTGCTG	267		
DB	1	MeMetProProtrIrpneuunlarhgrhIreunleleMetalaleuphneserCyIeu	20		
QY	268	ACAACGAGAACTTGATGATCCCTGCAATGAGGTAGTCTCTTAATATTACCTACCAATGATG	327		
DB	21	ThiProglYserIeuunProCyIleIleIuValAlProaenillethnTYrgInCymec	40		
QY	328	GATCAGAACTCAGCAAACTCCCTGATGATCATCTCTTTTAAACAGAAATAGATCTG	387		
DB	41	AspGlnIlyserIeuSerIyValAlProaspapIleProSerSerThrIlyAsnIleAspIeu	60		
QY	388	AGCTCAACCCCTTGAAAGATCTTAAAGACATATGACTCTCTCCATATTTTTCAGACTTCAG	447		
DB	61	SerPheasnProIeuunIlyIleuunIySerIySerPheSerIasnPheSerGluIeuGln	80		
QY	448	TGGCTGGATTATTCAGGTGTGAAATGAAACAATATGAGCAAGCATGGCATGGCTTA	507		
DB	81	TripleunspIeuSerIyrgIsegluIleIguIhnrIleIguIaSerlySAIatPrhIseGlyIeu	1000		
QY	508	CACCACTCTCAAACTTGATGATCAGACGAAACCTTATCCAGAGTTTTCACGAGAACT	567		
DB	101	HishIleuSerIasnIleuIleuThrIrgIlyasnProIleGlnSerPheSerProIySer	120		

QY 568 TTCTGTGACATAACAAGTTTAGACATCTGGTGGCTGAGAGACAAATTTGGCCTCTTA 627
 Db PheSerGlyLeuThrSerLeuGlnSerValAlaValGlnThrLyLeuAlaSerLeu 140
 QY 628 GAAAGCTTCCCTTATTTGACAGCTTAAACCTTAAAGAAATTCATGTGGCTCACAAATTT 687
 Db GluSerPheProIleGlyGlnLeuIleThrLeuLySLeuAsnValAlaHisAsn 160
 QY 688 ATACATTCCTGTAGTTACCTGCATATTTTCCATCTGACGAACCTTGTCATGCTGAT 747
 Db IleHisSerCysLySLeuProAlaTrpPheSerAsnLeuThrAsnLeuValHisValAsp 180
 QY 748 CTTTCTTATTAATCTATATCAACTATTAATCTGCAACGATTAAGTTCTACGTGAAT 807
 Db LeuSerTrpAsnTrpIleGlnThrIleThrValAsnAspLeuGlnPheLeuArgGlnSer 200
 QY 808 CCACAGTCAATCTCTCTTGAACATGTCTTTGAAACCAATGATTCATTCAGAACCA 867
 Db ProGlnValAsnLeuSerLeuAspIleSerLeuAsnProIleAspPheIleGlnAspGln 220
 QY 868 GCCTTTGAGGAAATTAAGCTCCAGTAAGTGAATCTTAAGAGTAATTTTAAATAGTCAAT 927
 Db AlaPheGlnGlyIleLySLeuHisGlnLeuThrLeuArgGlyAsnPheAsnSerSerAsn 240
 QY 928 ATATGAAAACTTGCTTCAAAACCTGGCTGTTTACAGTCCATCGGTGATCTGGGA 987
 Db IleLeuLySThrCysLeuGlnAsnLeuAlaGlyLeuHisValHisAspGlnIleLeuLy 260
 QY 988 GAATTTAAAGATGAAGGAATCTGAAATTTTGAACCTCTATCATGGAAGACTATGT 1047
 Db GluPheLySAspGluArgAsnLeuGlnIlePheGluProSerIleMetGlnGlyLeuCys 280
 QY 1048 GATGTGACATTTGATGAGTTCAAGTTAACATATACAAATGATTTTTCAGATGATTTGT 1107
 Db AspValThrIleAspGlnPheArgLeuThrHisThrAsnAspPheSerAspAspIleVal 300
 QY 1108 AAGTTCATGCTTGGCGAATGTTTCTGCAATGTCTCGGAGGTTGATCTATTAATAT 1167
 Db LysPheHisCysLeuAlaAsnValSerAlaMetSerLeuAlaGlyValSerIleLySThr 320
 QY 1168 CTAGAAGATGTTCTTAAACATTTCAATGAGCAATCTTATCATGATAGTCAACT- 1226
 Db LeuGlnAspValProLySHisPheLySThrPheGlnSerLeuSerIleIleArgCysGlnLeu 340
 QY 1227 AAGCAGTTTCCAACTCTGAGATCTACCTTTCTTAAAGTTTGACTTTAATGATGAACA 1286
 Db LysGlnPheProThrLeuAspLeuProPheLeuLySLeuThrIleThrMetAsnLyS 360
 QY 1287 GGGCTATCAAGTTTAAAGATGGGCCCTACCAAGTCTCAGCTATCTAGATCTTAGTA 1346
 Db GlySerIleSerPheLySValAlaLeuProSerLeuSerTrpLyLeuAspLeuSerTrp 380
 QY 1347 AATCAGCTGAGCTTATGAGTGGCTGTCTTATTTCTGATTTGGGAACAAACAGCCTGGA 1406
 Db AsnAlaLeuSerPheSerGlyCysCysSerTrpSerAspLeuGlyThrAsnSerLeuArg 400
 QY 1407 CACTTAAGCTCAGCTTCAATGATGTCATCATTAATGATGTCGAATTTGATGGTCTAGAA 1466
 Db HisLeuAspLeuSerPheAsnGlyAlaIleIleMetSerAlaAsnPheMetGlyLeuGln 420
 QY 1467 GAGGTGAGAGACCTGGAGTTTTCAGCACTCACTTTTAAAGGCTCACGAATTTCTCAGC 1526
 Db GlnLeuGlnHisLeuAsp-PheGlnHisSerThrLeuLySArgValThrGlnPheSerAla 440
 QY 1527 GTTCTTATCCCTTAAAAAGTACTTTTACCTTGACATCTTATTAATAACCAAAATTTGA 1586
 Db APhLeuSerLeuGlnLySLeuLeuTrpLeuAspIleSerTrpThrAsnThrLySLeuAs 460
 QY 1587 CTTGATGATATATTTCTTGCTTGACCAAGTCTCAACACATTAATAATGCTGGCAATTC 1646
 Db pPheAspGlyIlePheLeuGlnLyLeuThrSerLeuAsnThrLeuLySMetAlaGlyAsnSe 480

QY 1647 TTTCAGAGACACACCCCTTTCAAATGCTTTTGCAACACAAACAACTTGACATTCCTGGA 1706
 Db rPheLySAspAsnThrLeuSerAsnValPheAlaAsnThrThrAsnLeuThrPheLeuAs 500
 QY 1707 TCTTCTTAATGTCAATTTGAAACAAATATCTTGGGGGGTATTTGACACCTTCATGACT 1766
 Db pLeuSerLySLeuGlnLeuGlnGlnIleSerTrpGlyValPheAspThrLeuHisAspGly 520
 QY 1767 TCAATTTATTAATATGAGTCAACAAATCTATGTTTTTGGATTCATCCCATTTAACA 1826
 Db uGlnLeuLeuAsnMetSerHisAsnAsnLeuLeuPheLeuAspSerSerHisTrpAspGly 540
 QY 1827 GCTGTATTTCCCTCAGCACTCTTGATTCAGTTTCATTCGATAGACATCTTAAGGAAT 1886
 Db nLeuTrpSerLeuSerThrLeuAspCysSerPheAsnArgIleGlnThrSerLySLeuIle 560
 QY 1887 ACTGCAACATTTTCCAAAGAGTCTAGCCTTCTTCAATCTTAATACTAACATTTCTGTGCTTG 1946
 Db eLeuGlnHisPheProLySLeuAlaPhePheAsnLeuThrAsnAsnSerValAlaCys 580
 QY 1947 TATATGGAACATCAGAAATTCCTGCACTGGGTCAAGAACAGAAAGCACTTGCTGAA 2006
 Db sIleCysGlnHisGlnLySLeuGlnThrValLySAspGlnLySLeuPheLeuValAs 600
 QY 2007 TGTTGAACAAATGACATGTGCAACACCTGTAGAGATGAATPACTCTTAGGTGATTT 2066
 Db nValGlnGlnMetThrCysAlaThrProValGlnMetAsnThrSerLeuValLeuAspPh 620
 QY 2067 TAATTAATCTAACCTGTATATGTAACAAGACATCATGATGTCAAGTGTGAT 2126
 Db eAsnAsnSerThrCysTrpMetTrpLySThrIleIleSerValSerValIleSerValIle 640
 QY 2127 TGTGTATCCACTGATGACATTTCTGATATACACTTCTATTTTACCTGATACCTTATTCG 2186
 Db eValValSerThrValAlaPheLeuIleTrpHisPheTrpPheHisLeuIleLeuIleAl 660
 QY 2187 TGCGTGTAAAAAGTACAGCAGAGAGAGAAAGCATCTAGATGATCTGACTCGAG 2246
 Db aGlyCysLySLeuSerTrpSerArgLySLeuSerIleTrpHisPheAlaPheValIleTrpSerSe 680
 QY 2247 TCAGAAATGAGACTGGGTGAGAAATGAGCTGTGTAAGAAATTTAGAAAGAGAGTCCCG 2306
 Db rGlnAsnGlnAspTrpValArgAsnGlnLeuValLySAsnLeuGlnGlyValProArg 700
 QY 2307 CTTTCACTCTGCTTCACTACACAGACTTTATCTCGGTGTACCACTGTGTGCCAAT 2366
 Db gPheHisLeuCysLeuHisTrpArgAspPheIleProGlyValAlaIleAlaAsnIle 720
 QY 2367 CATCCAGAAAGGCTTCACAAAGACCGGAAGGTATGTTGGTAGTGTACACTTAT 2426
 Db eIleGlnGlnGlyPheHisLySLeuSerArgLySValIleValValValSerArgHisPheIle 740
 QY 2427 TCAGAGCGTGTGTATCTTTGAATATGAGATTTGCTCAAAACATGAGCATTTCTGACAG 2486
 Db eGlnSerArgTrpCysIlePheGlnLySLeuIleAlaGlnThrTrpGlnPheLeuSerSe 760
 QY 2487 CCGCTCTGCAATCATCTTCAATGTCTTGAAGAGTTGAGAAAGTCCCTGCTGAGGCGCA 2546
 Db rArgSerGlyIleIlePheIleValLeuGlnLySValGlnLySLeuSerLeuAspGlnGly 780
 QY 2547 GGTGGAATGTAATGCGCTTCTTGAAGAAACACTCCTGGAATGGAGAGCAATCTCCT 2606
 Db nValGlnLeuTrpArgLeuLeuSerArgAsnThrTrpLeuGlnTrpGlnAspAsnProLe 800
 QY 2607 GGGAGGACACATCTTCTGAGAGAACTTAAAAATGCCCTATTTGATGAGAAAGCCTGGA 2666
 Db uGlyArgHisIleIlePheTrpArgArgLeuLySValAlaLeuLeuAspGlyLySAlaSerAs 820
 QY 2667 TCTTGAGCAACACAGCAGAGAGAAACAAGAAACGCACTTGACCC 2712
 Db nProGlnGlnThrAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 835

RESULT 3

TLR4_RAT	ID	TIR4_RAT	STANDARD:	PRT:	835 AA.
AC		O9QX05			
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DE	Toll-like receptor 4 precursor (Toll14).				
GN	Name=Tlr4,				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_Taxid=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Sprague-Dawley; TISSUE=Heart;				
RA	MEDLINE=99362487; PubMed=10430608;				
RA	Frantz S., Kobzik L., Kim Y.-D., Fukazawa R., Medzhitov R., Lee R.T.,				
RA	Kelly R.A.;				
RT	"Toll14 (TLR4) expression in cardiac myocytes in normal and failing				
RT	myocardium.";				
RL	J. Clin. Invest. 104:271-280(1999).				
CC	-1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate				
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via				
CC	MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine				
CC	secretion and the inflammatory response (By similarity).				
CC	-1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a				
CC	multi-protein complex containing at least CD14, LY96 and TLR4.				
CC	Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via				
CC	their respective TIR domains (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).				
CC	-1- SIMILARITY: Belongs to the Toll-like receptor family.				
CC	-1- SIMILARITY: Contains 17 leucine-rich (LRR) repeats.				
CC	-1- SIMILARITY: Contains 1 TIR domain.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/				
CC	or send an email to license@isb-sdb.ch).				
CC	-----				
DR	EMBL	AF057025	MAC1313.1; --		
DR	HSSP	Q15399	1FYV.		
DR	InterPro	IPR001611	LRR.		
DR	InterPro	IPR000483	LRR_Cterm.		
DR	InterPro	IPR000157	TIR.		
DR	Pfam	PF00560	LRR; 10.		
DR	Pfam	PF01582	TIR; 1.		
DR	PRINTS	PR000019	LEURICHRPT.		
DR	SMART	SM00082	LRRCT; 1.		
DR	SMART	SM00255	TIR; 1.		
DR	PROSITE	PS50104	TIR; 1.		
KW	Glycoprotein; Immune response; Inflammatory response;				
KW	Leucine-rich repeat; Receptor; Signal; Transmembrane.				
FT	SIGNAL	1	25		Potential.
FT	CHAIN	26	835		Toll-like receptor 4.
FT	DOMAIN	26	638		Extracellular (Potential).
FT	TRANSMEM	639	659		Potential.
FT	DOMAIN	660	835		Cytoplasmic (Potential).
FT	REPEAT	32	52		LRR 1.
FT	REPEAT	53	75		LRR 2.
FT	REPEAT	76	99		LRR 3.
FT	REPEAT	100	123		LRR 4.
FT	REPEAT	148	172		LRR 5.
FT	REPEAT	173	196		LRR 6.
FT	REPEAT	201	224		LRR 7.
FT	REPEAT	227	251		LRR 8.
FT	REPEAT	305	330		LRR 9.
FT	REPEAT	370	393		LRR 10.
FT	REPEAT	396	419		LRR 11.
FT	REPEAT	420	443		LRR 12.
FT	REPEAT	468	492		LRR 13.

FT	REPEAT	493	516	LRR 14.
FT	REPEAT	518	540	LRR 15.
FT	REPEAT	542	563	LRR 16.
FT	REPEAT	565	589	LRR 17.
FT	DOMAIN	670	816	TIR.
FT	CARBOHYD	34	34	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	43	43	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	75	75	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	172	172	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	204	204	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	237	237	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	248	248	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	281	281	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	307	307	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	432	492	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	495	495	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	524	524	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	572	572	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	575	575	N-1linked (G1CNC. .) (potential).
FT	CARBOHYD	622	622	N-1linked (G1CNC. .) (potential).
SQ	SEQUENCE	835 AA;	96071 MW;	DFSEI6A30851B3A0 CRC64;
Alignment Scores:				
Pred. No.:	4.31e-279	Length:	835	
Score:	3683.00	Matches:	711	
Percent Similarity:	91.27%	Conservative:	72	
Best Local Similarity:	85.05%	Mismatch:	52	
Query Match:	71.14%	Indels:	0	
DB:	1	Gaps:	2	
US-09-396-985B-46 (1-2951) x TLR4_RAT (1-835)				
OY	208	ATGATGCCCTCCCTGGCTCCTGGCTAGACATCTGATATAGGACATGTTCTTCTCTGCTG	267	
DB	1	MetmetProleuLeuH1eLeuA1eG1YtrLeu11eMeLAlaLeuHeuSerYLeu	20	
OY	268	ACACCAAGAGGTTGAATCCCGCATAGAGGATGCTCAATATTTACCTACACATGACATG	327	
DB	21	ArgProGlySerLeuAsnProCys11eG1uValLeuProAsn11eHnTrYg1nCywec	40	
OY	328	GATCAGAAATCAGCAAAAGTCCCTGATGACATTCCTCTTCTTCAACCAAGACATAGATCTG	387	
DB	41	AbgG1nAsnLeuSerY1e1eProH1sAbP1eProTy1eSerH1rYsAsnLeuAbPLeu	60	
OY	388	AGCTTCAACCCCTTGAGAGATCTTAAAAAGCTATAGCTTCCAAATTTTTCAGAACTTCAAG	447	
DB	61	SeHrPheAsnProleuY1e1eLeuArgSerY1eSerPheH1rAsnPheSerG1nLeuG1n	80	
OY	448	TGGCTGGATTTATCCAGGCTGTGAATTTGAACAATTTGAAGACAAAGCATGGCATGGCTTA	507	
DB	81	TrPLeuAbPLeuSerY1eArgCysG1u11eG1uH1r11eG1uAspYsAlaTrP1eG1uLeu	100	
OY	508	CACCAACCTTCAAACTGTATGACATGACAGGAAACCTATCCAGAGATTTCCTCCAGAGAGT	567	
DB	101	AsnG1nLeuSerTh1eUValLeuHnTrG1YAsnPro11eYsSerPheSerProGlySer	120	
OY	568	TTCTCTGACATACAAAGTTTAAACAATCTGTGGCTGTGGAGACAAATTTGGCCTCTTA	627	
DB	121	PheSerG1YLeuH1rAsnLeuG1uAsnLeuValAla1eAlaG1uH1rYswecTh1rSerLeu	140	
OY	628	GAAAGCTTCCSTATTGGAACAGCTTATACCTTTAAAGAACTCAATGTGGCTCACAAATTTT	687	
DB	141	G1uG1YPhn1eG1eG1Y1nLeu11eSerLeuY1eY1eLeuAbnValAla1eAsnLeu	160	
OY	688	ATACATTCCTGTAGATTACCTGATATTTTCCAACTGACGAAACCTAGACATGTGCAT	747	
DB	161	11eH1sSerPheY1eLeuProG1uY1rPheSerAsnLeuH1rAsnLeuG1uH1sValAsp	180	
OY	748	CTTTCTTATACATATATTCAAACTATATCTGTCCAAAGACTTACAGTTTCTACGTGAAAT	807	
DB	181	LeuSerY1rAsnY1r11eG1nH1r11eSerValY1eAspPheuG1nPh1eLeuArgG1uAsn	200	
OY	808	CCAGCAATCAATCTCTTTAGACATGCTTTGAAACCAATTTGACATTCATTCAGAACCA	867	

Db 201 ProGlnValAsnLeuSerLeuAspLeuSerProIleAspSerIleGlnAlaGln 220
 Qy 868 GCCTTTGAGGAATTAAGCTCATGAATGACTTAAGAGGTAATTTAATAGCCAAAT 927
 Db 221 AlphegInGlyIleValGlnHisIleuThrLeuAlaGSerAspHisSerSerAsn 240
 Qy 928 ATAAAGAAACCTGGCTTCAAAACCTGGCTGGTTTACAGCTCAATCGGTGATCTTGGGA 987
 Db 241 ValLeuSerMetCysLeuGlnHisMetThrGlyLeuHisValHisArgLeuIleuGly 260
 Qy 988 GAATTTAAAGATGAAAGAAATCTGGAATTTTGAACCTCTATCATGAAAGACTATGT 1047
 Db 261 GluPheLeuAsnGluArgAsnLeuGlnSerPheAspArgSerValMetGluGlyLeuGly 280
 Qy 1048 GATGAGCACTTGAAGTGAAGTTACATATACATTAATGATTTTTCAGATGATTTGTT 1107
 Db 281 AsnValSerIleAspGlnPheArgLeuThrTyrlleAsnHisPheSerAspAspIleTyx 300
 Qy 1108 AAGTTCATGCTGGCGAATGTTTCTGCAATGCTCTGCGACAGGTGATCTATAAATAT 1167
 Db 301 AsnLeuAsnCysLeuAlaAsnIleSerAlaMetSerPheThrGlyValHisIleLeuHis 320
 Qy 1168 CTAGAAGATGTTCTTAAACATTTGCAATGCAATCTTATCAATCAATTAATGATCAACT- 1226
 Db 321 IleAlaAspValProArgHisPheLeuSerPheGlnSerLeuSerIleIleArgCysHisLeu 340
 Qy 1227 AAGAGATTTTCAACTCTGGAATCTACCTCTTAAAGTTTGAAGTTTGAATGACAA 1286
 Db 341 LysProPheProLysLeuSerLeuProPheLeuLysSerTrpThrLeuThrThraAsnArg 360
 Qy 1287 GGGCTCATACGTTTAAAGAGGCGCTTACCAAGTCTCAGCTATCTAGATCTTAGTGA 1346
 Db 361 GluAspIleSerPheGlyGlnLeuAlaLeuProSerLeuArgTyrlleAspLeuSerArg 380
 Qy 1347 AATGCACTAGCTTTAGTGTGGCTGTTCTTATTTCTGATTTGGAACAACAGCCTGGA 1406
 Db 381 AsnAlaMetSerPheArgGlyCysCysSerTyrlleAspPheGlyThrAsnAsnLeuGly 400
 Qy 1407 CACTTAAAGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1466
 Db 401 TyrlleuAspLeuSerPheAsnGlyValIleLeuMetSerAlaAsnPheMetGlyLeuGln 420
 Qy 1467 GAGCTGACGACCTGATTTTTCAGCACTTACTTAAAGAGGTCACAGAAATCTCAGC 1526
 Db 421 GluLeuGlnTyrlleuAsp-PheGlnHisSerThrLeuLysValThrGlnPheSerVal 440
 Qy 1527 GTTCTTATCCCTTAAAGACTTACTTATCTTGAATCTTATTAATCAACCAAAATTTGA 1586
 Db 440 PheLeuSerLeuGlnLysLeuLysTyrlleuAspIleSerTyrlleuAsnThrLysIleAs 460
 Qy 1587 CTTGATGATGATTTTCTGGCTTACAGCACTTCAACATTTAAATGCTGGCAATTC 1646
 Db 460 PheAspGlyIlePheLeuGlnTyrlleuIleSerLeuAsnThrLeuLysMetAlaGlyAsnSe 480
 Qy 1647 TTTCAGAGACACACCTTTCAAAATGCTTTCAGAAACACAACTTGAATTCCTGGA 1706
 Db 480 rPheLysAspAsnThrLeuSerAsnValPheThrAsnThrThrAsnLeuThrPheLeuAs 500
 Qy 1707 TCCTTTAAATGATCAATTTGAACAATATCTTGGGGGATTTTGAACCTCCATAGACT 1766
 Db 500 PheSerLysCysGlnLeuGlnGlnIleSerArgGlyValPheAspThrLeuTyrlleGly 520
 Qy 1767 TCATTTATTAATTAAGTCAACAACATCTATGTTTGGATTCATCCCATTTAACA 1826
 Db 520 uGlnLeuLeuAsnMetSerHisAsnAsnLeuPheLeuAspProSerHisTyrlleGly 540
 Qy 1827 GCTGATTTCCCTGACACTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1886
 Db 540 nLeuTyrlleSerLeuArgThrLeuAspCysSerPheAsnArgIleGlnThrSerLysGlyIle 560
 Qy 1887 ACTGCAACATTTTCCAAAGAGCTTACGCTTCTTCAATTTTCAACAATTTCTGTGCTTG 1946

Db 560 eLeuGlnHisPheProLysSerLeuAlaValPheAsnLeuThrAsnAsnSerValAlaCys 580
 Qy 1947 TATATGATCAATCAGAAATTCCTGAGTGGGTCAAGAGACAGAAAGCTTGTGTGA 2006
 Db 580 sIleCysGlnTyrlleGlnAsnPheLeuGlnTrpValIleAspGlnLysMetPheLeuValAs 600
 Qy 2007 TGTGAAACAAATGACATGTGCAACACCTGTAGAGANTGAATTCCTTGTAGTGTGATTT 2066
 Db 600 nValGlnGlnMetLysCysAlaSerProIleAspMetLysAlaSerLeuValLeuAspPh 620
 Qy 2067 TAAATATTTCACTGTTATATGTCACAGACATATCATGCTGTGTCAGTGTGAT 2126
 Db 620 eThrAsnSerThrCysTyrlleTyrlleTyrlleIleSerValSerValIleSerValLe 640
 Qy 2127 TGGGTATTCACCTGATGATTTTGTATATACCTTATGATTTTTCACCTGATGATTC 2186
 Db 640 uValValAlaThrValAlaPheLeuIleTyrlleHisPheTyrlleHisLeuIleValIleAl 660
 Qy 2187 TGGCTGTAAAGATGACAGACAGAGAGAGAAAGCATGATGATGATGATGATGATGAT 2246
 Db 660 aGlyCysLysLysTyrlleSerArgGlyGlnSerIleTyrlleAspAlaPheValIleTyrlleSe 680
 Qy 2247 TCAGATGAGGACTGGGTGAGAAATGAGCTGCTGTAAGATTTAAGAGAGAGTCCCG 2306
 Db 680 rGlnAsnGlnAspTrpValAlaArgAsnGlnLeuValLysAsnLeuGlnGlyValProAr 700
 Qy 2307 CTTTCACTGCTGCTTCACTTACAGAGACTTATTCCTGCTGATGATGATGATGATGAT 2366
 Db 700 gPheGlnLeuCysLeuHisTyrlleArgAspPheIleProGlyValAlaIleAlaAlaAsnIle 720
 Qy 2367 CATCCAGAAAGCTTCCACAAAGACCCGAGAGTATTTGTGTAGTGTGATGATGATGAT 2426
 Db 720 eIleGlnGlnGlyLysPheHisLysSerArgLysValIleValValAlaSerArgHisPheIle 740
 Qy 2427 TCAGAGCCGTGTGTGATTTTGAATTAAGATTTGCTCAACATGCGAGATTTCTGAGCAG 2486
 Db 740 eGlnSerArgTrpCysIlePheGlnTyrlleGlnIleAlaGlnThrTrpGlnPheLeuSerSe 760
 Qy 2487 CCGCTGAGGACATCATTCATGCTGAGAGAGTGAAGAGTCCGCTGAGAGGACGA 2546
 Db 760 rArgSerGlyIleIlePheIleValLeuGlnLysValGlnLysSerLeuLeuArgGlnI 780
 Qy 2547 GGTGAAATTTATGCTTCTTATGACAGAAACACTTACCTGGAATGAGAGACAACTCTCT 2606
 Db 780 nValGlnLeuTyrlleArgLeuLeuSerArgAsnThrTyrlleGlnTrpGlnAspAsnAlaLe 800
 Qy 2607 GGGAGGACACATCTTGTGAGAGACTTAAAGATGCTTATGATGAGAGAAAGCTTCGAA 2666
 Db 800 uGlyArgHisIlePheTrpArgLeuLysValAlaLeuLeuAspGlyLysAlaLeuAs 820
 Qy 2667 TCTGAGCAAAACAGACAGAGAAAGAAAGAAAGCGCAACTTGGACC 2712
 Db 820 nProAspGlnThrSerGlnGlnGlnGlnAlaThrThrLeuThr 835

RESULT 4
 ID TLR4_CRIGR STANDARD; PRT; 838 AA.
 AC Q9WV82;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OC NCBI_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Macrophage;
 RX MEDLINE=20148868; PubMed=10683379;
 RA Lien E., Means T.K., Heine H., Yoshimura A., Kusumoto S., Fukase K.,

RA	Fenton M.J., Oikawa M., Qureshi N., Monts B., Finberg R.W.,
RA	Innalls R.R., Goldenbock D.T.; 1; gold-1-like receptor, a
RT	Toll-like receptor, 4 impacts ligand-specific recognition of bacterial
RL	lipopolysaccharide."/;
J.	Clin. Invest. 105:497-504(2000).
-1	FUNCTION: Cooperates with Lyg6 and CD14 to mediate the innate
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via
CC	MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC	secretion and the inflammatory response (By similarity).
CC	SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC	multi-protein complex containing at least CD14, Lyg6 and TIR4.
CC	Binds Lyg6 via the extracellular domain. Binds MyD88 and TIRAP via
CC	their respective TIR domains.
CC	- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	- TISSUE SPECIFICITY: Detected in macrophages and the Chinese
CC	hamster ovary fibroblast cell line.
CC	- SIMILARITY: Belongs to the Toll-like receptor family.
CC	- SIMILARITY: Contains 1 leucine-rich (LRR) repeats.
CC	- SIMILARITY: Contains 1 TIR domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	The European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isdb-sib.ch/announce/
CC	or send an email to licenses@isdb-sib.ch).
CC	-----
DR	EMBL; AF153676; AAD41891.1; .
DR	HSSP; Q15399; 1PVV.
DR	InterPro; IPRO001611; LRR.
DR	InterPro; IPR000483; LRR_Cterm.
DR	InterPro; IPR000351; LRR_Typ.
DR	InterPro; IPR000157; TIR.
DR	Pfam; PF00560; LRR; 8.
DR	Pfam; PF01582; TIR; 1.
DR	PRINTS; PR00019; LEURICHRPT.
DR	SMART; SM00082; LRCT; 1.
DR	SMART; SM00369; LRR_TYP; 1.
DR	SMART; SM00255; TIR; 1.
DR	PROSITE; PS50104; TIR; 1.
KW	Glycoprotein; Immune response; Inflammatory response;
KW	Leucine-rich repeat; Receptor; Signal; Transmembrane.
FT	SIGNAL 1 25 Potential.
FT	CHAIN 26 838 Toll-like receptor 4.
FT	DOMAIN 26 629 Extracellular (Potential).
FT	TRANSMEM 630 650 Potential.
FT	DOMAIN 651 838 Cytoplasmic (Potential).
FT	REPEAT 31 52 LRR 1.
FT	REPEAT 53 75 LRR 2.
FT	REPEAT 76 99 LRR 3.
FT	REPEAT 100 123 LRR 4.
FT	REPEAT 127 148 LRR 5.
FT	REPEAT 149 172 LRR 6.
FT	REPEAT 173 196 LRR 7.
FT	REPEAT 200 224 LRR 8.
FT	REPEAT 227 251 LRR 9.
FT	REPEAT 305 330 LRR 10.
FT	REPEAT 351 370 LRR 11.
FT	REPEAT 371 393 LRR 12.
FT	REPEAT 396 419 LRR 13.
FT	REPEAT 420 443 LRR 14.
FT	REPEAT 468 492 LRR 15.
FT	REPEAT 494 516 LRR 16.
FT	REPEAT 517 538 LRR 17.
FT	REPEAT 541 563 LRR 18.
FT	REPEAT 565 589 LRR 19.
FT	DOMAIN 670 816 TIR.
FT	CARBOHYD 34 34 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 115 115 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 172 172 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
FT	CARBOHYD 237 237 N-linked (GlcNAc...) (Potential).

FT	CARBOHYD	307	307	N-linked (G1CNC. .)	(Potential).
FT	CARBOHYD	492	492	N-linked (G1CNC. .)	(Potential).
FT	CARBOHYD	495	495	N-linked (G1CNC. .)	(Potential).
FT	CARBOHYD	524	524	N-linked (G1CNC. .)	(Potential).
FT	CARBOHYD	572	572	N-linked (G1CNC. .)	(Potential).
FT	CARBOHYD	622	622	N-linked (G1CNC. .)	(Potential).
SO	SEQUENCE	838 AA;	96277 MW;	129B35966908B48 CMC64;	
Alignment Scores:					
	Pred. No.:	9.99e-255	Length:	838	
	Score:	3371.50	Matches:	652	
	Percent Similarity:	86.50%	Conservative:	72	
	Best Local Similarity:	77.90%	Mismatches:	109	
	Query Match:	65.12%	Indels:	5	
	DB:	1	Gaps:	1	
US-09-396-985B-46 (1-2951) x TLR4_CRIGR (1-838)					
QY	208	ATGATGCTCCCTGGCTGGCTGGCTGAGACTGCATGACGACATGTTCTCTCGCTG	267		
DB	1	MeMePrSeSerPheCysLeuAlaGlyThrLeuMetMetAlaLeuPheLeuSerSerLeu	20		
QY	268	ACACAGAGAACTGGTGAATCCCTGCATAGAGGATGTTCTTAATATTACCAATGATG	322		
DB	21	ArgProGlnSerLeuAspArgProCysValGluValAlaSerSerAsnThrSerTyrGlnCysMet	40		
QY	328	GATCAGAAACTCAGCAAAAGTCCCTGATGACATCTCTTCAACCAAGACATGATCTG	387		
DB	41	AspArgAsnLeuAsnLysIleProArgSerIleProSerSerValTyrLysIleAspLeu	60		
QY	388	AGCTTCAACCCCTTGAAAGTCTTAAAGAAGCTATGCTTCCATATTTTCAGAACTTCAG	444		
DB	61	SetPheAsnProLeuLysThrLeuGlySerLysSerPheAsnPheProGlnLeuLys	80		
QY	448	TGGCTGATTTTCCAGGTGTGAAATTTGAAACAAATTGAAACAAGGATGCGATGCTGTA	507		
DB	81	LeuLeuAspLeuSerArgCysGluIleGluThrIleGluLysArgLysIleTyrGlnGlyLeu	100		
QY	508	CACCACCTCTCAAACTTGATAGTGA CAGAAA CCGTATCCAGAGTTTTC C CAGAAAGT	567		
DB	101	HisGlnLeuThrThrLeuIleLeuThrGlyAsnProIleGlnAsnLeuSerTyrGlyThr	120		
QY	568	TTCTCTGACTAAACAGTTTATGACATCTGGTGGCTGTGGAGACAAATTTGGCTCTCTA	622		
DB	121	PheSerGlyLeuAlaAsnLeuGlnAsnLeuValAlaValGluIleLysLeuAlaSerLeu	140		
QY	628	GAAGAGTCCCTTATGACAGCTTGTATTAACCTTAAAGAACTCAATGTGGCTCAAAATTTT	687		
DB	141	AspSerLeuProIleGlyIleValAlaThrLeuLysLysLeuAsnValAlaHisAsnLeu	160		
QY	688	ATACATTTCTGTAAAGTTTACCTGCATATTTTTCATCTGACGAACTTAGTACATGTGAT	747		
DB	161	IleHisSerPheLysLeuProGlnTyrPheSerAsnLeuThrAsnLeuGluHisLeuAsp	180		
QY	748	CTTTCTTATATCATATTTTAAACATACTATGTCGACACGACTTACAGTTTCTACGTTAAAT	807		
DB	181	LeuSerAsnAsnTyrIleGlnThrIleTyrTyrThrAspLeuGlnThrLeuArgGluAsn	200		
QY	808	CCCAAGTCAATCTCTCTTAGACAGTCTTGAACCCCAATGAGCTTCATTCAGACACAA	865		
DB	201	ProGlnLeuAsnLeuSerLeuGlnLeuSerLeuAsnProIleAspPheIleGlnProGly	220		
QY	868	GCGTTTCAGGAAATTAAGCTCCATGACAGCTCAATAGAGGTTAATTTTAATAGCTCAAT	922		
DB	221	AlaPheGlnGlyIleArgLeuHisSerLeuThrLeuArgSerAsnPheAsnSerThrAsn	240		
QY	928	ATAAGAAAATTGCTCTTCAAAACCTGCTGTTTACAGTTCATCGGTGATCTTGCGA	987		
DB	241	ValMetCysThrCysIleHisAsnLeuAspGlyLeuGlnValHisArgLeuIleLeuGly	260		
QY	988	GAATTTAAAGATGAAGAATCTGGAATTTTGAACCCCTCTATCATGAGAAGACTATGT	1040		
DB	261	GlnPheLysAsnGlnIleArgAsnValGlnTyrPheAspArgTyrValIleGlnGlyLeuCys	280		


```

RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
RT locus (TLR4).";
RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
RN [4]
RN SEQUENCE FROM N.A. AND VARIANTS GLY-299 AND ILE-399.
RX MEDLINE=20296622; PubMed=10835634; DOI=10.1038/76048;
RA Arbour N.C., Lorenz E., Schutte B.C., Zahner J., Kline J.N., Jones M.,
RA Freese K., Walt J.L., Schwartz D.A.;
RT "TLR4 mutations are associated with endotoxin hyporesponsiveness in
RT humans.";
RL Nat. Genet. 25:187-191(2000).
RN [5]
RN SEQUENCE OF 24-38.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [6]
RN MUTAGENESIS OF GLU-697; ARG-710; ASP-711 AND PRO-714.
RX MEDLINE=20531768; PubMed=11081518; DOI=10.1038/35040600;
RA Xu Y., Teo X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.;
RT "Structural basis for signal transduction by the Toll/Interleukin-1
RT receptor domains.";
RL Nature 408:111-115(2000).
RN [7]
RN CARBOHYDRATE-LINKAGE SITES, AND MUTAGENESIS OF ASN-526 AND ASN-575.
RX MEDLINE=21648731; PubMed=11706042; DOI=10.1074/jbc.M109910200;
RA da Silva Correia U., Olevitch R.J.;
RT "MD-2 and TLR4 N-linked glycosylations are important for a functional
RT lipopolysaccharide receptor.";
RL J. Biol. Chem. 277:1845-1854(2002).
RN [8]
RN VARIANTS ARG-188; SER-246; GLY-289; SER-329; ILE-399; LEU-443;
RX LYS-474; HIS-510; ARG-694; HIS-763 AND HIS-834.
RA Shulnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RX MEDLINE=21405531; PubMed=11514453;
RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
RT in humans.";
RL Genetics 158:1657-1664(2001).
RL
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response.
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TIR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
CC their respective TIR domains.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Highly expressed in monocytes, macrophages,
CC peripheral blood leukocytes. Detected in placenta, spleen and
CC dendritic cells and several types of T-cells.
CC -1- PTM: N-glycosylated. Glycosylation of Asn-526 and Asn-575 seems to
CC be necessary for the expression of TLR4 on the cell surface and
CC the LPS-response. Likewise, mutants lacking two or more of the
CC other N-glycosylation sites were deficient in interaction with
CC LPS.
CC -1- POLYMORPHISM: Allele TLR4*B (Gly-299, Ile-399) is associated with
CC a blunted response to inhaled LPS.
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AF177765; AAF05316.1; -.
DR EMBL; AF177766; AAF07823.1; -.
DR EMBL; AF172171; AAF89753.1; -.
DR EMBL; AF172169; AAF89753.1; JOINED.
DR EMBL; AF172170; AAF89753.1; JOINED.
DR HSP; 060603; IFTM.
DR Genew; HGNC:11850; TLR4.
DR MIM; 603030; -.
DR GO; GO:0005867; C:integral to plasma membrane; TAS.
DR GO; GO:0046596; C:lipopolysaccharide receptor complex; NAS.
DR GO; GO:0001530; P:lipopolysaccharide binding; NAS.
DR GO; GO:0004888; P:transmembrane receptor activity; NAS.
DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO; GO:0016046; P:detection of fungi; NAS.
DR GO; GO:0009598; P:detection of pathogenic bacteria; NAS.
DR GO; GO:0006955; P:immune response; TAS.
DR GO; GO:0042116; P:macrophage activation; IMP.
DR GO; GO:0045576; P:mast cell activation; ISS.
DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; NAS.
DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; NAS.
DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR GO; GO:0042088; P:T-helper 1 type immune response; NAS.
DR Interpro; IPR001611; LRR.
DR Interpro; IPR000483; LRR_Cterm.
DR Interpro; IPR003591; LRR_Typ.
DR Interpro; IPR000157; TIR.
DR Pfam; PF00560; LRR_12.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00369; LRR_Typ; 2.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR POSITE; PS50104; TIR; 1.
KW Direct protein sequencing; Glycoprotein; Immune response;
KW Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;
KW Repeat; Signal; Transmembrane.
FT SIGNAL 1 223
FT CHAIN 24 839
FT DOMAIN 24 631
FT TRANSMEM 632 652
FT DOMAIN 653 839
FT REPEAT 52 76
FT REPEAT 77 100
FT REPEAT 101 124
FT REPEAT 128 149
FT REPEAT 150 173
FT REPEAT 174 197
FT REPEAT 203 225
FT REPEAT 228 252
FT REPEAT 277 303
FT REPEAT 307 330
FT REPEAT 332 350
FT REPEAT 351 372
FT REPEAT 373 398
FT REPEAT 400 421
FT REPEAT 422 445
FT REPEAT 447 469
FT REPEAT 470 494
FT REPEAT 495 518
FT REPEAT 520 541
FT REPEAT 543 566
FT REPEAT 568 592
FT REPEAT 672 698
FT REPEAT 722 748
FT REPEAT 772 798
FT REPEAT 822 848
FT CARBOHYD 173 173
FT CARBOHYD 205 205
FT CARBOHYD 282 282
FT CARBOHYD 309 309
FT CARBOHYD 497 497

```

FT	CARBONHD	526	526	N-linked (GlcNAc. . .)
FT	CARBONHD	525	525	N-linked (GlcNAc. . .)
FT	CARBONHD	624	624	N-linked (GlcNAc. . .)
FT	CARBONHD	630	630	N-linked (GlcNAc. . .) (potential).
FT	VARIANT	188	188	Q -> R.
FT	VARIANT			/FTId=VAR_018729.
FT	VARIANT	246	246	C -> S.
FT	VARIANT			/FTId=VAR_018730.
FT	VARIANT	299	299	D -> G (1n allele TLR4*B; reduced LPS-response; dbSNP:4986790).
FT	VARIANT			/FTId=VAR_012739.
FT	VARIANT	329	329	N -> S.
FT	VARIANT			/FTId=VAR_018731.
FT	VARIANT	399	399	T -> I (1n allele TLR4*B; reduced LPS-response; dbSNP:4986791).
FT	VARIANT			/FTId=VAR_012740.
FT	VARIANT	443	443	F -> L.
FT	VARIANT			/FTId=VAR_018732.
FT	VARIANT	474	474	E -> K.
FT	VARIANT			/FTId=VAR_018733.
FT	VARIANT	510	510	Q -> H.
FT	VARIANT	694	694	/FTId=VAR_018734.
FT	VARIANT			K -> R.

Alignment Scores:	
Pred. No.:	2,12e-209
Score:	2792.00
Percent Similarity:	79.35%
Best Local Similarity:	67.27%
Query Match:	53.93%
DB:	1
	Gaps: 4
	Length: 839
	Matches: 557
	Conservative: 100
	Mismatch: 166
	Indels: 6
	Gaps: 4

US-09-396-985B-46 (1-2951) X TLR4_HUMAN (1-839)

QY	208	ATGATGCTCTCTGGCTCTGGCTAGAACTGATCAGCACTG- - -TTCTTCTCTGC	26
Db	1	MeMeSeSerLaSeRaTrgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys	20
QY	265	CTGACACACAGAAAGCTTGAAATCCCTGCATAGAGAGAGTCCCAATATTAACCAATATGC	324
Db	21	ValArgProIuSerTrpGluProCysValGluValAlaProAsnIleThrTyrGlnCys	40
QY	325	ATGATCAGAAACTCAGCAAAAGTCCCTGTAGCATTCCTCTTTCACACAGAACATAGT	384
Db	41	MetGluLeuAsnAmpHeTyrLysIleProAspAenLeuProPheSerThrLysAenLeuAsp	60
QY	385	CTGAGCTTCAACCCCTTTGAAGATCTTAAAAAGCTATAGCTTTTCCAAATTTTCAGAACTT	444
Db	61	LeuSerPheAsnProLeuAlaTrgHisLeuGlySerTyrSerPhePheSerPheProGluLeu	80
QY	445	CAGTGGCTGATTTATTCACAGGTGTGAATTTGAACAATTGAAGACAGAGCAATGGCATGGC	504
Db	81	GlnValLeuAspLeuSerAraGlySerGlnIleGlnThrIleGlnAspGlyAlaTyrGlnSer	100
QY	505	TTACACACCCTCTCAAACTTGATTACTGACAGAGAAACCTATTCAGAGATTTTCCACAGA	564
Db	101	LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly	120
QY	565	AGTTTCTCTGGACTAACAGTTTAGACAATCTGGTGGCTGTGGAGACAAATTGGCCTCT	624
Db	121	AlaPheSerTrpLeuSerSerLeuGlnTrpLeuValAlaValaGluThrAsnLeuAlaSer	140
QY	625	CTAGAAAGCTTCCCTTAATGGACAGCTTATTAACCTTAAAGAAACATGATGGCTCACAT	684
Db	141	LeuGluAsnAmpHeProIleGlyHisLeuAspThrIleLeuTrpGluLeuAenValAlaHisAsn	160
QY	685	TTTATACATCTCTGTAAGTTACTGCAATATTTTCCAACTTGACAGCACTAGTACATGTG	744
Db	161	LeuIleGlnSerPheLysLeuProGluTyrPheSerAenLeuThrAsnLeuGlnHisLeu	180
QY	745	GATCTTTCTTAATACATTAATTCAAATATTAATCTGTCACAGCACTTACATTTCTACGGAA	804
Db	181	AspLeuSerAenAsnLysIleGlnSerTrpTyrCysThrAspLeuAspValLeuHisGln	200

OY	865	AATGCACAGTCATCTCTCTTTGAGACATGTCTTGAACCCAAATTGACTTGATTCAGAAGC	864
Dd	201	MctProLeuLeuAanLeuSerLeuAspLeuSerLeuAnPromeAanPheIleInPro	220
OY	865	CAAGCCCTTTGAGGAAATTAAGCTCCATGACATGACTTAAGAGGGTAATTTTAATGACTCA	924
Dd	221	GlyAlaPheIeuysGuIlIeArgLeuHlAbysLeuThrLeuAaArgAanPheaSperIeu	240
OY	925	AATATAATGAAAACCTTGCTTCAAAAACCTGGCTGGTTTACACGTCATCGGTTGATCTTG	984
Dd	241	AsnValMetIystrIyrCysIIeGIingIyLeuAlaGIyleugIuValHlsArgLeuValIeu	260
OY	985	GGAGAAATTTAAGAAGTGAAGCATCTGGAAATTTTTGAACCCTCATCATGAGAAAGACTA	1044
Dd	261	GIylguPheArGaengluGIyAsnLeuClIuIySpheApIybsSerAlaLeuclIuclIyeu	280
OY	1045	TGTGATGTGACCATTTGATGAGTTCAGGTTAACATTAACAATGATTTTTTCAGATGATVTT	1104
Dd	281	CysAnsnLeuThrlIeGIuGlIuPheArGLeuAlaTyxLeuAapTyTYrIyLeuAspAspIle	300
OY	1105	GTTAAAG---TTCACATGGCTTGAGCAAATGTTCTCGCAATGCTCTCGGACGAGTGATACMA	1164
Dd	301	IleAspLeuPheAanCySLeuThrAsnValSerIerPheaSerLeuValSerValThrIle	320

126	ACGACGAGS	1341	AGTGAAGATGAC	1401	CTGAGACACTT	1461	CTAAGAAGCTG	1521	CTCAGCGCTT	1581	AATTGACTTGA	1641	CAATTCTTTGA	1701	CCTGGATCTCT	1761	TAGACTTCAT	1821	TAACGACGTGA	1881	CTGAGCTGAT	1941	CTGAGCTGAT	2001	CTGAGCTGAT	2061	CTGAGCTGAT	2121	CTGAGCTGAT	2181	CTGAGCTGAT	2241	CTGAGCTGAT	2301	CTGAGCTGAT	2361	CTGAGCTGAT	2421	CTGAGCTGAT	2481	CTGAGCTGAT	2541	CTGAGCTGAT	2601	CTGAGCTGAT	2661	CTGAGCTGAT	2721	CTGAGCTGAT	2781	CTGAGCTGAT	2841	CTGAGCTGAT	2901	CTGAGCTGAT	2961	CTGAGCTGAT	3021	CTGAGCTGAT	3081	CTGAGCTGAT	3141	CTGAGCTGAT	3201	CTGAGCTGAT	3261	CTGAGCTGAT	3321	CTGAGCTGAT	3381	CTGAGCTGAT	3441	CTGAGCTGAT	3501	CTGAGCTGAT	3561	CTGAGCTGAT	3621	CTGAGCTGAT	3681	CTGAGCTGAT	3741	CTGAGCTGAT	3801	CTGAGCTGAT	3861	CTGAGCTGAT	3921	CTGAGCTGAT	3981	CTGAGCTGAT	4041	CTGAGCTGAT	4101	CTGAGCTGAT	4161	CTGAGCTGAT	4221	CTGAGCTGAT	4281	CTGAGCTGAT	4341	CTGAGCTGAT	4401	CTGAGCTGAT	4461	CTGAGCTGAT	4521	CTGAGCTGAT	4581	CTGAGCTGAT	4641	CTGAGCTGAT	4701	CTGAGCTGAT	4761	CTGAGCTGAT	4821	CTGAGCTGAT	4881	CTGAGCTGAT	4941	CTGAGCTGAT	5001	CTGAGCTGAT	5061	CTGAGCTGAT	5121	CTGAGCTGAT	5181	CTGAGCTGAT	5241	CTGAGCTGAT	5301	CTGAGCTGAT	5361	CTGAGCTGAT	5421	CTGAGCTGAT	5481	CTGAGCTGAT	5541	CTGAGCTGAT	5601	CTGAGCTGAT	5661	CTGAGCTGAT	5721	CTGAGCTGAT	5781	CTGAGCTGAT	5841	CTGAGCTGAT	5901	CTGAGCTGAT	5961	CTGAGCTGAT	6021	CTGAGCTGAT	6081	CTGAGCTGAT	6141	CTGAGCTGAT	6201	CTGAGCTGAT	6261	CTGAGCTGAT	6321	CTGAGCTGAT	6381	CTGAGCTGAT	6441	CTGAGCTGAT	6501	CTGAGCTGAT	6561	CTGAGCTGAT	6621	CTGAGCTGAT	6681	CTGAGCTGAT	6741	CTGAGCTGAT	6801	CTGAGCTGAT	6861	CTGAGCTGAT	6921	CTGAGCTGAT	6981	CTGAGCTGAT	7041	CTGAGCTGAT	7101	CTGAGCTGAT	7161	CTGAGCTGAT	7221	CTGAGCTGAT	7281	CTGAGCTGAT	7341	CTGAGCTGAT	7401	CTGAGCTGAT	7461	CTGAGCTGAT	7521	CTGAGCTGAT	7581	CTGAGCTGAT	7641	CTGAGCTGAT	7701	CTGAGCTGAT	7761	CTGAGCTGAT	7821	CTGAGCTGAT	7881	CTGAGCTGAT	7941	CTGAGCTGAT	8001	CTGAGCTGAT	8061	CTGAGCTGAT	8121	CTGAGCTGAT	8181	CTGAGCTGAT	8241	CTGAGCTGAT	8301	CTGAGCTGAT	8361	CTGAGCTGAT	8421	CTGAGCTGAT	8481	CTGAGCTGAT	8541	CTGAGCTGAT	8601	CTGAGCTGAT	8661	CTGAGCTGAT	8721	CTGAGCTGAT	8781	CTGAGCTGAT	8841	CTGAGCTGAT	8901	CTGAGCTGAT	8961	CTGAGCTGAT	9021	CTGAGCTGAT	9081	CTGAGCTGAT	9141	CTGAGCTGAT	9201	CTGAGCTGAT	9261	CTGAGCTGAT	9321	CTGAGCTGAT	9381	CTGAGCTGAT	9441	CTGAGCTGAT	9501	CTGAGCTGAT	9561	CTGAGCTGAT	9621	CTGAGCTGAT	9681	CTGAGCTGAT	9741	CTGAGCTGAT	9801	CTGAGCTGAT	9861	CTGAGCTGAT	9921	CTGAGCTGAT	9981	CTGAGCTGAT	10041	CTGAGCTGAT	10101	CTGAGCTGAT	10161	CTGAGCTGAT	10221	CTGAGCTGAT	10281	CTGAGCTGAT	10341	CTGAGCTGAT	10401	CTGAGCTGAT	10461	CTGAGCTGAT	10521	CTGAGCTGAT	10581	CTGAGCTGAT	10641	CTGAGCTGAT	10701	CTGAGCTGAT	10761	CTGAGCTGAT	10821	CTGAGCTGAT	10881	CTGAGCTGAT	10941	CTGAGCTGAT	11001	CTGAGCTGAT	11061	CTGAGCTGAT	11121	CTGAGCTGAT	11181	CTGAGCTGAT	11241	CTGAGCTGAT	11301	CTGAGCTGAT	11361	CTGAGCTGAT	11421	CTGAGCTGAT	11481	CTGAGCTGAT	11541	CTGAGCTGAT	11601	CTGAGCTGAT	11661	CTGAGCTGAT	11721	CTGAGCTGAT	11781	CTGAGCTGAT	11841	CTGAGCTGAT	11901	CTGAGCTGAT	11961	CTGAGCTGAT	12021	CTGAGCTGAT	12081	CTGAGCTGAT	12141	CTGAGCTGAT	12201	CTGAGCTGAT	12261	CTGAGCTGAT	12321	CTGAGCTGAT	12381	CTGAGCTGAT	12441	CTGAGCTGAT	12501	CTGAGCTGAT	12561	CTGAGCTGAT	12621	CTGAGCTGAT	12681	CTGAGCTGAT	12741	CTGAGCTGAT	12801	CTGAGCTGAT	12861	CTGAGCTGAT	12921	CTGAGCTGAT	12981	CTGAGCTGAT	13041	CTGAGCTGAT	13101	CTGAGCTGAT	13161	CTGAGCTGAT	13221	CTGAGCTGAT	13281	CTGAGCTGAT	13341	CTGAGCTG
-----	-----------	------	--------------	------	-------------	------	-------------	------	------------	------	-------------	------	-------------	------	-------------	------	------------	------	-------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	------------	-------	----------

Db 560 slysgIngluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAs 580
 QY 1938 TGTTGCTGTATATGTGACATCATGAATTCCTGACATGGGTCAAGGACAGACAGT 1997
 Db 580 pPheAlaCyThrCysGlnHisGlnSerPheLeuGlnTrpIleLeuAspGlnArgGlnLe 600
 QY 1998 CTTGTGTGATGTTGACAAATGACATGTGCAACACCTGTGATGATGAAATCCTCTTAA 2057
 Db 600 uLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspGlnGlnMetProVa 620
 QY 2058 GTTGTGATTTAAATTAATCTACCTGTTATATGATGACAAACATCATCATGCTGTG 2117
 Db 620 lLeuSerLeu---AsnIleThrCysGlnMetAsnIleThrIleIleGlyValSerValle 639
 QY 2118 CAGGTGATGTTGTGTATCCACTGAGATTTCTGATATACACTTCAATTTTCACTGAT 2177
 Db 639 uSerValLeuValValSerValValAlaValLeuValTyrLeuPheThrPheHisLeu 659
 QY 2178 ACTTATGCTGTGCTGTAAAGATACACAGACAGAGAGAAAGCATCTATGATGATGAT 2237
 Db 659 tLeuLeuAlaGlyCysIleLeuTyrGlnArgGlnGlnAsnIleTyrAspAlaPheValI 679
 QY 2238 CTACTGATGTCAGATGAGAGACTGGGTGAGAAATGACCTGTAAAGATTTAGAAAGG 2297
 Db 679 eTyrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValTyrAsnLeuGlnGlnG 699
 QY 2298 AGTGCCTGCTTACCTGCTGCTTCACTGAGAGATTTATCTGCTGTGAGCATTGCTG 2357
 Db 699 yValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyAlaAlaIle 719
 QY 2358 TGCCACATCATCTCAGAGAGGCTTCCACAAGAGCGGAGAGGTTATGTTGTAGTGTAG 2417
 Db 719 aAlaAsnIleIleHisGlnGlnPheHisTyrSerArgLeuValIleValValValSerG 739
 QY 2418 ACACTTATTCAGAGCGCTGTGTATCTTGAATATGAGATTCTCTCAACATGTGCGCT 2477
 Db 739 nHisPheIleGlnSerArgTrpCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnP 759
 QY 2478 TCTGAGAGCGCGCTGTCGATCATCTTCACTGCTGAGAGAGGTTAGAGAGTCCCTGCT 2537
 Db 759 eLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIleValGlnTyrAsnTrpLe 779
 QY 2538 GAGGACAGAGTGTGATTTGATTCGCTTCTTACGAGAAACATCACTGAGATGAGAGA 2597
 Db 779 uArgArgGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnAs 799
 QY 2598 CAATCTCTGTGGGAGGACATCTTCTGAGAGAACTTAAATCCCTATTGATGAGAA 2657
 Db 799 pSerValLeuGlnTyrGlnHisIlePheTrpArgArgLeuArgGlyAlaLeuLeuAspGly 819
 QY 2658 AGCCTGCAATCTGAGCAACA 2679
 Db 819 sSerTrpAsnProGlnGlnTyr 826
 RESULT 7
 TLR4 HORSE
 ID TLR4 HORSE STANDARD: PRT: 843 AA.
 AC QMWT#3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Vandepol M.L., McNeill B.W., Barton M.H., Moore J.N.,
 RT "Cloning and sequencing of equine Toll-like receptor 4 (TLR4).",
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate

CC CC Immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TRAF6
 CC binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC HSBP; AY005808; AAF91076.1; -.
 DR DR
 DR GO: GO:0046896; C:lipopolysaccharide receptor complex; ISS.
 DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO: GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO: GO:0016046; P:detection of fungi; ISS.
 DR GO: GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO: GO:0042116; P:macrophage activation; ISS.
 DR GO: GO:0045576; P:mast cell activation; ISS.
 DR GO: GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO: GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO: GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO: GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 DR GO: GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR00157; TIR.
 DR Pfam; PF00560; LRR; 13.
 DR Pfam; PF01562; TIR; 1.
 DR PRINTS; PR00019; LEURCHRP.
 DR SMART; SM00369; LRR_TYP; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KW Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 843
 FT DOMAIN 24 633
 FT TRANSMEM 634 654
 FT DOMAIN 655 843
 FT REPEAT 53 76
 FT REPEAT 77 100
 FT REPEAT 101 124
 FT REPEAT 128 149
 FT REPEAT 150 173
 FT REPEAT 174 197
 FT REPEAT 203 225
 FT REPEAT 277 300
 FT REPEAT 311 334
 FT REPEAT 351 373
 FT REPEAT 374 399
 FT REPEAT 401 422
 FT REPEAT 423 446
 FT REPEAT 447 470
 FT REPEAT 471 495
 FT REPEAT 496 519
 FT REPEAT 521 544
 FT REPEAT 545 566
 FT REPEAT 569 593
 LRR 1.
 LRR 2.
 LRR 3.
 LRR 4.
 LRR 5.
 LRR 6.
 LRR 7.
 LRR 8.
 LRR 9.
 LRR 10.
 LRR 11.
 LRR 12.
 LRR 13.
 LRR 14.
 LRR 15.
 LRR 16.
 LRR 17.
 LRR 18.
 LRR 19.
 Toll-like receptor 4.
 Extracellular (Potential).
 Potential.
 Cytoplasmic (Potential).

FT DOMAIN 674 820 TIR.
 FT CARBOHYD 35 189 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 189 205 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 205 205 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 282 282 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 295 295 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 498 498 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 527 527 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 576 576 N-linked (GlcNAc . . .) (Potential) .
 FT CARBOHYD 626 626 N-linked (GlcNAc . . .) (Potential) .
 SQ SEQUENCE 843 AA; 96495 MW; B5976898AD6F7A69 CRC64;

 Alignment Scores:
 Pred. No.: 2,54e-209 Length: 843
 Score: 2791.00 Matches: 556
 Percent Similarity: 78.08% Conservative: 103
 Best Local Similarity: 65.88% Mismatches: 174
 Query Match: 53.91% Indels: 12
 DB: 1 Gaps: 4

 US-09-396-985b-46 (1-2951) x TLR4_HORSE (1-843)
 QY 208 ATGATGCTCCCTGGCTCTGCTGCTGATGATGCACTG---TTCTTCTCTGC 264
 Db 1 MetMetProProThrArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 265 CTGACACGAGAACTTGAATCCCTGCATGAGGTAGGTCTCTATATTACTACCAATGC 324
 Db 21 LeuArgProGluSerThrPheProCysValGlnValProAsnThrThrTyGlnCys 40
 QY 325 ATGATGACAAAGCTCAGCAAAAGTCCCTGATGACATCTCTTCTTCAACCAAGACATGAT 384
 Db 41 MetAspLeuAsnLeuTyrlsIleProGluAsnIleProThrSerThrTyGlnLeuAsp 60
 QY 385 CTGAGCTTCAACCCCTTGAAGATCTTAAAGCTATAGCTTCTCCAAATTTTCAAACTT 444
 Db 61 LeuSerPheAsnProLeuTyrlsGlnLeuGlySerHisSerPheSerAsnPheProGluLeu 80
 QY 445 CAGTGGCTGATTTATTCAGGTGTGAATGAACATTTGAAGACCAAGGATGGCATGGC 504
 Db 81 GlnAlaLeuAspLeuSerAspGlyIleGlnMetIleGlnAspAspAlaTyrlsGlnGly 100
 QY 505 TTACACCACTCTCAAACTGATGATGACAGAAACCTATCCAGATTTTCCCGCAGA 564
 Db 101 LeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleArgSerLeuAlaLeuGly 120
 QY 565 AGTTTCTCTGACTTAACAAGTTTGAACAATGTGGTGGCTGTGAGACAAATTTGGCTCT 624
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnThrLeuValAlaValGluThrTyLeuSerSer 140
 QY 625 CTGAAGAGCTTCCCTATTTGACAGCTTATACTTAAAGAACTCATGTGGCTCAACAT 684
 Db 141 LeuGlnTyrlsPheProIleGlyHisLeuTyrlsThrLeuTyrlsGlnLeuAsnValAlaHisAsn 160
 QY 685 TTTATACATTCCTGTAGTTACTGACATATTTTCCATCTCAAGCAAGTATGATCATGTG 744
 Db 161 LeuIleHisSerPheTyrlsLeuProGluTyrlsPheSerTyrlsMetProAsnLeuGlnHisLeu 180
 QY 745 GATCTTTCTTATACTATATTCAAATCTATTAAGTCAACAAGTTCAGTTTCTAAGTAA 804
 Db 181 AspLeuSerAsnLeuTyrlsIleGlnAlaSerHisGlnLeuAspLeuValLeuHisGln 200
 QY 805 AATCCCAAGATCATCTCTTGTAGACATGCTTTGAACCCAAATGATGATCTTCAAGAC 864
 Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuGlnPheIleGlnPro 220
 QY 865 CAAGCTTTCAAGGAAATTAAGCTCAGTGAAGTCAAGTAAAGTAAATTTTAAATAGTCA 924
 Db 221 AsnAlaPheTyrlsGlnTyrlsLeuHisTyrlsLeuThrLeuArgSerAsnPheAspSerIle 240
 QY 925 AATATAATGAAGAACTTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 984
 Db 241 AspValMetCysSerCysIleGlnGlyLeuAlaGlyLeuTyrlsValAsnArgLeuValLeu 260

QY 985 GGAATATTTAAAGATGAAGAAATCTGAAATTTTGAACCCCTCTATCATGAAGAGCTA 1044
 Db 261 GlnGlnPheTyrlsAsnGlnTyrlsGlyIleGlnTyrlsPheAspThrSerAlaLeuArgGlyLeu 280
 QY 1045 TGTGATGTCACCATTTGATGAGTTCAGGTTCATATACATTAACAATGATTTTTCAT 1098
 Db 281 HisAsnLeuThrIleGlnGlnPheArgLeuValAlaTyrlsLeuAsnTyrlsSerSerTyrlsAsp 300
 QY 1099 GATTTTGTTAAGTTCCATCTGCTGGCAAGTGTTCGCAATGTCTCTGGCAGGTGTATCT 1158
 Db 301 SerIleAspLeuLeuAsnTyrlsLeuAlaAspIleSerTyrlsIleSerLeuValSerLeuAsp 320
 QY 1159 ATAAATATCTAGAGATGTCTCAAACTTTCAAAATGTCATTCATTCATTCATTAAGA 1218
 Db 321 LeuGlnTyrlsAsnLeuTyrlsAspPheProTyrlsGlyIlePheGlyTyrlsPheAsnPheGlnLeuValAsn 340
 QY 1219 TGTCAACTGAACAG-TTTCCAACTGTGATCTACCTTTCTTAAAGTTCGACTTAACT 1277
 Db 341 CysArgIleGlnGlyPheProThrLeuGlnLeuThrSerLeuTyrlsArgLeuValPheThr 360
 QY 1278 ATGAACAAAGGCTCTACATTTTAAAAAGTGCCCTTACCAAGTCTCAGTATCTAGT 1337
 Db 361 SerAsnTyrlsAspMetTyrlsSerPheAsnGlnValTyrlsLeuProSerLeuGlnPheLeuAsp 380
 QY 1338 CTATAGTAAGTAATGACTGAGCTTTAGTGTGGCTGCTTATTCGATTTGGGAAACAAC 1397
 Db 381 LeuSerArgAsnArgLeuSerPheTyrlsSerCysCysSerGlnAlaAspLeuTyrlsThr 400
 QY 1398 AGCCTGACACACTTGAACCTCAAGCTTCATGATGTGCCATTCATTAAGTGGCAATTTGAT 1457
 Db 401 ArgLeuTyrlsHisLeuAspLeuSerPheAsnAspValIleSerMetSerSerAsnPheMet 420
 QY 1458 GGTCTAGAAGAGCTGACAGCACTGTGATTTTTCAGACATCTACTTTAAAGGTCACAGA 1517
 Db 421 GlyLeuGlnGlnLeuGlnHisLeuAsp-PheGlnHisSerThrLeuTyrlsGlnAlaSerAs 440
 QY 1518 ATTCTGAGCTTCTTATCCCTGAAAAAGTACTTACTTGAACATCTCTTAACTAACAAC 1577
 Db 440 PheProValPheLeuSerLeuTyrlsAsnLeuTyrlsGlyTyrlsAspIleSerTyrlsHisAsn 460
 QY 1578 CAAAATGACTCGATGTATATTTCTTGTGGCTTGACAGATCTCAACAATTAATAATGAC 1637
 Db 460 ArgValValPheHisGlyIlePheAspGlyLeuValSerLeuGlnValLeuTyrlsMetAl 480
 QY 1638 TGGCAATTTCTTCAAGACACACCTTTCAAAATGTCTTTGCAACACAAACATTTGAC 1697
 Db 480 ArgTyrlsSerPheTyrlsAspAsnPheLeuProAsnIlePheArgGlnMetThrAsnLeuThr 500
 QY 1698 ATTCTGAGCTTCTTAAATGTCAATTTGAACAAATATCTTGGGGGGTATTTTGACACCT 1757
 Db 500 ThrTyrlsAspLeuSerTyrlsCysAsnLeuGlnValSerGlnGlnAlaPheCysTyrlsLeu 520
 QY 1758 CCATAGACTTCAATTTAATATATGATGACCAACAATCTATTTTGTGATTCATCCCA 1817
 Db 520 TyrProArgLeuArgValLeuAsnMetSerHisAsnAsnLeuLeuPheLeuAspMetLeuP 540
 QY 1818 TTATTAACAGCTGATTTCCCTCAGACACTTGTGATTTGAGTTTCAATGCAATGACATC 1877
 Db 540 TyrTyrlsProLeuHisSerLeuGlnIleLeuAspCysSerPheAsnArgIleValAlaPhe 560
 QY 1878 TAAAT---GGAATCTGCAACATTTTCCAAAGAGTTCAGCTTCTCAATCTTCAATCAAA 1934
 Db 560 eLysTrpGlnGlnLeuGlnHisPheProSerSerLeuAlaSerLeuAsnLeuThrGlnHis 580
 QY 1935 TTCTGTGCTTGTATATGTGAACATGAGAATTTCTGCAATGAGTCAAGAGCAAGAACA 1994
 Db 580 AsnPheAlaCysValCysGlnTyrlsGlnSerPheLeuGlnTrpValTyrlsAspGlnArgGly 600
 QY 1995 GTTCTTGTGATGATTTGAACAAATGACATGTGCAACCTGTGAGATGATATCTCTCTT 2054
 Db 600 PheLeuValGlnValGlnHisLeuValCysAlaIleProLeuGlnMetArgIleMetP 620

FT	REPEAT	571	592	LRR	20.
FT	DOMAIN	672	818	TR.	
FT	CARBOHYD	35	35	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	173	173	N-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	205	205	N-1-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	282	282	N-1-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	309	309	N-1-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	497	497	N-1-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	526	526	N-1-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	575	575	N-1-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	624	624	N-1-linked (GlcNAc. . .)	(Potential).
FT	CARBOHYD	630	630	N-1-linked (GlcNAc. . .)	(Potential).
SO	SEQUENCE	826 AA;	94678 MW;	4227731855F1769	CR664;

Alignment Scores:

```

Pred. NO.:      1,076-208      Length:      826
Score:          2783.00        Matches:      554
Percent Similarity: 79.23%    Conservative: 97
Best Local Similarity: 67.48% Mismatches:    155
Query Match:    53.76%       Indels:        6
DB:             1           Gaps:         4

```

US-09-396-985B-46 (1-2951) X TLR4_PAPAN (1-826)

QY	226	CTGCCTAGAGACTTCGATCATGGCACTG--TTCTTCTCTCTGCTGCACAGAGAACTGCT	282
Db	7	LeuIaGlyThrLeuIleIleProAlaMetAlaPheLeuSerCysValAlaArgProGluSerThrP	26
QY	283	AATCCCTGCATAGAGAGTAGTCTTAATAATATTCATCAACATGCATGCATCAAGAACTCAAC	342
Db	27	GluProCysValAlaGluValAlaProAsnIleThrTyrgInCysMetGluIleuAsnPheTy	46
QY	343	AAATCCCTGATGACATCTCTCTTCAACCAAGAACTATGATCTGAGCTTCAACCCCTTG	402
Db	47	LysIleProAspAsnIleProPheSerThrTyrsAsnLeuAspLeuSerPheAsnProIleu	66
QY	403	AAGATCTTAAAAAGCTATAGCTCTTCCCAATTTTTCAGAACTTCAGAGGCTGATTTATCC	462
Db	67	ArgHisIleuGlySerTySerPheIleuArgPheProGluIleuGlnValIleuAsnPleuSer	86
QY	463	AGGTGTGAATTTGAACCAATTGAAGACAAAGGCATGGCTTACACCACTCTTCAAC	522
Db	87	ArgCysGluIleGlnIleThrIleGluAspGlyAlaTyrgInSerLeuSerHisIleuSerThr	106
QY	523	TTGATCTGCACAGGAACCTATCTCAAGTTTTCCTCCAGAGATTTCTCTGCATACA	582
Db	107	LeuIleLeuThrTrgIysAsnProIleGlnSerLeuAlaIleuGlyAlaPheSerGlyLeuSer	126
QY	583	AGTTTAGACATCTGGTGGCTGGTGAGCAAAATGGGCTCTCTGAAGATTCCTCTATT	642
Db	127	SerIleuGlnIlysLeuValAlaValAlaGluThrAsnLeuAlaSerLeuGluAsnPheProIle	146
QY	643	GGAAGCTTATTAACCTTTAAAGAAATCTCAAGTGGCTGCACAAATTTATACATCTCGTAG	702
Db	147	GlyHisIleuTystrIleuIlyGluIleuAsnValAlaHisAsnLeuIleGlnSerPheIys	166
QY	703	TTACTCTGCATATTTTTCCAATCTGACGAACCTAGTACATGTGGATCTTCTTATACATAT	762
Db	167	LeuProGluTyrrPheSerAsnLeuThrAsnLeuGlnIlyHisIleuAspLeuSerSerAsnIys	186
QY	763	ATTCAAACTATTACTGTCATCAAGCATTTACAGTTTCTACGTGAATAATCCACAACTCAATCTC	822
Db	187	IleGlnAsnIleTyrrCysIlyAspIleuGlnValIleuHisGlnMetProIleuProAsnLeu	206
QY	823	TCCTTAAACATGTCTTTGAACCCCAATTGATCTTATTAAGACCAAGCCTTTCAGGAGATT	882
Db	207	SerIleuAspLeuSerLeuAsnProIleAsnPheIleGlnProGlyAlaPheIlyGluIle	226
QY	883	AAGCTTCATCAACTGCATCTTAAGAGGTATTTTATACCTCAAAATTAAGAAATTCG	942
Db	227	ArgIleuHisIlysIleuThrLeuArgSerAsnPheAspAlaIleuAsnValMetIlyThrCys	246
QY	943	CTTCAAAACCTGGCTGTTTACACAGTCCATGGTGTATCTGGAGAAATTTAAAGATGA	1002

Dp	247	11e6c1n1yLeuAlaGlyLeuGluValHisArgLeuValLeuGlyGluPheAlaGlnGlu	266
Qy	1003	AGGAATGTGAAAATTTTGAACCCCTTCATCGAGTGAAGACATATGTGATGACCAATGAT	1062
Dp	267	ArgsnLeuGluGluPheAspLysSerAlaLeuGluGlyLeuGlySerAsnLeuThrIleGlu	266
Qy	1063	GAGTTGAGGTTTACATATACAAATGATTTTCAGATGATATTTGTTAAG---TTCCATGTC	1119
Dp	287	GluPheArgLeuThrTyrLeuAsnArgTyrTyrLeuAspAsnIleIleAspLeuPheAsnGly	306
Qy	1120	TTGGCGAAATGTTTCTGCAATGTCCTGGGAGGTGATCTTAATAATCTGAAGAAGATGT	1179
Dp	307	LeuAlaAsnAlaSerSerPheSerLeuValSerValAsnIleLysArgValGluAspPhe	326
Qy	1180	CTTAACATTTCAAAATGGCAATCCTTTCATCATATTAGATGATGCAACT--AAGCAGTTTCCA	1238
Dp	327	SerTyrAsnPheArgTrpGlnHisIleGluValLeuValAsnGlyLysPheGluGlnPhePro	346
Qy	1239	ACTCTGAGTATCACCTTTCTTAAAGATTGACTTTAATCTATGAACAAAGGCTTATCAGT	1298
Dp	347	ThrLeuGluLeuGluSerLeuLysArgLeuThrPheThrAlaAsnLysGlyIleAsnAla	366
Qy	1299	TTTAAAAAATGGCCCCACCAATCTCCAGTATCTGATCTTGTAGTGAATGCACTGAC	1358
Dp	367	PheSerGluValAspLeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSer	386
Qy	1359	TTTATGTTGGTGGCTGTTCTTATTCCTGATTTGGAAACAAACGCGTGACACTTAAGACTC	1418
Dp	387	PheLysGlySerGlySerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeu	406
Qy	1419	AGCTTCATGATGTCATCATATTAGTGGCCAAATTTGATGGGTCTAGAAGACTGCACAC	1478
Dp	407	SerPheAsnArgValIleThrMetGlySerAsnPheLeuGlyLeuGluGlnHis	426
Qy	1479	CTGGATTTTTCAGACACTCTACTTTTAAAGGGTCAACGAATTTCTCAGCGTTCTTATCCCT	1538
Dp	427	LeuAsp-PheGlnHisSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerIle	446
Qy	1539	TGAAAAGCTACTTTACCTTGACACTCTCTTAATCTTAACACCAAAATGACTTGAGTGAT	1598
Dp	446	ValArgAsnLeuIleTyrLeuAspIleSerHisIleSerHisIleSerHisIleValAlaPheAsnGlyIle	466
Qy	1599	ATTTCTTGCTGACCAAGTCTCAACACATTTAAATGGCTGGCAATTTCTTCAAGACA	1658
Dp	466	PheAspArgGlyLeuLeuSerLeuLysValLeuLysMetAlaGlyAsnSerPheGlnIleAs	486
Qy	1659	CACCCTTTCAAATGCTTTTGCAAAACACAAACCTTGACATTTCTGTGATCTTCTAAATG	1718
Dp	486	nPheLeuProAspIlePheThrAspLeuLysAsnLeuThrPheLeuAspLeuSerGlnGly	506
Qy	1719	TCAATTTGAAACAATATCTTGGGGGGTATTTTGACACCCCTCAAGACTTCAATATTAAT	1778
Dp	506	ArgIleLeuGluGlnLeuSerProThrAlaPheAspIleLeuAsnLysLeuGlnAlaLeuAs	526
Qy	1779	TATAGTGCACAACAATCTATTGTTTGTGATTTATCCACTTAATTAACAGCTGATTCCTCT	1838
Dp	526	MetSerHisAsnAsnPhePheSerLeuAspValPheProTyrLysCysLeuProSerIle	546
Qy	1839	CAGCACTTTGATGAGTTTCAATGCAATGAGACATTAAGGA--ATACTGCACA	1895
Dp	546	uGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLysAsnGlnGluProGlnHis	566
Qy	1896	TTTTTCCAAAGACTGACCTTCTCAATCTTCAATCTTCAATCTTCTGTTCTGTATATGTA	1955
Dp	566	SPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrGlySerG	586
Qy	1956	ACATCAAGAAATTTCTCAGTGGGTCAAGACAAGACAGATTTCTTGTAATGTTGAACA	2015
Dp	586	uHisGlnSerPheLeuGlnThrIleTyrAspArgGlnAsnGlnLeuLeuValAGluAlaGly	606
Qy	2016	AATGACATGTGCAACCTGTAGAGATGAATACCTCTTAGTGTGGATTTTAATATATTC	2075

FT CARBOHYD 526 526 N-linked (GLCNAC. . .) (Potential1)
 FT CARBOHYD 570 570 N-linked (GLCNAC. . .) (Potential1)
 FT CARBOHYD 575 575 N-linked (GLCNAC. . .) (Potential1)
 FT CARBOHYD 625 625 N-linked (GLCNAC. . .) (Potential1)
 SQ SEQUENCE 833 AA; 95592 MW; 383A84F2BEB55EA CRC64;

Alignment Scores:

Pred. No.: 4,296-207 Length: 833
 Score: 2762.50 Matches: 546
 Percent Similarity: 79.09% Conservative: 112
 Best Local Similarity: 65.62% Mismatches: 170
 Query Match: 53.36% Indels: 5
 Gaps: 3

US-09-396-985b-46 (1-2951) x TLR4_FELCA (1-833)

QY 208 ATGATGCTCCCTGGCTCTGCTGCTGAGACCTGATCATGACATG--TTCTTCTCTGCG 264
 Db 1 MetMetProProthrlArgLeuAlaGlyThrIleuileProAlaMetAlaPheLeuSerCys 20
 QY 265 CTGACACAGAGAACTTGAATCCCTGCTAGAGTAGTACTTCTATATATCTTACCTACCAATGC 324
 Db 21 LeuArgProGluSerThrPaspProCysValGluValAlaProAlaIleThrIleGlnCys 40
 QY 325 ATGATGACGAAGAACTCAGCAAGTCCCTGATGACATTCCTCTTCAACCAAGAAATAGAT 384
 Db 41 MetAspLeuMetLeuHisIleGlyIleProAspAsnIleProSerSerThrIleAspLeuAsp 60
 QY 385 CTGAGCTTCAACCCCTTGAAGATCTTAAAGCTATAGCTTCTCCAAATTTTTCAGAACTT 444
 Db 61 MetSerPheAsnProLeuArgAsnLeuGlySerHisSerPheSerAsnPheProGluLeu 80
 QY 445 CAGTGGCTGATTTATATCATGCTGTAAGTGAATGAACAATGAAGCAAGCATGCGATGCG 504
 Db 81 GlnAlaIleuAspLeuSerArgCysGluIleGlnIleIleGluAspAspAlaIleGlnGly 100
 QY 505 TTACACACACCTCTCAAACTTATAGTACTGACAGAAACCTATCCAGAGTTTTCGCCAGAG 564
 Db 101 LeuAsnHisLeuSerIleLeuIleLeuThrGlyAsnProIleGlnIleArgLeuPheProGly 120
 QY 565 AGTTTCTCTGACTTAACAGTTTGAACAATGCTGGTGGCTGAGACAAATTTGCGCTCT 624
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnThrLeuValAlaValGluThrAsnIleAlaSer 140
 QY 625 CTGAAAAGCTTCCCTATATGACACAGCTTATACCTTTAAAGAACTCAATGTGGCTCAAT 684
 Db 141 LeuGluAspPheProIleGlyHisLeuIleGlySerHisLeuAspValAlaHisIleAsn 160
 QY 685 TTATATCATTCCTGTAAGTACTGACATATTTTTCATCTGACGAGACCTAGTACATGTG 744
 Db 161 LeuIleHisSerPheLeuPheProGluIlePheSerAsnMetSerAsnLeuGluIleu 180
 QY 745 GATCTTTCTTATATCTATATTAATCAACTATATCTGACAGACTTACAGTTTCTACGTGA 804
 Db 181 AspLeuSerAsnAsnLeuIleGlnAlaAsnIleGlyHisLeuAspLeuGlnValLeuHisGln 200
 QY 805 AATCCACAGTCAATCTCTCTTGAACATGTCTTTGAACCCCAATGACTTATTCAGAAC 864
 Db 201 LysProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAspPheIleGlnPro 220
 QY 865 CAACGCTTTCAGGAATTAAGCTCATGACATGACATGACATGAGGAATTTTAAATAGTCA 924
 Db 221 GlnAlaPheLeuGluValIleLeuArgGluLeuThrIleuAspSerAsnPheAsnSerThr 240
 QY 925 AATATATGAAGAACTTCAAAACCTGCTGGTGTATTCACGTCATCGGTGATCTTG 984
 Db 241 AspValMetLysAlaSerIleGlnGlyLeuAlaGlyLeuGlnIleHisGlnLeuValLeu 260
 QY 985 GGAAATTTAAAGTGAAGAAATCTGGAATTTTGAACCTCTATCATGGAAGACTA 1044
 Db 261 GlnIleuPheLysAsnGluArgAsnLeuGlyArgPheAspLysSerIleLeuGlnGlyLeu 280
 QY 1045 TGTGATGTGACATGATGAGTTCAGGTTACATATACAAATGATTTTTCAGATGATAT 1104

Db 281 CysAsnLeuIleIleGlnLysPheArgIleAlaIleArgPheAspLysPheSerGluAspAla 300
 QY 1105 GTT---AAGTTCCATGCTGGCCGAATGTTTTCGCAATGTCCTGGCAGCGTATCTATA 1161
 Db 301 IleAspSerPheAsnCysLeuAlaAsnValSerThrIleSerLeuValHisIleuIleu 320
 QY 1162 AATATATGAGAAAGTTCCTTAACATTTTCAATGAGCAATCTTATCATCATGATGATGAT 1221
 Db 321 LysGlnLeuLysGlnLeuProLysAsnLeuGlyTrpGlnArgLeuGluLeuValAsnCys 340
 QY 1222 CAAGT-AAGCAGTTTCCAACTCTGATCTACCTCTTCTTAAAGTTGACTTTAATGATG 1280
 Db 341 GluPheGlnGluPheProThrIlePheLeuAspProLeuLysGluLeuValPheSerAla 360
 QY 1281 AACAAAGGCTTATCAGTTTAAAAAGTGCCCTTACCAAGTCTCAGTATCTAGATTT 1340
 Db 361 AsnGluValAlaArgAsnAlaPheThrGlnValIleLeuGluSerLeuGluPheLeuAspLeu 380
 QY 1341 AGTGAAGATGACCTGACCTTTAGTGGTGGCTCTTATTCGATTTGGGAACAACAGC 1400
 Db 381 SerArgAsnAspPheSerLeuLysSerCysCysSerGluArgAspLeuGlyThrArg 400
 QY 1401 CTGACACACTTGAACCTCAGCTTCAATGATGACATGATATGATGATGATGATGATGAT 1460
 Db 401 LeuLysHisLeuAspLeuSerPheAsnAsnIleIleThrIleSerSerAsnPheLeuGly 420
 QY 1461 CTGAAGAAGCTGACGACCTCGATTTTTCAGACATCTTATTAAGAGGCTCAGCAAT 1520
 Db 421 LeuGlnGlnLeuGluIleuArgPheGlnHisSerSerLeuLysGlnValSerAsp 440
 QY 1521 CTGACGCTTCTTATCCCTGAAAGCTACTTATCTTGAACATCTTATATCAACCA 1580
 Db 440 eSerValPheLeuProLeuLysAsnLeuArgGlyLeuAspIleSerIleuHisIleGln 460
 QY 1581 AATGACTGATGATGATATTTCTTGGCTTGCACAGTCTCAACATTTAAATAGCTGG 1640
 Db 460 nValAlaPheHisIleGlyIlePheAsnGlyLeuIleIleSerLeuGlnIleLeuLysMetAlaG 480
 QY 1641 CAATCTTTCAAGACAAACCTTTCAATATGCTTTTGAACAAACAAACAACTTGACATT 1700
 Db 480 LysSerPheGlnAspAsnPheLeuProAsnIlePheMetCyluLeuThrAsnLeuThrI 500
 QY 1701 CTTGAGCTCTTGAAGTCAATGTAAGCAAAATATCTGGGGGATTTTGAACCCCTCA 1760
 Db 500 eLeuAspLeuSerAspCysGlnLeuGlnGlnValSerGlnValAlaPheAsnSerLeuP 520
 QY 1761 TAGACTCAATTAATATAGTCAACAACATCTATGTTTGGATTCATCCCATTA 1820
 Db 520 oLysLeuGlnLeuLeuAsnMetSerHisAsnHisLeuLeuSerLeuAspThrLeuProTy 540
 QY 1821 TAACAGCTGATATCCCTCAGACACTCTTGAATGAGTTTCAATGACATAGACATCTAA 1880
 Db 540 rGluProLeuHisSerLeuGlnThrLeuAspCysSerPheAsnArgIleValAlaSerIle 560
 QY 1881 A---GGAATCTGAAATTTTCCAAAGAGTCAAGCTTCTTCAATGTTTAAACAATTC 1937
 Db 560 eGlnGlnGlnLeuArgHisPheProSerAsnLeuSerSerLeuAsnLeuThrArgAsnAs 580
 QY 1938 TGTGCTTGTATATGTAACATCAGAAATTTCTGACATGGGCTCAAGAAACAGAACTT 1997
 Db 580 pPheAlaCysValCysGlnHisGlnSerPheLeuGlnThrValLysAspGlnArgGlnLe 600
 QY 1998 CTGCGAATGTTGAACAAATGACATGTCACAACTGTGAGAGATGAATACCTCTTAGT 2057
 Db 600 uLeuValGlnValGlnIleMetValCysAlaLysProLeuAspMetGlnGlyMetProMe 620
 QY 2058 GTTGATTTTAAATATCTACCTGTTATATGTAACAACAATCATCATGATGATGATGAT 2117
 Db 620 tLeuAsnPheArgAsnAlaThrCysGlnValArgLysThrIleIleThrGlySerValP 640
 QY 2118 CAGTGTATGTGTATCCACTGAGCATTTCTGATATACCACTTCTATTTTCACTGAT 2177

D 640 ethrValleuLeuValpheuValValleuValtyrtyepheThyphHisleu 660
Q 2178 ACTTATGCTGCGCTGTAAGTAACAGAGAGAAAGCATCTATATGATTTGGAT 2237
D 660 tleuLeuValleuGlyCySerlySerlySerlySerlyGlyGlySerlyThyTyraPheVal 680
Q 2238 CTACTCGAGTCAG 2297
D 680 eTySerSerGlnApeGlnApeGlnApeGlnApeGlnApeGlnApeGlnApeGln 700
Q 2298 AGTCCCGCGCTTTCACCTGCTGCTTTCATCAGAGAGAGAGAGAGAGAGAGAG 2357
D 700 yValProProPheGlnleuGlySerlySerlySerlySerlySerlySerlySerly 720
Q 2358 TGGCAATATCATCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2417
D 720 aAlaAsnleileileileileileileileileileileileileileileileile 740
Q 2418 ACACTTATTCAG 2477
D 740 nhisPheileileileileileileileileileileileileileileileile 760
Q 2478 TCTGAG 2537
D 760 eleuSerSerArglyArglyArglyArglyArglyArglyArglyArglyArgly 780
Q 2538 GAGGACAG 2597
D 780 uArgGlnGlnValGlnleuTyArgleuTyArgleuTyArgleuTyArgleuTyArg 800
Q 2598 CAATCTCTGAG 2657
D 800 pSerValleuGlyArgHisleilePheleileValleuGlnleuGlnleuGlnleu 820
Q 2658 AGCCTCGAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2691
D 820 sProArgCySerProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 831
RESULT 10
Q 837 PRELIMINARY; PRT; 837 AA.
AC Q8SP8;
DT 01-JUN-2002 (TREMBlurel. 21, Created)
DT 01-JUN-2002 (TREMBlurel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlurel. 26, Last annotation update)
DE Toll-like receptor 4.
GN Name=TLR4;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21405531; PubMed=11514453;
RA Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
in humans";
RL Genetics 158:1657-1664(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Beutler B., Smirnova I., Hamblin M.T., McBride C., Di Rienzo A.;
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF497565; AAM18617.1; JOINED.
DR EMBL; AF497565; AAM18617.1; JOINED.
DR HSP; O60603; 1077.
DR GO; GO:0046666; C:lipopolysaccharide receptor complex; ISS.
DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR GO; GO:0007205; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR GO; GO:0042116; P:macrophage activation; ISS.

DR GO; GO:0045576; P:mast cell activation; ISS.
DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR GO; GO:0045672; P:negative regulation of interleukin-1 biosyn. . .; ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR000157; TIR.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF00560; LRR_1; 10.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00369; LRR_TYP; 2.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PSS0104; TIR; 1.
DR Receptor.
SQ SEQUENCE 837 AA; 95497 MW; 5A177BAB341396DD CRC64;
Alignment Scores:
Pred. No.: 2.38e-206 Length: 837
Score: 2753.00 Matches: 553
Percent Similarity: 78.86% Conservative: 100
Best Local Similarity: 66.79% Mismatches: 168
Query Match: 53.18% Indels: 8
DB: 2 Gaps: 5
US-09-396-985b-46 (1-2951) x Q8SP8 (1-837)
Q 208 ATGATGCTCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 264
D 1 MecMesSerAlaSerArgleuAlaGlyThleuileProAlaPheleuSerCys 20
Q 265 CTGACACAG 324
D 21 ValArgProGlnSerTyrGlnProGlnProGlnProGlnProGlnProGlnProGln 38
Q 325 ATGATGAG 384
D 39 MecGlnleuAsnPheTyrlsleProAspAsnleuProPheSerThyAsnleuAsp 58
Q 385 CTGAGCTTCAACCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 444
D 59 leuSerPheAsnProleuArgHisleuGlySerTySerPheSerPheProGlnleu 78
Q 445 CAGTGCCTGATTTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 504
D 79 GlnValleuAsnleuSerArgGlyGlnleuGlnleuGlnleuGlnleuGlnleuGln 98
Q 505 TTACACCACTTCAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 564
D 99 leuSerHisleuSerThyrlsleleuThyGlyAsnProleuGlnleuGlnleuGln 118
Q 565 AGTTCTCTGAGCTCAACAACTTGAACAACCTGAGAGAGAGAGAGAGAGAGAGAG 624
D 119 AlaPheSerGlyleuSerSerleuGlnleuValAlaValGlnThrAsnleuAlaSer 138
Q 625 CTAGAAGCTTCCCTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 684
D 139 leuGlnAsnPheProileGlyHisleuTyThleuysGlnleuAsnValAlaHisAsn 158
Q 685 TTATATACCTTCTGTAAGTATGATGATGATGATGATGATGATGATGATGATG 744
D 159 leuileGlnSerPheTyrlsleuProGlnTyPheSerAsnleuThrAsnleuGlyleu 178
Q 745 GATTTCTTAT 804
D 179 AspPheSerSerleuTyrlsleuGlnleuTyrlsleuGlnleuGlnleuGlnleuGln 198
Q 805 AATCACAAGTCAATCTCTTATGACATGCTTGAACCAATTGACTTATCAAGAC 864


```

Db      199 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetThrPheIleGlnPro 218
Qy      865 CAAGCCTTTCAGGAAATTAAGCTCAGTCACTGATCTTAAGAAGTAATTTAATATGCTCA 924
Db      219 G1yAlaPheLysGlnIleArgLeuH1sLysLeuThrIleuArgAsnAspPheAspSerLeu 238
Qy      925 AATTAATAAGAAACTTGGCTTCAAAACCTGGCTGTTTACAGCTCCATCGGTGATCTTG 984
Db      229 AsnValMetLysThrCysIleGlnIleuAlaGlyLeuGluValArgArgLeuValLeu 258
Qy      985 GGAGAAATTTAAAGATGAAGAAGAAATCTGAAATTTTGAACCTCTATCATGGAAGACTA 1044
Db      259 GlyGluPheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 278
Qy      1045 TGATGATGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1104
Db      279 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyrlleuAspTyrlleuAspAspIle 298
Qy      1105 GTTAAG--TTCCATTGGCTGGCGAATGTTCTGCAATGTCTGCGAGAGTGATCTATA 1161
Db      299 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 318
Qy      1162 AAATATCTAGAAGATGTTCTTAACATTTTCAATGCGAATCTTATCATGATAGATGT 1221
Db      319 GluArgValLysAspPheSerTyrlasPheGlyTrpGlnH1sLeuGlnLeuValAsnGly 338
Qy      1222 CAACTAG-CAGTTTCCACTCTGATCTTACCCTTTTAAAGTTGACTTTAATCTATG 1280
Db      339 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 358
Qy      1281 AACAAAGGCTATAGTTTAAATAAGTCCCAAGCCCAAGTCCAGTATCTAGATCTT 1340
Db      359 AsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeu 378
Qy      1341 AGTAAAGATGACATGAGCTTTAGTGGCTGCTGTTTATCTGATTTGGGAAACAACAC 1400
Db      379 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 398
Qy      1401 CTGAGACACTTGAACCTTCAATGCTGATCATGATGATGATGATGATGATGATGATGAT 1460
Db      399 LeuLysTyrlleuAspLeuSerPheAsnGlyValIleThrMetSerSerAspPheLeuGly 418
Qy      1461 CTAGAAGAGCTGACACCTGATTTTACAGATCTTCTTAATAAAGGTCACAGATTT 1520
Db      419 LeuGlnGlnLeuGlnH1sLeuAsp-PheGlnH1sSerAsnLeuLysGlnMetSerGlnPhe 438
Qy      1521 CTCAGCGTTCTTATCCCTTGAAGACTACTTATCTGACATCTTATCTTAAACACCA 1580
Db      438 eSerValPheLeuSerLeuArgAsnLeuIleTyrlleuAspIleSerH1sThrH1sThrAr 458
Qy      1581 AATGACTCTGATGATATATTTCTTGGCTTACACAGTCTCAACACATTTAAATAGCTGG 1640
Db      458 GValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly 478
Qy      1641 CAATCTTTTCAAGACACACCTTTTCAATAGCTTTTGAACAACACAACTGACATTT 1700
Db      478 YAsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 498
Qy      1701 CCTGATGCTCTTAAATGCTCAATTTGAACAATATCTGGGGGGGATTTTGAACACCTTCA 1760
Db      498 eLeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSe 518
Qy      1761 TAGACTTCAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1820
Db      518 rSerLeuGlnValLeuAsnMetSerH1sAsnAsnPheSerLeuAspThrPheProTy 538
Qy      1821 TAACCACTGATTTCCCTCAGACACTTGTGATGATGATGATGATGATGATGATGATGAT 1878
Db      538 rLysCysLeuAsnSerLeuArgValLeuAspTyrlSerLeuAsnH1sIleMetThrSerLys 558
Qy      1879 -AAAGAAATATCTGCAACATTTTCCAAAGAGTCTAGCTCTTCAATCTTAAACAATTC 1937

```

```

Db      558 sLysGlnGlnLeuGlnH1sPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAs 578
Qy      1938 TGTTGCTTGTATATGTAACATCTCAAAATTCCTCAGCGGCTCAAGAGACAGAGCTT 1997
Db      578 pPheAlaCysThrCysGlnH1sGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLe 598
Qy      1998 CTGGTGAATTTTGAACAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2057
Db      598 uLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlnMetProVa 618
Qy      2058 GTTGCAATTTTAATTAATCTTATCTTATATGTAACAACAATCATCATGATGTGCACTGT 2117
Db      618 lLeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLe 637
Qy      2118 CAGTGTATGTGGTATTCACCTGATGATGATGATGATGATGATGATGATGATGATGAT 2177
Db      637 uSerValLeuValSerValValAlaValLeuValTyrlleLysPheTyrlleH1sLeuMe 657
Qy      2178 ACTTATTTGCTGGCTGTAATAAGTACACAGAGAGAGAAAGCATCTATGATGATGATGAT 2237
Db      657 tLeuLeuAlaGlyCysIleLysTyrlArgGlyGlnAsnValTyrlAspAlaPheValIle 677
Qy      2238 CTACTGAGTCAAGATGAGACTGGGTGAGAATGATGATGATGATGATGATGATGATGATGAT 2297
Db      677 eTyrlSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGln 697
Qy      2298 AGTGGCCCGCTTTCACCTCTGCTTCACTACAGAGACTTATTTCTGCTGATGATGATGAT 2357
Db      697 yValProProPheGlnLeuCysLeuH1sTyrlArgAspPheIleProGlyValAlaIleAl 717
Qy      2358 TGCCACATCATCCAGGAAGCTTCCACAAGAGCGGAGAGGTTATTTGGTATGATGATGAT 2417
Db      717 AlaAsnIleIleH1sGlnGlnPheH1sLysSerArgLysValIleValValValSerGly 737
Qy      2418 ACACTTATTCAGACCGCTGTGTGTATCTTGAATATGATGATGATGATGATGATGATGAT 2477
Db      737 nH1sPheIleGlnSerArgTrpCysIlePheGlnTyrlleAlaGlnIleThrTrpGlnPhe 757
Qy      2478 TCTGAGACCGCGCTCTGATCATCTTCTGATGATGATGATGATGATGATGATGATGATGAT 2537
Db      757 eLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnTyrlleLeu 777
Qy      2538 GAGGACAGAGTGAATTTGATGCTCTTCTTACAGAAACCTTACCTGGAATGGAGAGA 2597
Db      777 uArgGlnGlnValGlnLeuTyrlArgLysLeuSerArgAsnH1sTyrlleuGlnIleTrpGlnAs 797
Qy      2598 CAATCTCTGGGAGAGACATCTTCTGAGAGAGACTTAAATAATCCCTATTTGATGAGAA 2657
Db      797 pSerValLeuGlyArgH1sIlePheTrpArgLysLeuArgLysAlaLeuLeuAspGlyLys 817
Qy      2658 AGCCTGCAATCTGAGCAACA 2679
Db      817 sSerTrpAsnProGlnGlyThr 824

```

RESULT 11
 TLK4_PONPY STANDARD; PRT; 828 AA.
 AC Q8SPB9;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, last sequence update)
 DT 05-JUL-2004 (Rel. 44, last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLK4;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21405531; PubMed=11514453;
 RA Saitou N., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
 RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
 in humans."

RL Genetex 158:1657-1664(2001).
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TRAF4.
 CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the toll-like receptor family.
 CC -1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements/>
 CC or send an email to license@ebi.ac.uk).

CC -----
 DR EMBL; AF497562; AAM18616.1; -
 DR EMBL; AF497560; AAM18616.1; JOINED.
 DR EMBL; AF497561; AAM18616.1; JOINED.
 DR HSSP; O60603; 1PYM.
 DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001350; P:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007320; P:activation of NF-kappa-B-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0045216; P:macrophage activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
 DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR_Typ.
 DR Pfam; PF00560; LRR; 12.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_Typ; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS01004; TIR; 1.
 KW Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 828 TIR-like receptor 4.
 FT DOMAIN 24 650 Extracellular (Potential).
 FT TRANSMEM 630 650 Potential.
 FT DOMAIN 631 828 Cytoplasmic (Potential).
 FT REPEAT 50 74 LRR 1.
 FT REPEAT 75 98 LRR 2.
 FT REPEAT 99 122 LRR 3.
 FT REPEAT 126 147 LRR 4.
 FT REPEAT 148 171 LRR 5.
 FT REPEAT 172 195 LRR 6.
 FT REPEAT 201 223 LRR 7.
 FT REPEAT 226 250 LRR 8.
 FT REPEAT 275 301 LRR 9.
 FT REPEAT 325 348 LRR 10.
 FT REPEAT 349 370 LRR 11.
 FT REPEAT 371 396 LRR 12.
 FT REPEAT 398 419 LRR 13.
 FT REPEAT 420 443 LRR 14.

FT REPEAT 445 467 LRR 15.
 FT REPEAT 468 492 LRR 16.
 FT REPEAT 493 516 LRR 17.
 FT REPEAT 518 539 LRR 18.
 FT REPEAT 541 564 LRR 19.
 FT REPEAT 566 590 LRR 20.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 33 33 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 171 171 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 203 203 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 280 280 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 307 307 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 524 524 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 573 573 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 622 622 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 628 628 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 828 AA; 94340 MW; 51AC0984E5970DFD CRC64;

Alignment Scores:

Pred. No.: 3,4e-206 Length: 828
 Score: 2751.00 Matches: 551
 Percent Similarity: 78.74% Conservative: 101
 Best Local Similarity: 66.55% Mismatches: 169
 Query Match: 53.14% Indels: 8
 DB: 1 Gaps: 5

US-09-396-985b-46 (1-2951) x TLR4_PONPY (1-828)

QY 208 ATGATGCTCCCTGGCTCTGCTGAGCATCTGATCATGCGACTG---TTCTTCTCTGCG 264
 1 MetMetSerLaseArGleuIaGlyThleuIleProIaMetLaPheLeuSerCys 20
 QY 265 CTGACACGAGGAGCTTGAATCCCTGATGAGGTGCTTATATATCTCAATGAC 324
 21 ValArgProGluSerThrGluProCys-----ValValProSerIleThrGlnCys 38
 QY 325 ATGATGACGAAAGCTCAGCAAGTCCCTGATGATCTCTTTCACCAAGAAATGATGAT 384
 39 MetGluLeuSerPheThrGlySerIleProAspAsnLeuProPheSerThrGlySerLeuAsp 58
 QY 385 CTGAGCTTCAACCCCTTGAAGATCTTAAAGCTATAGCTTTCCTCAATTTTTCAGAACT 444
 59 LeuSerPheAsnProLeuArgIleGluIleGlySerTyrSerPhePheSerProGluLeu 78
 QY 445 CAGTGGCTGATTTATTCAGAGTGAATGAACAATGAAGCAATGAGCATGGCATGGC 504
 79 GlnValLeuAspLeuSerArgCysGluIleGlnThrIleGluSerGlyAlaTyrGlnSer 98
 QY 505 TTACACCACTCTCAACTGATGATGACAGCAAGAACTTATCCAGAGTTTTCCTCCAGCA 564
 99 LeuSerIleLeuSerThrLeuIleLeuThrGlyAsnProIleGlnAsnLeuAlaLeuGly 118
 QY 565 AGTTTCTCTGAGCTTACCAAGATTTGACAACTGTGGCTGTGAGACAAATTGGCTCT 624
 119 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGluThrAsnLeuAlaSer 138
 QY 625 CTAAAGACTTCCCTATTTGACAGCTTAAAGCTTAAAGAACTCAATGGGCTCACAAT 684
 139 LeuIleAsnProPheProIleGlyAsnIleLeuThrGlySerLeuAsnValAlaAsn 158
 QY 685 TTTATACATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 744
 159 LeuIleGlnSerPheLeuProGluTyrPheSerAsnLeuThrAsnLeuGlnIleLeu 178
 QY 745 GATCTTTCTTAAATCTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 804
 179 AspLeuSerSerAsnLeuIleGlnSerIleTyrCysIleAspLeuGlnValIleGlnIle 198
 QY 805 AATCCACAAGCATCTCTCTTGAACATGCTTGAACCAATGATGATGATGATGATGATGAT 864
 199 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnAlaMetAsnPheIleGlnPro 218

QY 985 GGAGAAATTTAAGATGAAGAAATCTGGAATTTTGAACCCCTCATCATGGAAGACTA 1044
 Db 261 G1ygluPheLysaangluArgLysleuGlnArgPheAspArgSerPheleuGluGlyLeu 280
 QY 1045 TGTGATGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1101
 Db 281 CysasnleuThrIleGluGlnPheArgIleAlaTyLeuAspLysPheSerGlyAspAsp 300
 QY 1102 ATTGTAAATCTCAATGCTGGCAATGCTGCAATGCTGCAATGCTGCAATGCTGCAAT 1161
 Db 301 ThrAspLeuPheAsnGlyLeuAlaAsnValSerValIleSerLeuSerIleSerLeu 320
 QY 1162 AAATATCTGAGAAGATGTTCTTAAACATTTCAATGAGCAATCTTATCAATCATTAAGAT 1221
 Db 321 GlySerleuGlnAlaLeuLysAspPheArgTrpGlnIleAsnGlyIleIleAsnGly 340
 QY 1222 CAATTAAG-CAGTTTCCAACTCTGATATCACTCTTCTTAAAGTTGACTTTAACTATG 1280
 Db 341 AspPheAspLysPheProAlaLeuLysLeuSerSerLeuLysLysPheValPheThrAsp 360
 QY 1281 AACAAAGGCTCTACAGTTTAAAGTGGCCCTACCAAGTCTCAGCTATCTAGATCTT 1340
 Db 361 AsnLysAspLysSerThrPheThrGluPheGlnLeuProSerLeuGlnTyLeuAspLeu 380
 QY 1341 AGTAGAATGCACTGAGCTTTAGTGGTGGTCTTCTTATCTGATTTGGGAACAACAGC 1400
 Db 381 LysArgAsnIleAsnSerPheLysGlyCysCysSerIleThrAspPheGlyThrThrAsn 400
 QY 1401 CTGAGACCTTAAACCTCAGCTTCAATGCTGCCATCATTAAGTCCCAATTTCAATGGGT 1460
 Db 401 LeuTyshIleuAspLeuSerPheAsnAspValIleThrLeuGlySerAsnPheMetGly 420
 QY 1461 CTAGAAGCTGAGCACTGCTGATTTTCAAGCACTTAAAGGTCACAGAAAT 1520
 Db 421 LeuGlnGlnleuGlnIshleuAsp-PheGlnIshSerThrleuLysGlnIleAsnAlaPhe 440
 QY 1521 CTCAGCTTCTTATCCCTTGAAGAACTATTAACCTTGAACATCTTATTAACCAACAA 1580
 Db 440 eSerAlaPheleuSerleuArgAsnleuArgTyLeuAspIleSerTyThrAsnIleAsp 460
 QY 1581 AATTGACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1640
 Db 460 gIleValaPheIshGlyIlePheThrGlyLeuValSerleuGlnIshleuLysMetAlaGly 480
 QY 1641 CAATTCTTGAAGAAACCCCTTCAATGCTTGAAGAAACCAACCAATCTGACAT 1700
 Db 480 YAsnSerPheGlnIshAsnleuLeuProAspIlePheThrGlyLeuThrAsnleuThrIsh 500
 QY 1701 CTTGATCTCTTCAATGCTCAATGGAACAATATCTTGGGGGCTTATTTGACACCTCA 1760
 Db 500 IleAspLeuSerIshCysGlnleuGlnValAlaGlnThrAlaPheIshSerleu 520
 QY 1761 TAGACTTCAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 1820
 Db 520 rSerleuGlnValleuAsnMetSerIshAsnLysleuLeuSerleuAspThrPheLys 540
 QY 1821 TAACCACTGATCTCTCAAGCACTCTTGAATGAGTTCAATGCTTGAAGAAATCTTA 1880
 Db 540 rGluProleuIshSerleuArgIleleuAspCysSerPheAsnArgIleMetAlaSerLys 560
 QY 1881 A---GGAATACGCAACATTTTCCAAAGAGCTAGCTCTTCAATCTTCAATCAATTC 1937
 Db 560 sGluGlnGlnleuGlnAsnleuProArgSerleuThrTrpleuAsnleuThrGlnAla 580
 QY 1938 TGTGCTTGTATATGTAACATCAAGAAATCTCTGAGTGGTCAAGAAAGAGAGCTT 1997
 Db 580 aPheAlaCysValCysGlnIshGlnSerPheleuGlnTrpAlaLysAspGlnArgIle 600
 QY 1998 CTGGTGAATGTTGAAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 2057
 Db 600 uLeuValaGlyAlaGlnIshMetCysAlaGlnProleuAspMetIshAspMetProVal 620
 QY 2058 GTTGATTTTAATTAATCTACTGTTATGTAACAACAATCATCATGCTGCTGCTGCT 2117

Db 620 lLeuSerPheArgAsnAlaThrCysGlnleuSerLysThrIleleuSerValSerVala 640
 QY 2118 CAGTGTATGTGTATGATCACTGATGATGATGATGATGATGATGATGATGATGATGAT 2177
 Db 640 lThrValleuValSerValValGlyValleuValTyIshPheTyPheIshleu 660
 QY 2178 ACTTATGCTGGCTGTAAAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2237
 Db 660 tLeuLeuAlaGlyCysLysLysTyGlyArgGlyGlnSerIleTyAspAlaPheVal 680
 QY 2238 CTACTGAGTCGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 2297
 Db 680 eTySerSerGlnAspIshLysPheValArgAsnGlnleuValLysAsnleuGlnGln 700
 QY 2298 AGTGGCCCGCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2357
 Db 700 yValProProPheGlnleuCysleuIshTyArgAspPheIleProGlyValAlaIleAl 720
 QY 2358 TGCCACATCATCCAGAGAGCTTCCACAGAGCGGAGAGGTTATGTTGATGCTGAT 2417
 Db 720 aAlaAsnIleIleGlnGlnIshPheIshLysSerArgLysValIleValValIshSerGly 740
 QY 2418 ACACTTATTCAGAGCGGTGCTGATCTTGAATGATGATGATGATGATGATGATGATGAT 2477
 Db 740 nHisPheIleGlnSerArgTrpCysIlePheGlnTyGlnIleAlaGlnThrTrpGlnPhe 760
 QY 2478 TCTGAGACGCGCTCTGAGCATCATCTTCAATGCTTGAAGAGTTGAGAGAGTCCCTGCT 2537
 Db 760 eLeuSerSerArgAlaGlyIleIlePheIleValleuGlnLysleuGlnLysSerleuLe 780
 QY 2538 GAGGACAGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2597
 Db 780 uArgGlnGlnValaGlnleuTyArgleuLeuSerArgAsnThrTyLeuGlnTrpGlnAs 800
 QY 2598 CAATCTCTGGGAGAGGACATCTTCTGAGAGAGATTAATAATGCTTATTTGATGAGAA 2657
 Db 800 pSerValleuGlyArgIshValPheTrpArgArgLeuArgLysAlaLeuLeuAlaGlyLys 820
 QY 2658 AGCTCGAATCTGAGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2717
 Db 820 sProGlnSerProGlnGlyThrAlaAspAlaGlnThrAsnProGlnGlnAlaThrIsh 840
 QY 2717 GACC 2712
 Db 840 rThr 841

RESULT 13
 Q8S055 ID PRELIMINARY; PRT: 841 AA.
 AC Q8S055;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RA Ito T., Morimatsu M.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB056444; BAB86840.1; -.
 DR HSSP: O60603; 1077
 DR GO: GO:0046966; C:lipopolysaccharide receptor complex; ISS.
 DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO: GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO: GO:0016046; P:detection of fungi; ISS.

OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovinae; Bos.
 CC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.133957100;
 RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Mowack J.E.;
 RT "haplo type variation in bovine TOLL-like receptor 4 and computational
 RT prediction of a positively selected ligand-binding domain."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369 (2003).
 DR EMBL; AY297043; AA062701.1; -
 DR EMBL; AY297041; AA062701.1; JOINED.
 DR EMBL; AY297042; AA062701.1; JOINED.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003885; LRR_CySt.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF00560; LRR_1; 12.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00365; LRR_SD22; 6.
 DR SMART; SM00369; LRR_Typ; 13.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS0104; TIR; 1.
 KW Receptor.
 SQ SEQUENCE 841 AA; 95954 MW; AD6D06ACBF44CC91 CRC64;

Alignment Scores:

Pred. No.: 1.5e-204 Length: 841
 Score: 2730.00 Matches: 547
 Percent Similarity: 77.08% Conservative: 102
 Best Local Similarity: 64.96% Mismatches: 186
 Query Match: 52.73% Indels: 8
 Gaps: 4

US-09-396-985b-46 (1-2951) x Q6WCD4 (1-841)

QY 208 ATGATGCTCCCTGCTGCTGCTGAGACTGATGATGCA---CTGTTCTTCTCTGC 264
 DB 1 MetMetAlaArgAlaArgLeuAlaAlaLeuLeuProLaThrAlaIleLeuSerCys 20
 QY 265 CTGACACGAGAACTGATGATCCCTGACATAGAGTAGTTCCTAATATTACCTACATGC 324
 DB 21 LeuAlaGlnArgIleuSerTrpAspProCysValGlnValProAsnIleSerTrpGlnCys 40
 QY 325 ATGATGAGAACTGACGAAAGTCCCTGATGATGATCTCTTCTTCAACGAAAGCATAGAT 384
 DB 41 MetGlnLeuAsnLeuTrpIleProAsnIleProIleSerThrIleMetLeuAsp 60
 QY 385 CTGAGCTTCAACCTTGAAGATCTTAAAGCTATAGCTTCCAAATTTTCAAGACTT 444
 DB 61 LeuSerPheAsnTrpLeuArgIleuGlnSerHisAsnPheSerPheProIleu 80
 QY 445 CAGTGGCTGATTTTCAAGGTGTAATGAAATTTGAAACAATTGAAAGACGATGGATGCG 504
 DB 81 GlnValLeuAspLeuSerTrpCysIleLeuValIleGlnAspAspThrPheGlnGly 100
 QY 505 TTACACCACTCTCAACTGTATCTGACAGGAAACCTATCCAGAGTTTTCCTCCACAGA 564
 DB 101 LeuAsnHisLeuSerThrLeuIleuThrGlnAsnProIleGlnSerLeuAlaTrpGly 120
 QY 565 AGTTTCTCTGACATACAGATTGACATCTGGTGGCTGTGAGACAAATTTGGCTCT 624
 DB 121 AlaPheSerGlnLeuSerSerLeuGlnIleuValAlaValGlnThrAsnIleuValSer 140
 QY 625 CTAGAAAGCTTCCATTGACAGCTTAATACCTTAAGAAACGTAATGTGGCTCAAT 684

DB 141 LeuAsnAspPheProIleGlnHisLeuIleAsnLeuIleuGlnLeuAsnValAlaHisAsn 160
 QY 685 TTTATACATTCCTGTATGATTAACCTGCATATTTTCCATGACGAGCACTGATCATGTG 744
 DB 161 PheIleHisSerPheIleuPro****PheSerAsnLeuProAsnLeuGlnHisLeu 180
 QY 745 GATTTCTTATATCTTATTAATCAACTTATTAAGTCTGACAGCACTTACAGTTTCTACGTGA 804
 DB 181 AsnLeuSerAsnAsnIleuGlnAsnIleuTrpGlnuAspValIleuValLeuHisGln 200
 QY 805 AATCCACAGTCAATCTCTCTTATGACATCTTGAACCCATGACCTTATTCACAGAC 864
 DB 201 MetProLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAspPheIleGlnPro 220
 QY 865 CAACCTTCAAGGAAATTAAGCTTCACATGACCTGATTAAGAGGTAATTTAATAGCTCA 924
 DB 221 GlyThrPheIleuGlnIleuLeuAsnGlnIleuThrLeuArgSerAsnPheAsnSerSer 240
 QY 925 AATATTAATGAAAACTTGCTCCCAAAACCTGGCTGTTTACACGTCACTCGGTGATCTTG 984
 DB 241 HisValMetIleuThrCysIleGlnGlnIleuAlaGlnIleuIleuSerThrAsnArgLeuValLeu 260
 QY 985 GGAGAAATTTTAAAGATGAAAGGAAATCTGAAATTTTGAACCTCTATCAGGAGACTA 1044
 DB 261 GlnIleuPheIleuAsnGlnArgIleuGlnArgPheAspArgSerPheLeuGlnGlyLeu 280
 QY 1045 TGTGATGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1101
 DB 281 CysAsnLeuThrIleGlnGlnPheArgIleuAlaIleuLeuIleuAspIleuSerGlnAspAsp 300
 QY 1102 ATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1161
 DB 301 ThrAspLeuPheAsnCysLeuAlaAsnValSerValIleSerLeuLeuSerIleSerLeu 320
 QY 1162 AAATATGTAGAAGATGTTCTTAACATTTGCAATGAGCAATCTTATCATGATGATGAT 1221
 DB 321 GlnSerLeuGlnAlaLeuLeuIleuAspPheArgTrpGlnHisLeuGlnIleuIleuAsnCys 340
 QY 1222 CAACCTAAG-CAGTTTCCACCTGTGAGATCTACCTTTCTTAAAGTTGACCTTAACTATG 1280
 DB 341 AspPheAspIleuPheProAlaLeuIleuLeuSerSerIleuIleuSerPheValPheThrAsp 360
 QY 1281 AACAAAGGATCTACAGTTTAAATAAGTGAGCCCTCAACCAAGCTCAGCTATCTGATGAT 1340
 DB 361 AsnIleAspIleSerThrPheThrGlnPheGlnLeuProSerLeuGlnIleuAsnLeu 380
 QY 1341 AGTGAATGACATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1400
 DB 381 LysArgAsnHisLeuSerPheIleuGlnCysCysSerHisThrAspPheGlnThrThrAsn 400
 QY 1401 CTGAGACACTTGAACCTCAGCTTCAATGAGGCCATCATATGAGTGCCAAATTTGATGGGT 1460
 DB 401 LeuIleHisLeuAspLeuSerPheAsnAspValIleThrLeuGlnSerAsnPheMetGly 420
 QY 1461 CTAGAGAGCTGACGACCTGATTTTACACACTTACTTAATAAGGATGACAGAAAT 1520
 DB 421 LeuGlnGlnLeuGlnHisLeuAsp-PheGlnHisSerThrIleuIleuGlnIleuAsnAlaPhe 440
 QY 440 eSerAlaPheLeuSerLeuArgAsnLeuArgTrpLeuAspIleSerTrpThrAsnIleArg 460
 QY 1581 AATTGACTTGCATGATATATTTCTTGCTTGAACAGCTTCAACATTTAAATGAGCTGG 1640
 DB 460 GlnLeuAlaPheHisGlnIlePheThrGlnLeuValSerLeuGlnIleuIleuSerMetAlaGln 480
 QY 1641 CAATTTCTTGAAGACAAACCTTGAATGCTTGAACCTTGAACCAACAACTTGAACAT 1700
 DB 480 LysAsnSerPheGlnAsnAsnLeuLeuProAspIlePheThrGlnLeuThrAsnLeuThrVal 500
 QY 1701 CTTGATTCCTTCAATGATCAATGAAACAATATCTTGGGGGATTTTGAACACCTTCA 1760

Db 500 lleuAspIeuSerLysCysgluIeuGluInValAlaGluThrAlaPheHisSerLeuSe 520
QY 1761 TAGACTTCATTAATTAATTAAGTCAACAATCTATGTTTGGATTCATCCCATTA 1820
Db 520 rSerLeuGluValIeuAsnMetSerHisAsnLysLeuIeuSerLeuAspThrPheLeuTy 540
QY 1821 TAACCAAGCTGATTCCTCAGACACTTGTGATTCAGTTTCATCGCATAGACATCTAA 1880
Db 540 rGluProIeuHisSerLeuArgIleLeuAspCysSerPheAsnArgIleMetAlaSerLy 560
QY 1881 A---GGAAATCTGCAACATTTCCAAAGAGCTTAGCCTTCTCAATCTTACTAAATTC 1937
Db 560 sGluGluIleuGluInAsnLeuProArgSerLeuThrLTrpLeuAsnLeuThrGluAsnAl 580
QY 1938 TGTTCCTGTATATGTGACATCAGAAATCCCTGACAGGGTCAAGGACAGAAAGCAGTT 1997
Db 580 aPheAlaCysValCysgluHisSerPheLeuGluInTrpValLysAspGluArgGluLe 600
QY 1998 CTTGTGATGATGTGACAAATGACATGTGCAACACTGTAGAGATGAATACCTCCTTAGT 2057
Db 600 uIeuValGlyAlaGluInMetMetCysAlaGluProIeuAspMetGluAspMetProVa 620
QY 2058 GTTGGATTTAATTAATCTTACCTGTATATGATACAGACATCATCATGCTGTACATGCT 2117
Db 620 lIeuSerPheArgAsnAlaThrCysgluIeuSerLysThrIleIleSerValSerValVa 640
QY 2118 CAGTGATGATGTGATTCACCTGTAGCATTTCTGATATACCACTTCTATTTTCACTGAT 2177
Db 640 lThrValIeuIeuValSerValValGlyValIeuValTyIlyPheTyIlyPheHisLeuMe 660
QY 2178 ACTTATTCCTGGCTGTAAAAAGTACACAGACAGAGAAAGCATCTATGATGATTTGTGAT 2237
Db 660 tIeuLeuAlaGlyCylSerLysTyIlyArgGlyGluSerIleTyIlyAspAlaPheValIl 680
QY 2238 CTACTCGAGTCAGATAGAGACTGGGTGAGAAATGACGTGTAAAGATTTAGAGAGAG 2297
Db 680 eTyIlySerSerGluAspGluAspTrpValArgAsnGluIeuValLysAsnIeuGluGluGl 700
QY 2298 AGTGCCCGCGCTTCACCTGCGCTTCACCTACAGAGACTTATTCCTGTGTAGCCATGCG 2357
Db 700 yValProProPheGluIeuCysLeuHisTyIlyArgAspPheIleProGlyValAlaIleAl 720
QY 2358 TGCCACATCATCCAGAGAGGCTTCACAAGAGCCGAGAGGTTATGTGTAGTGTCTAG 2417
Db 720 aAlaAsnIleIleGluIeuTyIlyPheHisLysSerArgLysValIlleValValValSerGl 740
QY 2418 ACACCTTATTCAGAGCCGTTGGTGTATCTTGAATATGAGATTCCTCAACATGCGAGTT 2477
Db 740 nHisPheIleGluIeuSerArgTrpCysIlePheGluTyIlyIleAlaGluInThrTrpGluInPh 760
QY 2478 TCTGAGACAGCGGCTCTGGCATCATCTTCATTCCTTGAGAAAGGTTGAGAAAGTCCCTGCT 2537
Db 760 eIeuSerSerArgAlaGlyIleIlePheIleValIeuGluInLysLeuGluLysSerLeuLe 780
QY 2538 GAGGACAGAGGTGAAATTTGATTCGCTTCTTAGCAGAAACACTACCTGGAATGGAGAGA 2597
Db 780 uArgGluInValGluIeuTyIlyArgLeuIeuSerArgAsnThrTyIlyIeuGluIuTrpGluAs 800
QY 2598 CAATCTCTGGGGAGGCACTTCCTTGAGAAAGCTTAAAAATGCCCTATTTGAGATGGAAA 2657
Db 800 pSerValIeuGlyArgHisValPheTrpArgArgLeuArgLysAlaIeuIeuAlaGlyLy 820
QY 2658 AGCCTCGAATCTGACGAAACAGAGAGAGAA-----CAAGAAACGGCAACTTG 2708
Db 820 sProGluIeuSerProGluGlyThrAlaAspAlaGluThrAsnProGluInGluAlaThrThrSe 840
QY 2709 GACC 2712
Db 840 rThr 841

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 09:56:53 ; Search time 755 Seconds
(without alignments)
19454.816 Million cell updates/sec

Title: US-09-396-985B-47

Perfect score: 33065
Sequence: 1 tccccctactcttcacatt.....catgaabdcabdcabydc 18989

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p model -DEV=xlh
-Q=cg22_1/USFT0.spool/US0939685/Runat_28032005_155742_21135/app_query.fasta_1.85098
-DB=A-Geneseq_16Dec04 -QMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US0939685 @CGN 1.1_4007 @runat_28032005_155742_21135 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESUBSTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A-Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3905.5	11.8	839	6	ABU04773 Human exp
2	3905.5	11.8	839	6	ABU04774 Human exp
3	3905.5	11.8	839	6	ABU04775 Human exp
4	3905.5	11.8	839	7	ADDC78785 Human PRO
5	3905.5	11.8	839	7	ADDC48826 Human PRO
6	3903.5	11.8	799	2	AAW86352 Human DNA
7	3903.5	11.8	799	5	AAE16093 Human DNA
8	3903.5	11.8	799	5	ABR83162 Human Tol
9	3903.5	11.8	799	6	ABR42963 Human Tol
10	3903.5	11.8	799	7	ADB39121 Human tol

11	3903.5	11.8	799	8	ADP56656
12	3903.5	11.8	799	8	ADP48597
13	3903.5	11.8	837	2	AAW86361
14	3903.5	11.8	837	5	AAE16102
15	3903.5	11.8	837	6	ABU04776
16	3896.5	11.8	837	5	AAE16116
17	3889.5	11.7	808	8	ADOS7782
18	3878.5	11.7	808	8	ADOS7785
19	3875.5	11.7	808	8	ADOS7803
20	3794	11.5	728	8	ADP29455
21	3751.5	11.3	801	8	ADOS7788
22	3629.5	11.0	795	8	ADOS7791
23	3612.5	10.9	795	8	ADOS7800
24	3544.5	10.7	801	8	ADOS7797
25	3501	10.6	745	8	ADOS7794
26	1090	3.3	208	3	AAW86059
27	919	2.8	178	8	ADN12270
28	785	2.4	179	7	ADC42707
29	561.5	1.7	784	2	AAW86350
30	561.5	1.7	784	5	AAE16091
31	561.5	1.7	784	5	ABR83161
32	561.5	1.7	784	8	ADN02005
33	560.5	1.7	784	2	AAW05869
34	560.5	1.7	784	6	ABU61956
35	560.5	1.7	784	7	ADL15005
36	560.5	1.7	784	8	ADP56652
37	560.5	1.7	784	8	ADP48593
38	560.5	1.7	784	8	ADQ66397
39	560.5	1.7	784	8	ADP23787
40	560.5	1.7	784	8	ADQ39727
41	560.5	1.7	784	8	ADQ39728
42	557.5	1.7	784	2	AAW48245
43	557.5	1.7	784	2	AAW90069
44	557.5	1.7	784	5	ABG73879
45	557.5	1.7	784	5	AAW50618

ALIGNMENTS

RESULT 1	ABU04773	standard; protein; 839 AA.
ID	ABU04773	
AC	ABU04773	
XX		
DT	29-JAN-2003	(first entry)
XX		
DE	Human expressed protein tag (EPT) #1439.	
XX		
KW	Transational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein;	
KW	receptor; transcription factor; cancer; MHC;	
KW	major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200278524-A2.	
XX		
PD	10-OCT-2002.	
XX		
PF	28-MAR-2002; 2002WO-US009671.	
XX		
PR	28-MAR-2001; 2001US-0279495P.	
PR	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326370P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358985P.	
XX		
PA	(ZYCO-) ZYCOS INC.	
XX		
PI	Chicz RM, Tomlinson AJ, Urban RG;	

```

XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX PT tracing cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX PS Example 2; SEQ ID NO 1439; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that bind to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIP0 at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 839 AA:

Alignment Scores:
Pred. No.: 0 Length: 839
Score: 3905.50 Matches: 773
Percent Similarity: 93.46% Conservative: 13
Best Local Similarity: 91.91% Mismatches: 20
Query Match: 11.81% Indels: 35
DB: Gaps: 6

US-09-396-985b-47 (1-18989) x ABU04773 (1-839)
QY 11992 TGCTTATGCTGATGCTTAAACATGACAAAAAGCCTATCATTTGACGCCAGTATGATAA 12051
DB 29 CyvalalgluValalProaenilleThryrGlnCymetGluLeuAen----- 44
QY 12052 TACTCACTCTGTGGGGCTTCTTATTCCTT-----ATTCATCATCATCTGTCTG 12102
DB 45 -----PheTyrlYsileProaPhanLeuProPheSerThrlYsAsn 58
QY 12103 CTTGATGCTTTGGCCTATGACATCATATGACCCA---TCACATCTGTATGAAGAGCTG 12159
DB 59 LeuAsnLeu-----SerPheAsnProLeuAenrghis----- 68
QY 12160 GATGACATGAGTAAATATTCTATTATTTAGGTTCTTATTC---GCAGAAATATTAGATTAAT 12216
DB 69 -----LeuGlySerTySerPhePheSerPheProGluLeu 80
QY 12217 CAATGCTTTTATTCTCTGATGCTGTAAGATTCAGCAATTAAGATGGGCAATTCAGA 12276
DB 81 GlValAlaLeuAsnLeu--SerArgCysGluIleGlnTrlIleGluAspGlyAlaTyrlGlns 100
QY 12277 GCCTAAGCCACCTCTTACCTTATATTATGACAGAAACCCCATCCAGAGTTTACCGCTGG 12336
DB 100 erLeuSerHisbueSerThrlleuThrGlyAenProIleGlnSerLeuAlaLeuG 120
QY 12337 GAGCCTTTTTCGACTATCAAGATTACAGAAAGCTGTGCTGTGAGAGCAAAATTCAGAT 12396
DB 120 lYalAlaPheSerGlyLeuSerSerLeuGlnYsLeuValAlaValGluThrAsnLeuAlas 140
QY 12397 CTCTAGAGAACTTCCCATTTGAGACATCTCAAAACTTTGAAAGACTTAATGTGCTACA 12456
DB 140 erLeuGluAsnPhProIleGlyHisLeuYsrThrLeuYsGluLeuAsnAlaAlaHisA 160
QY 12457 ATCTTATCAATCTTTCAAAATTAACCTAGATATTTTCTTATCTAGCAACATCTAGACACT 12516

```

```

DB 160 snLeuIleGlnSerPheYsLeuProGluTyPheSerAsnLeuThrAsnLeuGluHisIel 180
QY 12517 TGGACCTTTCCAGCAACAAAGATTTCAAAAGATTTATTTGACACAGCTTGGGGTTTCAATC 12576
DB 180 euaSpLeuSerSerAsnYsIleGlnSerIleTyrcTySerThrsPheuAaGValLeuHisG 200
QY 12577 AAATGCCCTTACTCAATCTCTCTTTAGACCTGTCCCTGAACCTTGAACCTTATTCACAC 12636
DB 200 lmetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPhelIleGlnP 220
QY 12637 CAGGTGCATTTTAAAGAAATTAAGCTTCATTAAGCTGACTTTAAAGAAATTTGATAGTT 12696
DB 220 rodYlAlaPheYsGluIleArgLeuHisIeYsLeuThrLeuXrGAsnAsnPhaSerI 240
QY 12697 TAAATGTATGAAAACTTGTATTCMAAGCTGTGGCTGTTAAGACCCATCCGTTGCTTC 12756
DB 240 euaAsnValMetYsrThrCysIleGlnGlyLeuAlaIleuGluValAlaSarGLeuValL 260
QY 12757 TGGGAAATTTTGAATGAAAGAACTTGAAAGAAAGTTTGACAAATCGCTTAGAGGGCC 12816
DB 260 eudYlGluPheAsnGAsnGluGlyAsnLeuGluYsPheAspYsSerAlaLeuGluGly 280
QY 12817 TGTGCAATTTGACCATTTGAAAGAAATTCGATTAAGCATTAAGACTAATCCTCGATGATA 12876
DB 280 eucYsAsnLeuThrIleGluGluPheArgLeuAlaTyrlLeuAspTyrlYrYrLeuAspAspI 300
QY 12877 TTTATGACTTATTTAATTTGTTTGAACAAATGTTTCTTCAATTTCCCGTGAGAGTACATA 12936
DB 300 lelleAspLeuPheAsnCySleuThrAsnValSerSerPheSerLeuValSerValThrI 320
QY 12937 TTGAAAGGGTAAAGAACTTTTCTTAAATTTCCGATGAGCAACTTATAGATTAATTAAGT 12996
DB 320 ledIuXrYValIyAsaPheSerTyAsnPhelYrIrgIlnHisleuGluLeuValAsn 340
QY 12997 GTAATTTTGACAGTTTCCCACTTGAAATCTCAAACTCTGCAAAAGGCTTACTTCACTT 13056
DB 340 yslYsPheGlyGlnPheProThrLeuYsLeuYsSerLeuYsArgLeuThrPheThrS 360
QY 13057 CCACAAAGGTGGGAATGCTTTTTCAGAGCTGATCTTACCAAGCCTTGAGTTCTTGATGC 13116
DB 360 exAsnYsGlyYsAlaAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspI 380
QY 13117 TCAGTGAAGATGGCTGAGTTTCAAGAGTTGCTGTTCTCAAGATGATTTTGGACAACCA 13176
DB 380 euaSerArgAsnGlyLeuSerPheYsGlyCySerserGlnSerAsnPhaGlyThrThrs 400
QY 13177 GCCTAAAGATTTAGATCTGAGCTTCAATGTGTGTTATTCACATGAGTTCAAACTTTGG 13236
DB 400 erLeuYsrTyrlleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPhaLeuG 420
QY 13237 GCTTAAAGCAACTGAAACATCTGAGATTTCCAGATTCCAATTTGAAACAAATGAGTACG 13296
DB 420 lYleuGluGlnLeuGluHisIeLeuAspPheGlnHisSerAsnLeuYsGlnMetSerGlu 440
QY 13297 TTTCAAGATTCATATCAGACCTAGAAACCTCATTAACCTTGACATTTCTCATATCTCACACCA 13356
DB 440 heserValPheLeuSerLeuAsnArgAsnLeuIleYrLeuAspIleSerHisThrHis 460
QY 13357 GAGTTCCTTTCATGAGCATCTTCAATGCTGTGTCAGATCTCGAAGCTTGGAAAAAGGCTG 13416
DB 460 rGValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuYsMetAlaG 480
QY 13417 GCAATTCCTTCCAGAAAACCTTCTTCCAGATATCTTCACAGAGCTGAGAAAACCTTGACCT 13476
DB 480 lYAsnSerPheGlnGluAsnPhaLeuProAspIlePheThrGluLeuAaGAsnLeuThr 500
QY 13477 TCCGTGACCTCTCTCAGTGCATCTGAGAGAGTGTCTCCAAACAGACTTAACTCACTCT 13536
DB 500 heLeuAspLeuSerGlnCySglnLeuGluIleuSerProThrAlaPheAsnSerLeuS 520
QY 13537 CCAAGCTTCAGTACTTAATATATGAGCACAAACCTTCTTTGATGATACGTTTCCTT 13596

```

Db	520	erserleuGlnValleuAsnmeSerHisAsnAsnAsnPhenPheSerleuAspThrPheProT	540
QY	13537	ATMAAGTCTGAACATCCCTCCAGGTTCTTGAATPACGTCTCAATCAATATGACTTCCA	13656
Db	540	yrLysCybLeuAsnSerleuGlnValleuAspTrySerleuAsnHisIleMetThrSerL	560
QY	13657	AAAAACAGGAACSTACAGATTTTCCAGATGAGTGTAGTCTTCTTAATCTTACTCSGAAG	13716
Db	560	ybLysGlnGluLeuGlnHisPheProSerSerleuAlaPheLeuAsnLeuThrGlnAspA	580
QY	13717	ACTTGGCTTGTACTTGTGAACACACAGAGTTTCTGTCAATGATCAAGACCCAGAGCAGC	13776
Db	580	sPheIleAcysThrCysGluHisGlnSerPheLeuGlnTrpIleuysAspGlnAArgGln	600
QY	13777	TCTTGGTGAAGATTGAACGAATGGATGTGCAACACCTTCAGTAAAGAGGAGATGCCGTG	13836
Db	600	euleuValGluValGlnAArgMcGluCysAlaThrProSerAspLysGlnGlyMetProV	620
QY	13837	TGCGAGTGTGAATATACCTGTCCAGATGAATGAATGAACATCATGGTGTGTGGTCTCA	13896
Db	620	AlIuSerleuAsnHisLeThrCysGlnMetAsnLysThrIleIleGlyAlaSerValLeuS	640
QY	13897	GTGTGCTTGTAGATTCCTGTGTGAGAGCTTGTGGCTATGAAGTCTATTTTCACTGATGC	13956
Db	640	erValleuValValSerValValAlaValleuValYrLysPheIleYrPheHisbleuMetL	660
QY	13957	TTCTTGCTGTGCGATMAAGTATGTAGAGGTGAACAAACATCTATGATGCCCTTGTATCT	14016
Db	660	euleuAlaGlyCysIleLeuTyrcLysGluLysAsnIleTyrcAlaPheAlaPheValIleT	680
QY	14017	ACTCAACCCAGATGAGAGGACTGGGTGAAGAAATGAGCTATGAAGAATTGAAGAAAGGG	14076
Db	680	ybSerSerGlnAspGlnAspTrpValAArgAsnGluLeuValLysAsnLeuGlnGluGlyV	700
QY	14077	TGCTTCATTTACAGCTGTGCTTTCACATCAAGAGACTTTATCCCGGTGTGGCATTTGCG	14136
Db	700	AlProPhePheGlnLeuCysLeuHisGlyrAspAspPheIleProGlyAlaAlaIleAlaA	720
QY	14137	CGAACATCATTCATGAAGTTTCCATMAAACCGAAAGGTGATTTGTGTGTGCCAGC	14196
Db	720	IaAsnIleIleHisGlnGlyPheHisblySerAspGlyValIleValValSerGlnH	740
QY	14197	ACTTCATCCAGAGCCGCTGGTGTATCTTTGAATATGAAGTTGCTCAGACCTGGCAGTTTC	14256
Db	740	IsPheIleGlnSerAspTrpCysAlaPheGluTyrcLuiIleAlaGlnTrpGlnPheL	760
QY	14257	TGAGCAGTCCGAGCGGTATCATCTTCATTTGCTGTGAGAGAGGTGAGAAAGCCGTGCA	14316
Db	760	eulerSerAspAlaGlyIleIlePheIleValleuGlnLysValGlnLysThrIleLeuA	780
QY	14317	GCGCAGAGGTGAGCTGTACCGGCTTCTCAGCAGAAACAATTACCTGAGTGGAGAGCA	14376
Db	780	rgGlnGlnValGluLeuTyrcArgLeuLeuSerAspGlnHisThrLysGlnLutrpGluAspS	800
QY	14377	GTGTCCCTGGGGCGGACATTTTCTGAGAGAGCACTCAGAAAGCCGTGCTGATGGTAAT	14436
Db	800	erValleuGlyAspHisIlePheTrpAspArgLeuAspGlyValaLeuLeuAspGlyLysS	820
QY	14437	CATGGAATCCAGAAAGGAACGTGGGTACAGAAATGCAATTGGAGAGGAACAAATCATATC	14495
Db	820	erTrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle	839
RESULT 2			
ID	ABU04774	standard; protein; 839 AA.	
XX	ABU04774;		
AC	29-JAN-2003	(first entry)	
XX			
DT		Human expressed protein tag (EPT) #1440.	
XX			
DE			
XX			
XX		Translational profiling; expressed protein tag; EPT; kinase; phosphatase;	

KM protease, protease inhibitor; transporter; cytoskeletal protein;
 KM receptor; transcription factor; cancer; MHC;
 KM major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KM adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 XX WO200278524-A2.
 XX
 XX 10-OCT-2002.
 XX
 PD 28-MAR-2002; 2002WO-US009671.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 XX 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1440; 134p; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPR) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 839 AA;
 XX
 Alignment Scores:
 Pred. No.: 0 Length: 839
 Score: 3905.50 Matches: 773
 Percent Similarity: 93.46% Conservative: 13
 Best Local Similarity: 91.91% Mismatches: 20
 Query Match: 11.81% Indels: 35
 DB: Gaps: 6
 XX
 US-09-396-985B-47 (1-18989) x ABU04774 (1-839)
 QY 11992 TGCTTATCATGTAAGCTTAAGCAAAAGAGGCTATCATTCAGCGCAGATGATTA 12055
 DB 29 CyvaValgluValValProbenlleIrrYrGlhCymecGluLeuasn----- 44
 QY 12052 TACTCAGTCTGTGGGAGCTTCTTATTTGCTT-----ATTCCATCATCATCTGTCTG 12102
 DB 45 -----PheTyxrlYsIlleProaPasnleuProheSerhrlYrsaen 58
 QY 12103 CTTGATGTCTTTGGCCATATGACATGACATATATGACCC---TACATCTGTATGAAAGAGCTG 12155
 DB |||||||::: |||::: |||

Db 59 LeuAspLeu-----SerPheAsnProLeuArgHis----- 68
QY 12160 GATGACTAGGATTAATATTCTATTTAGGCTCTATTCA---GCAGAAATATTAGATTAAT 12216
Db 69 -----LeuGlySerTyrSerPheSerPheProGlnLeu 80
QY 12217 CAATGCTTTTATTCCTGTAGTGTGAATAATCCAGACAAATTGAAAGTGGGCAATATCAGA 12276
Db 81 GlnValLeuAspLeu--SerArgCysGlnIleGlnIleThrIleGlnAspGlyAlaTyrGlnHis 100
QY 12277 GCTTAAGCCACTCTCTACTCTTAATATTTGACAGAAACCCCATCCAGAGTTTATGCCCTGG 12336
Db 100 etLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaIleGln 120
QY 12337 GAGCCTTTCTGGACATATCAAGTTTACAGAGCTGGTGGTGGAGACAAATCTAGCAT 12396
Db 120 LysAlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaHis 140
QY 12397 CTCTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAAAGAACTTAAATGTGGCTCAGA 12456
Db 140 etLeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGlnLeuAsnValAlaHisAs 160
QY 12457 ATCTTATCCAAATTTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGAGCACT 12516
Db 160 snLeuIleGlnSerPheLysLeuProGlnTyrPheSerAsnLeuThrAsnLeuGlnHisIle 180
QY 12517 TGGACCTTTCCAGCAACAAGATTCAAAAGTATTATTTGACAGACTTGGCGGTCTCAATC 12576
Db 180 euAspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisG 200
QY 12577 AAAATGCCCTACTCAATCTCTCTTTAGACCTGTCCCTGAACCCCTATGAACTTTATCCAAAC 12636
Db 200 lmeProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnP 220
QY 12637 CAGGTGCATTTAAAGAAATTTAGGCTTCATAGCTGACTTAAAGAAATTAATTTGATGATT 12696
Db 220 rGlyLysAlaPheLysGlnIleArgLeuHisLysLeuThrLeuArgAsnPheAspSerI 240
QY 12697 TAAATGTATTAAGAAACTTGATATTCAGAGCTGGCTGGTGTAAAGTCCATCCGTTGGTTC 12756
Db 240 euAsnAlaIleCysIleTyrCysIleGlnGlyLeuAlaGlyLeuGlnValHisAspGlyLeuValHis 260
QY 12757 TGGAGAAATTTAGAAATGGAAGAAACTTGGAAAAGTTTGCAAAATGTGCTAGAGGACC 12816
Db 260 euGlyLysPheArgAsnGlnLysAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyHis 280
QY 12817 TGTGCATTTTGACATTTGAAGAATTCGATTAGCAATCTTACACTACTGCTGATGATA 12876
Db 280 euCysAsnLeuThrIleGlnGlnPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspI 300
QY 12877 TTAATGACTTAATTAATTTGTTGACAAAGTTTCTCATTTTCCCTGGAGGTGAGTACTA 12936
Db 300 lLeIleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrI 320
QY 12937 TTGAAAGGGTAAAGAACTTTTCTTAATTAATTCGATGGCAACATTTAGAAATTAATTAAGT 12996
Db 320 lGlyLysArgValLysAspPheSerTyrAsnPheGlyTyrGlnHisLeuGlnLeuValAsnG 340
QY 12997 GTTAAATTTGACAGTTTCCCACTTGAACATTAATCTCAAAAGGCTTACTTCACTT 13056
Db 340 yelLysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrHis 360
QY 13057 CCAACAAAGGTGGAGATGCTTTTTCAGAGTTGATCTACCAACCTTGAAGTTTCTAGATC 13116
Db 360 etAsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspI 380
QY 13117 TCAGTGAAGATGGCTTGAAGTTTCAAAAGTTTGTCTCAAAAGTGAATTTTGGACAACA 13176
Db 380 euSerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrHis 400
QY 13177 GCCTAAAGTATTTAGTCTGAGCTTCAATGTGTGTTATTAACGATGATCAAACTTCTTGG 13236
Db 400 etLeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuG 420

QY 13237 GCTTAGAACAACTAGAACATCTGGAATTCACAGATTCCAATTTTGAAACAAATGAGTACT 13296
Db 420 LysLeuGlnIleuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnImeSerGlnP 440
QY 13297 TTTCAATATTCCTATCACTCAGAAAACCTTATTAACCTTGACATTTCTCACTACACCA 13356
Db 440 heSerValPheLeuSerLeuAsnLeuIleTyrLeuAspIleSerHisThrHisThrAs 460
QY 13357 GAGTTCCTTCAATGGCATCTTCAATGGCTTGTCCAGTCCGAAAGCTTGGAAAATGGCTGG 13416
Db 460 rGValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaG 480
QY 13417 GCAATCTTCTCCAGGAAAACCTTCCCTCCAGATATCTTCACAGAGCTGAGAAACTGACCT 13476
Db 480 LysAsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGlnLeuAsnLeuThrP 500
QY 13477 TCTTGACCTCTCTCAGTGTCAACTGAGACAGTTGTCTTCAACAGCATTTAACTCATCTCT 13536
Db 500 heLeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuS 520
QY 13537 CCAAGCTTCAAGTACTTAATATAGACCCACACAACCTTCTTTCATTTGATAGTTTCCTT 13596
Db 520 etSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProT 540
QY 13597 ATTAAGTGTGAAACTCCCTCCAGAGTTCTTGATTAAGCTGCAATGACATTAATGACTTCCA 13656
Db 540 yTrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetHisSerL 560
QY 13657 AAAAACAGGAACATAACAGATTTTCCAGAGTACTAGCTTTCTTAAATCTTACTCAGAAATG 13716
Db 560 yelLysGlnGlnIleuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnA 580
QY 13717 ACTTTGCTTGATCTTGTGAACACCAAGATTTCTTGCAATGATCAAGAACCAAGGCAAC 13776
Db 580 spPheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnHis 600
QY 13777 TCTTGGTGGAAGTTGAACGAAGGAATGTGCAACACCTTCAGATTAAGCGGCACTGCTG 13836
Db 600 euLeuValGlnValGlnAspMetGlnCysAlaThrProSerAspLysGlnLysMetProV 620
QY 13837 TGTGAGTTGGAATATCACCTGTCAAGATGAATGAACCATCATTTGGTGTGTGCTGTCA 13896
Db 620 alLeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuS 640
QY 13897 GTGTGCTTGTATATCTGTGTGAGCAAGTTCTGTCTTAAGTTCTTAATTTTCACTGATGC 13956
Db 640 etValLeuValAlaSerValAlaValLeuValTyrLysPheTyrPheHisLeuMetL 660
QY 13957 TTTCTGCTGGCTGAATAAAGTATGGTGAAGTGAAGAAACATCTATGATGCTTTGTTATCT 14016
Db 660 euLeuAlaGlyCysIleLysTyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIleT 680
QY 14017 ACTCAAGCCAGAGATGAAGACTGGGTGAAGGAATGAGCTAGTAAAGATTTTGAAGAGGG 14076
Db 680 ySerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlnLys 700
QY 14077 TGCCTTCATTTAGCTCTGCTTCACTACAGAGACTTATTTCCCGGTGGCCATTTGCTG 14136
Db 700 alProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleValAs 720
QY 14137 CCAACATATCCATGAAGGTTTCCATTAAGCCGAAAGGTAATGTGTGGTGGTCCCAAG 14196
Db 720 lAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValValSerGlnHis 740
QY 14197 ACTTATCCAGAGCCGCTGGTGTATCTTGAATATGAGATTTGCTGACCTGGCAGTTTC 14256
Db 740 lAspHeIleGlnSerThrArgTrpCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPheI 760
QY 14257 TGAAGAGTGTGCTGGTATCATTTCAATTTGCTTGTGCAAGAGGTGAGAAAGACCTGTCTCA 14316
Db 760 euSerSerArgLacGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuA 780

QY 14317 GCGACAGAGTGGAGCTGTACCGCCTTCTTCAGAGCAACCTTACCTGAGTGGAGGACA 14376
 DB 780 TGGTGGTGGGCGGACACATCTTCTGAGACCACTTCAAGAAAGCCCTGCTGATGATTAAT 14436
 QY 14317 GTCCTCTGGGCGGACACATCTTCTGAGACCACTTCAAGAAAGCCCTGCTGATGATTAAT 14436
 DB 800 erValLeuGlyARghisIstlePheTrpArgLeuARlyAlaLeuLeuaspGlyLys 820
 QY 14437 CATGGAATTCAGAGAGACAGTGGTACAGATGCAATTTGGCAGAGCAACATCTATC 14495
 DB 820 erTrpAsnProGluGlyThrValGlyThrGlyCysAsnTrpGlnAlaThrSerIle 839
 RESULT 3
 ABU04775
 ID ABU04775 standard; protein; 839 AA.
 AC ABU04775;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1441.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN MO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PE 28-MAR-2002; 2002MO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOs INC.
 XX
 PI Chiciz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1441; 134p; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIP0 at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 839 AA;
 Alignment Scores:
 Pred. No.: 0
 Score: 3905.50
 Percent Similarity: 93.46%
 Best Local Similarity: 91.91%
 Query Match: 11.81%
 DB: 6 Gaps: 6
 US-09-396-985B-47 (1-18989) x ABU04775 (1-839)
 QY 11992 TGCCTTATCATGTATGCTTACATGACAAAGAGCCATCATGAGCCAGTATGATTA 12051
 DB 29 CysValGluValValProAsnIleThrTyrGlnCysMetGluLeuAsn----- 44
 QY 12052 TACTCAGTCTGTGGGCTTCTTATTTGCTT-----ATTCATCATCATCTGCTCTG 12102
 DB 45 -----PheTyrLysIleProAsnLeuProPheSerThrLysAsn 58
 QY 12103 CTTCATGCTCTTGGCTTATGACATCATATGACCCA---TCACATCTGTATGAAGAGCTG 12159
 DB 59 LeuAspLeu-----SerPheAsnProLeuArgHis----- 68
 QY 12160 GATGACTAGATTAATATTCATTTTATGTTCTTATTCAC---GCAGAAATATTAGATTAAT 12216
 DB 69 -----LeuGlySerTyrSerPhePheSerPheProGluLeu 80
 QY 12217 CAATGCTTTTATTCCTGAGTGTGAAATTCAGACATATGAAATGGGCAATATGAGA 12276
 DB 81 GlnValLeuAspLeu--SerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlns 100
 QY 12277 GCCTAACCCACCTTCTTACCTTAATATTGACAGAAACCCCATCATCAAGTTTACCCCTGG 12336
 DB 100 erLeuSerHisLeuSerThrLeuIleuThrGlyAsnProIleGlnSerLeuAlaLeuG 120
 QY 12337 GAGCCTTTTTCGAGCTATCATGATTTACAGAAAGCTGTGGTGGAGACAAATATGACT 12396
 DB 120 lValaPheSerGlyLeuSerSerLeuGlnIlySerValAlaValGlnThrAsnLeuAla 140
 QY 12397 CTTAGAGAACTTCCCATTCAGACATCTCAAACTTTGAAGAAGACTTAATGTGGCTACA 12456
 DB 140 erLeuGluAsnProIleGlyHisLeuIlyThrLeuIlySGluLeuAsnValAlaHisA 160
 QY 12457 ATCTTATCCAAATCTTTCAAAATTAACGTGATTTTCTAATCTGACCAATCTAGACACT 12516
 DB 160 snLeuIleGlnSerPheIlyLeuProGluIlyrPheSerAsnLeuThrAsnLeuGluHis 180
 QY 12517 TGCACCTTTCAGAGCAACAAATTCAGATTTTATTATTCAGACAGCTTCCGGCTTACATC 12576
 DB 180 euAspLeuSerSerAsnIlyIleGlnSerIleTyrCysThrAspLeuArgValLeuHisG 200
 QY 12577 AAATGCCCTTACTCAATCTCTCTTTAGACCTGTCCCTGAAACCCATGAACTTTATCCAAC 12636
 DB 200 lmetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnP 220
 QY 12637 CAGGTGATTTAAAGAAATTAAGGCTTCATTAAGCTTATTAAGAAATATTGTATAGTT 12696
 DB 220 roGlyAlaPheIlySGluIleArgLeuHisIlySerLeuThrLeuArgAsnAsnPhaSerI 240
 QY 12697 TAAATGAAGAAGAACTGTATTCAGAGCTGTGCTGTTTGAAGCCATCAGTGTGCTC 12756
 DB 240 euAsnValMetLysTrpHisIleGlnIlyLeuAlaGlyLeuGluValHisArgLeuVal 260
 QY 12757 TGGGAGATTTAAGAAATGAAGAACTTGAGAAAGTTTGAACAATCTGCTTGAAGGGCC 12816
 DB 260 euGlyGluPheArgAsnGluIlyAsnLeuGluIlyrPheAspIlySerAlaLeuGluGly 280
 QY 12817 TGTGCAATTTGACCATTTGAAGAAATTCGATTTAGCATTTAGACTACTACCTGATGATA 12876
 DB 280 euCysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspIlyrTyrLeuAspAspI 300

QY 12877 TTAATGACTATTATTAATGTTTGACAAGATGTTTCTTCATTTCCCTGGTGGAGTGTGACTA 12936
 Db 300 IeIleAapleupheAserCybleuthrAsnValIserSerPheSerleuValIserValThrI 320
 QY 12937 TTGAAAGGGTAAAGACTTTTCTTAATAATTCGGATGGCAACATTAGAATTAGTTAACT 12996
 Db 320 legIuATgValIyAspPheSerTyzAsnPhelGlyTrpGlnIleleuGluIleuValIAsnC 340
 QY 12997 GTAATTTGACAGTTTCCACATTTGAACCAATCTCTCAAAAGGCTTAACCTTCACTT 13056
 Db 340 yslYsPheglYgInPheProthrleuYsleuYsSerleuYsArgleuthrPheThrS 360
 QY 13057 CCAACAAGGTGGAAATGCTTTTTCAGAAGTTGATCTACCAAGGCTTGAGTTCTAGATC 13116
 Db 360 eArEnlySglYglYAsnAlaPheSerGluValIAspIleuProSerleuGluPheleuAspI 380
 QY 13117 TCAGTAGAAATGGCTTAGATTTCAAAGTGTCTGTCTCAAGATGATTTGGAGAACCA 13176
 Db 380 euserATgAenGlyLeuSerPheYsGlyCySserGlnSerAspPheGlyThrThrS 400
 QY 13177 GCCTAAGTATTTTGAATCTGAGCTTCATAGTGTATTAACAGTAGTTCAAACTTCTGG 13236
 Db 400 eArEnlySlyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheleuG 420
 QY 13237 GCTTAGAACAACTAGACATCTGGAATTCAGACTTCACATTTGAAACAAATAGAGTAGT 13296
 Db 420 lYleuGlnGlnleuGlnIhIleuAspPheGlnIhIserAsnleuYlYsGlnMetSerIuP 440
 QY 13297 TTTTCAGTATTCCTATCTCACTGAGAAACCTCATTTACCTTGACATTTCTCATCTACA 13356
 Db 440 heSerValPheleuSerleuYrAsnleuIleYrleuAspIleSerHleThrHleThrA 460
 QY 13357 GAGTTGCTTTCAAGGCACTCTTCAATGGCTTGCCAGCTCGAAGTCTTGAAATGGCTG 13416
 Db 460 rGValAlaPheAsnGlyrlePheAsnGlyleuSerSerleuGlnValleuYsPheCAlaG 480
 QY 13417 GCAATTCCTTTCAGAGAAACCTTCCTCCAGATATCTTTCACAGAGCTGAGAACTGACT 13476
 Db 480 lYAsnSerPheGlnGlnAsnPheleuProAspIlePheThrGlnleuYrAsnleuThrP 500
 QY 13477 TCCTGAACTCTCTCAAGTGTCACTGAGAGAGTGTGTCTCAACAGCAATTTAACTACT 13536
 Db 500 heleuAspLeuSerGlnCySglInleuGlnleuSerProThrAlaPheAsnSerleuS 520
 QY 13537 CCACTCTTCAGGTACTAAATATGAGCCACCAACACTTCTTTTCATGGAATACGTTTCTT 13596
 Db 520 eArSerleuGlnValleuAsnMetSerHIsaenAsnPhePheSerleuAspThrPheProt 540
 QY 13597 ATAAGTGTGAATCTCCCTCCAGGTTCTTGATTAACAGTCTCAATCACTAATGACTTCCA 13656
 Db 540 yrlYsCySbleuAsnSerleuGlnValIleuAspYrSerleuAsnHleIleThrIserL 560
 QY 13657 AAAAAACAGAACTACAGCAATTTTCCAAAGTGTCTAGCTTTCTTAATCTTAACAGAAATG 13716
 Db 560 yslYsGlnGlnleuGlnIhIAspPheProSerSerleuAlaPheleuAsnleuThrGlnAsn 580
 QY 13717 ACTTGTCTTGAATCTTGGAACACAGAGTTTCCGCGAATGATGAAGACACAGAGGACG 13776
 Db 580 sPheAlaCySthrCySglInHleGlnSerPheleuGlnTrpIleYsAspGlnArgGlnL 600
 QY 13777 TCTTGAGTAGAGTTGAACGAATGGAATGTGCAACACTTCAGATAGACAGGAGCTGCTG 13836
 Db 600 euleuValGlnValGlnArgMetGlnCySAlaThrProSerAspIYsGlnIleYMetProV 620
 QY 13837 TGCTGAGTTTGAATATCACTGTCAGATGAATGAAGACCATTTGGTGTGGTCTCTCA 13896
 Db 620 alIeuserleuAsnIleThrCySglInMetAsnYsThrIleIleGlyAlaIserValleuS 640
 QY 13897 GTGTGCTTTGATATCTGTGTAGACAGTCTGTGCTAATAAATCTCATTTTCACTGTATGC 13956
 Db 640 eArValleuValIserValValAlaValleuValYrlySphethyrPheHIsleuMetL 660
 QY 13957 TTCTTGCTGGCTGCATAAAGTAGGTAGAGGTAAGAAACATCATATGATCCTTTGTATCT 14016

Db 660 euleuAlaGlyCySleIeYslyrGlyArgGlyGlnleuAsnIleYrAspAlaPheValIleT 680
 QY 14017 ACTCAAGCCAGATGTAGGACTGGGTAAAGAAACGACTACTAAAGATTTTGAAGAGGGG 14076
 Db 680 yArSerSerGlnAspGlnAspTrpValIArgAsnGlnleuValIyAsnleuGlnGlnIy 700
 QY 14077 TGCCTCCATTTGAGCTGTGCTCTTCACTACAGAGACTTATTTCCCGGTGTGGCCATTGCTG 14136
 Db 700 alProProPheGlnleuCySbleuHleYrArgAspPheIleProGlyValAlaIleAla 720
 QY 14137 CCAACATCATTCAGTAGAGTTTCCATTAAGCCGAAAGGTGATTTGTGTGCTCCAGC 14196
 Db 720 laAsnIleIleHIsGlnGlyPheHleYsSerArgYsValIleValIserGlnH 740
 QY 14197 ACTTCATCCAGACCCCTGTGATCTTGAATAAGATGCTGACCTGGACGCTTTC 14256
 Db 740 lArPheIleGlnSerArgYrCySlePheGlnYrGlnIleAlaGlnThrTrpGlnPheL 760
 QY 14257 TGAGCAGTGGTGGTATCATCTTCATTTGCTTCGACAGAGGTGAGAGACCTGCTCA 14316
 Db 760 euserSerArgAlaGlyIleIlePheIleValleuGlnYsValGlnYsThrleuLeu 780
 QY 14317 GGCAGCAGGTGAGCTGTACCGCTTCTCAGCAGAACCTTAACCTGAGTGGAGAGACA 14376
 Db 780 rGlnGlnValGlnleuYrArgleuLeuSerArgAsnThrYrleuGlnIuTrpGluAspS 800
 QY 14377 GTGTCTGGGGCGGCACTTTTGTGAGAGAGACTCAAGAAAGCCCTGGAGGTAAAT 14436
 Db 800 eArValleuGlyArgHIslePheTrpArgTrgleuYrGlySalaleuLeuAspGlyYsS 820
 QY 14437 CATGGAATCCAGAGAGAACAGTGGGTACAGAGATGCAATTTGGCAGAGAACATCTATC 14495
 Db 820 eArTrpAsnProGlnGlnYrThrValGlyThrGlyCySAsnTrpGlnAlaThrSerIle 839
 RESULT 4
 ID ADC78785 standard; protein; 839 AA.
 AC ADC78785;
 DT 01-JAN-2004 (first entry)
 XX
 DE Human PRO protein #7.
 KW human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease.
 OS Homo sapiens.
 PN NC02003034984-A2.
 XX
 PD 01-MAY-2003.
 XX
 PF 15-OCT-2002; 2002M0-US033070.
 XX
 PR 19-OCT-2001; 2001US-0340083P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Goddard A, Gurney AL;
 XX
 DR WPI; 2003-481990/45.
 DR N-PSDB; ADCT8784.
 XX
 PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
 PT medicament for diagnosing or treating cancer or inflammatory bowel
 PT disorder e.g., ulcerative colitis or Crohn's disease.
 XX
 PS Claim 12; SEQ ID NO 14; 327bp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of human PRO
 CC proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
 CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
 CC sequence represents a human PRO protein of the invention.

XX Sequence 839 AA;

Alignment Scores:

Pred. No.:	0	Length:	839
Score:	3905.50	Matches:	773
Percent Similarity:	93.46%	Conservative:	13
Best Local Similarity:	91.91%	Mismatches:	20
Query Match:	11.81%	Indels:	35
		Gaps:	6

US-09-396-985b-47 (1-18989) x ADC78785 (1-839)

```

QY 11992 TGCTTATCATGTAATGCTTAACATGCAAAAAAGACCTATGTCAGCCAGTATGATAA 12051
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      29 CysValGluValAlaProAsnIleThrTyrGlnCysMetGluLeuAsn----- 44
QY 12052 TACTCAGTCTGTGGGGCTTCTTATTTGCTT-----ATTCGATCATCATGTCCTG 12102
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      45 -----PheTyrLysIleProAspAsnLeuProPheSerThrLysAsn 58
QY 12103 CTGATGCTTGTGCTTATGCAACAATCATATGACCCA--TCACATCTGTATGAAGAGCTG 12159
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      59 LeuAspLeu-----SerPheAsnProLeuArgHis----- 68
QY 12160 GATACACTAGATTAATATTCTTATTAGTTCTTATTC---GCAGAAATATTGATAT 12216
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      69 -----LeuGlySerTyrSerPhePheSerPheProGluLeu 80
QY 12217 CAATGCTCTTTTATTCTCGTAGTGTGAATCCAGACAATTGAGATGGGCATATGCA 12276
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      81 GlnValIleuAspLeu--SerArgCysGlnIleGlnThrIleGlnAspGlyValAlaTyrGlns 100
QY 12277 GCCTTAAGCACTCTCTACTTAAATATTGACAGAAACCCATCCAGATTAGCCCTG 12336
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      100 erLeuSerHisLeuSerThrIleuIleuThrGlnAsnProIleGlnSerIleuAlaLeuG 120
QY 12337 GAGCCTTTTCTGACATATCAAGATTACAGAGCTGTGTGAGACAAATTTAGCAT 12396
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      120 LysAlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnIleuAla 140
QY 12397 CTCTAGAGAACTTCCCATTTGAGATCTCAAACTTTGAAGAACTTAATGTGCTACA 12456
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      140 erLeuGlnAsnPheProIleGlyHisLeuLysTrpLeuLysGlnLeuAsnValAlaHisAla 160
QY 12457 ATCTTATCAATCTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGACAT 12516
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      160 snLeuIleGlnSerPheLysLeuProGlnLysTrpPheSerAsnLeuThrAsnLeuGlnHis 180
QY 12517 TGAACCTTTCCAGACAAGATTCAGATATTATTCAGACAGACTTGCGGGTTCTACATC 12576
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      180 euAspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValIleuHisG 200
QY 12577 AAATGCCCTACTCAATCTCTCTTACAGCTGTCCCTGGAACCCATATGAATTTTCAAC 12636
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      200 InMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnHisIleGlnP 220
QY 12637 CAGGTGATTTAAAGAAATTAAGCTTCATAGCTGACTTAAAGAAATTAATTTGATAGTT 12696
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      220 roGlyAlaPheLysGlnIleArgLeuHisLysLeuThrIleuArgAsnAsnPheAspSerL 240
QY 12697 TAAATGTAATGAAAATTTGATTCAGAGTCTGGGTGTTTGAAGTCCATGTTGGTTC 12756
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      240 euAsnValIleMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValL 260
QY 12757 TGGAGAAATTTAGAAAGAAAGAACTTGAAGAAAGTTTGAACAATCTGCTCTAAGAGCC 12816
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      260 euGlyGlnPheArgAsnGlnIleGlnLeuGlnLysPheAspLysSerAlaLeuGlnGlyL 280
QY 12817 TGTCAATTTGACCATTTGAAGAAATTCGATTAGCATCTTACTACTGATGATA 12876

```

```

Db 280 euCysAsnLeuThrIleGlnIlePheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspI 300
QY 12877 TTAATGCACTTAATTAATTTGTCACAAATGTTCTTCAATTTCCCTGAGTGTGACTA 12936
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      300 IleIleAspLeuPheAsnCysLeuThrAsnValIleSerPheSerLeuValSerValThrI 320
QY 12937 TTGAAGAGGTAAAGACTTTTCTTAATTAATTTGCGATGGCAACATTTGAATTAATTAAT 12996
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      320 IeGluArgValLysAspPheSerTyrAsnPheGlyTrpGlnHisLeuGlnLeuValAsn 340
QY 12997 GTAAATTTGACAGTTTCCACATTTGAACCTCAAAATCTCTCAAAAGGCTTACTTCACTT 13056
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      340 LysLysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheHis 360
QY 13057 CCACAAAGGTGGGAATGCTTTTCCAGAACTTGATCTACCAAGCTTGAAGTCTTCAATC 13116
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      360 erAsnLysGlyGlnAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspL 380
QY 13117 TCAGTGAAGATGGCTGATGTTTCAAGAGTGTGCTGTTCTCAAGATTTTGGACAACCA 13176
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      380 euSerArgAsnGlyLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrHis 400
QY 13177 GCCTTAAATTTAGATCTGAGCTTCAATGCTGTATTAACATGATGATCAAACTTCTGG 13236
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      400 erLeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuG 420
QY 13237 GCTTAAGACAACATGACATCTGATTTCCAGCATTCCTCAATTTGAACAAATGATGAGT 13296
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      420 LysLeuGlnIleuGlnLysIleAsnAspPheGlnHisSerAsnLeuLysGlnMetSerL 440
QY 13297 TTTCAAGATTCCTATCATCTCAGAAACCTCATTAACCTTGAACATTTCTCATCTACACCA 13356
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      440 heserValPheLeuSerLeuAspAsnLeuIleTyrLeuAspLysSerHisThrHisAla 460
QY 13357 GAGTGTCTTCAATGGCATCTTCAATGCTTGTCCAGTCTCGAAGTCTTGAAGATGGCTG 13416
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      460 rGlyAlaPheAsnGlyLysPheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaG 480
QY 13417 GCATTTCTTCCAGAAACCTTCTCTCCAGATATCTTCAACAGCTGAGAAACCTTGACCT 13476
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      480 LysAsnSerPheGlnGlnLysAsnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrP 500
QY 13477 TCCGTGACCTCTCAGTGTCACTGGAGAGATTTGTCCAAAGCACTTAATCACTCATCT 13536
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      500 heLeuAspLeuSerGlnCysGlnMetGlnIleuLysSerProHisAlaPheAsnSerLeu 520
QY 13537 CCAAGTCTTCAAGTACTAATATATGAGCCACAACAACTTTTCAATTTGATACGTTTCTT 13596
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      520 erSerLeuGlnValIleuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPhePro 540
QY 13597 ATAAGTGTCTGAACCTCCCTCAGGTTCTTGATTAACGTCATCATCATATATGACTTCCA 13656
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      540 YrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerL 560
QY 13657 AAAAAGCAAGAACTACAGCATTTTCCAAAGTGTCTGAGCTTTCTTAATCTTACACAGATG 13716
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      560 YsLysGlnGlnLysLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsn 580
QY 13717 ACTTTGCTTGTACTTTGTAACACAGATTTCTCTGCAATGATATCAAGACAGAGGAGC 13776
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      580 spPheHisLysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnL 600
QY 13777 TCTTGGTGAAGTTGAACGAATGGAATGTGCAACACTTGAATTAAGCAGGAGCTGCTG 13836
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      600 euLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlyMetPro 620
QY 13837 TGTGAGTTGATATCACCTGTCAGATGAATTAAGCAACATCATTTGGTGTGGTCTCTCA 13896
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
      620 alLeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 640
QY 13897 GTGTGCTTGTAGTATCTGTGTGATGAGACTTCTGCTATTAAGTTCTATTTTCACTGATGC 13956

```

D	b	640	erValleuValValSeValValAlaValleuValYlrylrsPhreYrPhheIsleuMeL	660
Q	y	13957	TYCTTGCTGGCTGCATMAAGATGATGTAAGAGTGAAGAAAACATCTATGATGCCCTTGTATCT	14016
D	b	660	euleuAlaGlyCySlleYerTYGlyArgGlYglIuAenlleYrAaPaAlaPheValIleT	680
Q	y	14017	ACTCAAGCCGAGATGAGGAATCTGGGTAAAGAAATGAGCTAGTAAAGATTTTAAAGAAAGGGG	14076
D	b	680	ySeISerSerGlnAspGluAspTrYValArGheNlIuValuLVsAenleuGluGluYlV	700
Q	y	14077	TGCCTCATTTTCAGCTCTGCCTTCACTACAGAGACTTTATTTCCGGGTGGCCATGTCG	14136
D	b	700	alProPheProPheGlnleuCYleuHlStYrArGspheIleProGlyValAlaIleAla	720
Q	y	14137	CCAACATCATTCATGAAAGTTTCCATMAAACCGAAAGGTGATGTGTGTGTCCACG	14196
D	b	720	laAenlleIleHISgluGlyPheHleYSerArGlySValIleValIValISerGlnH	740
Q	y	14197	ACTTCATCCAGAGCGCGTGGTGTATCTTTGAATATGAGATTTGCTCAGACTCGCAATTTC	14255
D	b	740	ISpHeIleGlnSerArGTrpCYslePheGluYrGluIleAlaGlnThrTrpGlnPheL	760
Q	y	14257	TGAGCAGTGCNGCTGGTATCATCTTCATTTGCTCCGAGAGAGTGGAGAAGACCTGCTCA	14316
D	b	760	eueISerArGAlaGlyIlellePheIleValleuGlnYsValGluYsthrleuDeH	780
Q	y	14317	GGCAGCAGGTGAGAGCTGTACCGCCTTCTCAGCAGAAACATTACCTGAGTGGAGAGACA	14376
D	b	780	rgGlnGlnValIGluIeutyArGleuIeuSerArGheNThrYrleuGluTTrpGluAspS	800
Q	y	14377	GTCGCTCGGGGGCGGCAATCTTCTGAGAGAGACTCAGAAAAAGCCCTGCTGAGTGTAAAT	14433
D	b	800	erValleuGlyArGHisIlePheThrParGArGleuArGlyValAlaIleuAspGlyLys	820
Q	y	14437	CATGAATCCGAAAGAAAGAGTGGGTACAGATGCAATTGGCAGAGAAACATCTATC	14495
D	b	820	erTrpAenProGluGlyThrValaGlyThrGlyCySAenThrGlnGluAlaThrSerIle	839
RESULT 5				
AC	AD	ADD48826	standard; protein; 839 AA.	
XX	XX	ADD48826;		
XX	XX	02-DEC-2004 (revised)		
DT	DT	29-JAN-2004 (first entry)		
DE	XX			
DE	XX	Human Protein AAF05316, SEQ ID NO 14536.		
XX	XX			
KW	KW	Human; pain; neuronal tissue; gene therapy;		
KW	KW	spinal segmental nerve injury; chronic constriction injury; CCI;		
KW	KW	spared nerve injury; SNI; Chung.		
XX	XX			
OS	OS	Homo sapiens.		
OS	OS	Unidentified.		
XX	XX			
XX	XX	MO2003016475-A2.		
PD	PD	27-FEB-2003.		
XX	XX			
XX	XX	14-AUG-2002; 2002WO-US025765.		
XX	XX			
PR	PR	14-AUG-2001; 2001US-0312147P.		
PR	PR	01-NOV-2001; 2001US-0346382P.		
PR	PR	26-NOV-2001; 2001US-0333347P.		
XX	XX			
PA	PA	(GEHO) GEN HOSPITAL CORP.		
PA	PA	(FARB) BAYER AG.		
XX	XX			
PI	PI	Woolf C, D'Urso D, Befort K, Costigan M;		
XX	XX			
XX	XX	WPI; 2003-268312/26.		
DR	DR	GENBANK; AAF05316.		

XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page: 101pp; English.

The invention discloses a composition comprising two or more isolated RNA or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNi) in an animal (e.g. gene injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy)). The sequence presented is a human protein (described in Table 3 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at http://wipo.int/pub/publ/published_pct_sequences.

SQ Sequence 839 AA;

Alignment Scores:	
Pred. No.:	0
Score:	3905.50
Percent Similarity:	93.46%
Best Local Similarity:	91.91%
Query Match:	11.81%
DB:	7
Length:	839
Matches:	773
Conservative:	13
Mismatches:	20
Indels:	35
Gaps:	6

US-09-396-985B-47 (1-18989) X ADD48826 (1-839)

Qy 11992 TGGTTATCATGTATGCTTAACATGACAAAAAGAGCCTATATTCGAGCCAGTATGATTA 12051

Db 29 CysValGluValValProAsnIleThrTyrglnCysmetGluLeuAsn----- 44

QY 12052 TACTCAGTCTGTGGGGCTTCTTATTGCTT-----ATTCCATCATCATCTGCTCTG 12102

Db 45 -----Phe¹Y¹L¹S¹I¹L¹E¹Pro¹Asp¹Asn¹u¹Le¹Pro¹His¹Se¹Thr¹Ly¹Asn¹ 58

12103 CTGATGCTTTGGCTATGACAAATCATATGACCA ---TCACATCTGATGAAAGCTG 12155

```
Db      59 LeuAspLeu-----SerPheAsnProLeuArgHis-----66
```

Qy 12160 GATGACTAGGATTAATTCATTCTATTGTTCTATTCA--GCAGAAATATTGATTAAT 12216

Db 69 -----LeuGlySerTyrSerPhePheSerPheProGluLeu 80

QY 12217 CATGCTTTTATTCCTGTAGGTGTAAATCAGACAAATTGAAGATGGGCATATCAGA 12276

Db 81 GlnValLeuAspLeu--SerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlns 100

QY 12277 GCCTAAGCACCCTCTACCTTAATATTGACAGAAACCCCATCCAGAGTTAGCCCTGG 12338

Db 100 erLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuG 120

QY 12337 GAGCCTTTCTGCACTATCAAGTTTACAGAGAGCTGGTGGCTGTGGAGACAAATCTAGCAT 12396

Db 120 IyAlAPhSeSergIyLeuSeSerLeuGInIyLeuValAlaValGInuThrAsnLeuAlaAs 140

QY 12397 CTGAGAACTTCCCATGACATCTCAAACTTTGAAAAGAACTTAATGTGGCTACA 12456
 DB 140 erleuGluaSnPheproIleGlyHisleuYsthrleuYleuGlueuSnValAlaHisA 160
 QY 12457 ATCTTATTCATCTTTCAAAATTTACTGTAGTATTTTCTTAATCTGACCAATCTTACGACT 12516
 DB 160 snleuIleGlnSerPheYsleuProGluYrPheSerAsnleuThrAsnleuGlnHisL 180
 QY 12517 TGACCTTCCAGAAACAAGATTCAAATTTATTTAGCAGACTGGGGCTTCTACATC 12576
 DB 180 euasPheSerSerAsnYsIleGlnSerIleYrCystrAspLeuYrValIleuHisG 200
 QY 12577 AAATGCCCTACTCAATCTCTCTTTAGACCTGTCCCTGAAACCTTAAGACTTTATCCAAC 12636
 DB 200 lmetProleuLeuAsnleuSerleuAspLeuSerleuAsnProMetAsnHelleGlnP 220
 QY 12637 CAGGTGCAATTTAAAGAAATAGGCTTCATTAAGCTGACTTTAAGAAATATTTGATGATT 12696
 DB 220 roGlyAlaPheYleGlnIleArGleuHisYsleuThrleuYrAsnAsnDheAspSerL 240
 QY 12697 TAAATGTAATGAATCTGTATTTGAAGCTCTGGCTGGTTTGAAGTCCATGCTTTGCTTC 12756
 DB 240 euasnValMetLysThrCysIleGlnGlyleuAlaGlyleuGlnValHisArGleuValL 260
 QY 12757 TGGAGAAATTTAGAAATGAAGAAACTTGAAGAAAGTTTGAACAATCTGCTCTAGAGGGCC 12816
 DB 260 euGlyGluPheArGAsnGluClnYsAsnleuGlnYrPheAspYsSerAlaIleuGlnGlyL 280
 QY 12817 TGTCAATTTGACCAATTTGAAGAATTCGATTTAGCACTTACTACTCTGATGATA 12876
 DB 280 euCyAsnleuThrIleGlnGluPheArGleuAlaYrleuAspYrTytleuAspAspI 300
 QY 12877 TTATTTGCTTATTTATTTGTTTGAACAATGTTTCTTCAATTTCCCTGGTGTGATGACTA 12936
 DB 300 IeIleAspLeuPheAsnCySleuThrAsnValSerSerPheSerleuValSerValIthrI 320
 QY 12937 TTGAAGGGGTAAAGACTTTTCTTAATATTTCCGATGGCAACTTTAGAAATTAAGTTAACT 12996
 DB 320 IeGluAlaGlyValYAspPheSerYrAsnDheGlyTrpGlnHisIleuGlnleuValAsnC 340
 QY 12997 GTAAATTTGACAGCTTCCCATGATTAATCAATCTCTCAAAAGGCTTACTTCACTT 13056
 DB 340 YsYsPheGlyGlnPheProThrleuYsleuYsSerleuYrArGleuThrPheThrS 360
 QY 13057 CCAACAAGGTGGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAGTTTCTAATC 13116
 DB 360 eIraenYsGlyGlyAsnAlaPheSerGlnValAspLeuProSerleuGlnPheleuAspL 380
 QY 13117 TCAGTAGAAATGGCTTGATTTCAAGGTTGCTGTCCTCAAGATTTTGGACAACA 13176
 DB 380 euSerArGAsnGlyLeuSerPheYsGlyCySserGlnSerAspDheIlyThrTrS 400
 QY 13177 GCCTAAAGTATTTAGATCTGAGCTTCAATGCTGTTATTAATCCAGATTTCAACTCTTGG 13236
 DB 400 eIreleuYrTytleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnHelleuG 420
 QY 13237 GCTTGAACAACATTTGAAATTTCCAGATTTCCAAATTTGAAACAAATGATGACT 13296
 DB 420 YleuGlnGlnleuGlnHisIleuAspPheGlnHisSerAsnleuYsGlnMetSerGluP 440
 QY 13297 TTTGAGTATTCCTATCACTGAGAAACCTCATTTACTTGAATTTCTCATCTACACA 13356
 DB 440 heSerValPheLeuSerleuYrAsnleuIleYrYleuAspIleSerHisThrHis 460
 QY 13357 GAGTTGCTTTCATGAGCATCTTCAATGCTTGTCCAGTCTCGAAGCTTTGAAAATGGCTG 13416
 DB 460 rGValAlaPheAsnGlyIlePheAsnGlyLeuSerSerleuGlnValleuYsMetAlaG 480
 QY 13417 GCATTTCTTTCCAGAGAAACTTCTTCCAGATATCTTCCACAGAGCTGAGAACTTGACCT 13476
 DB 480 YAsnSerPheGlnGlnleuAsnPheleuProAspIlePheThrGlnleuYrAsnleuThrP 500

QY 13477 TCTGAGCTCTCTCACTGATCACTGAGAGATTGTCTCAACAGACTTTAACTCACTCT 13536
 DB 500 heIleuAspLeuSerGlnCySleuGlnleuGlnleuSerProThrAlaPheAsnSerleuS 520
 QY 13537 CCACTTTCAAGGTAATTAATGAGCCACAACAACCTTTCTTTCAATTTGATACGTTTCTT 13596
 DB 520 eIserleuGlnValleuAsnMetSerHisAsnAsnDhePheSerleuAspThrPheProT 540
 QY 13597 ATTAAGTCTGAACCTCCCTCAGGTTCTTGAATTAACATCACTCAATCATATATGACTTCCA 13656
 DB 540 YrTySCySleuAsnSerleuGlnValleuAspYrSerleuAsnHisIleMetThrSerL 560
 QY 13657 AAAACAGAACTACAGACTTTTCCAAATGATGATGATGATGATGATGATGATGATGATG 13716
 DB 560 YsYsGlnGlnleuGlnHisPheProSerSerleuAlaPheleuAsnleuThrGlnAsnA 580
 QY 13717 ACTTGTCTTGTACTTGTGAAACACCAAGTTTCTGCAATGATGATGATGATGATGATGATG 13776
 DB 580 spPheAlaCyStrnCysGlnHisGlnSerPheleuGlnTrpIleYrAspGlnArGlnL 600
 QY 13777 TCTTGTGGAAGTTGAACGAATGGAATGGAACACCTTGACATGATGATGATGATGATGATGATG 13836
 DB 600 euIleuValGlnValGlnArGleuGlnCysAlaThrProSerAspYsGlnGlyMetProV 620
 QY 13837 TGCTGATTTGAATATCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 13896
 DB 620 AlIeUserleuAsnIleThrCySleuGlnMetAsnYsThrIleGlyValSerValleuS 640
 QY 13897 GTGTGCTTGTGATCTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 13956
 DB 640 eYValleuValIleSerValIleAlaValleuValYrYsPheTyPheHisIleuMetL 660
 QY 13957 TTTCTGTGCTGCTGATTAAGTATGATGATGATGATGATGATGATGATGATGATGATGATG 14016
 DB 660 euIleuAlaGlyCySleuYrGlyArGlyGlnGlnIleYrAspAlaPheValIleT 680
 QY 14017 ACTCAAGCCAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 14076
 DB 680 YrSerSerGlnAspGlnAspTrpValArGAsnGlnleuValYrAsnleuGlnGlnIlyY 700
 QY 14077 TGCTTCCATTTAGACTCTGCTTCTTCACTACAGAACTTTATTTCCGGTGTGACATGCTG 14136
 DB 700 AlProPheGlnleuCySleuHisIleYrArGAspPheIleProGlyValAlaIleAla 720
 QY 14137 CCAACATCAACCAATGAAGTTTCCATTAAGCCGAAAGGATGATGATGATGATGATGATG 14196
 DB 720 IAsnIleIleHisGlnGlyPheHisYsSerArGlyValIleValValSerGlnH 740
 QY 14197 ACTTCATCAGAGCCGCTGTGATCTTGAATATGATGATGATGATGATGATGATGATGATG 14256
 DB 740 IspHeIleGlnSerArGTrpCyIlePheGlnYrGlnIleAlaGlnThrTrpGlnPheL 760
 QY 14257 TGAAGAGTCTGTGATCATCTTCAATGCTCTGCAAGAGTGAAGAGACCTGTGCTCA 14316
 DB 760 euSerSerArGAlaGlyIleIlePheIleValleuGlnYsValGlnYrThrleuEuA 780
 QY 14317 GCGACAGGTGGAGCTGATACCGCTTCTGACGAGAAACATTAACCTGAGTGGAGAGACA 14376
 DB 780 rGlnGlnValGlnleuYrArGleuLeuSerArGAsnThrYrleuGlnTrpGlnAspS 800
 QY 14377 GTGTCTGGGGCGGACATCTTGTGAGAGAGCTCGAAAGCCGTGAGATGGTAAAT 14436
 DB 800 eYValleuGlyArGHisIlePheTrpArGArGleuHisGlySalAlaIleuAspGlyYsS 820
 QY 14437 CATGGAATCCAGAGAAACAGTGGGTAACAGATGCAATTTGGACAGAGAAACATCTATC 14495
 DB 820 eTrTrAsnProGlnGlyThrValGlyThrGlyCySAsnTrpGlnGlnAlaThrSerIle 839
 RESULT 6
 ID AAM86352 standard; protein; 799 AA.
 ID AAM86352
 AC AAM86352;


```

Db      451  ILlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnGln 470
QY      13509 TTGCTCCAAAGAGATTAACTCACTCCAGTCTTGAGTACTAAATAATAGACACAC 13568
Db      471  LeuSerProtnAlaPheAsnSerLeuSerLeuGlnValLeuAsnMetSerHisAsn 490
QY      13569 AACTCTCTTTCAATGATACGTTTCTTATAGTGTCTGAATCCCTCCAGTCTTGAT 13628
Db      491  AsnHepSerLeuAspThrPheProTyrIleCysLeuAsnSerLeuGlnValLeuAsp 510
QY      13629 TACAGTCTCAATCAATATATGATCTTCCAAAAAGAGAACTACAGCATTTTCCAGTAT 13688
Db      511  TyrSerLeuAsnHisIleMetThrSerIleGlnGlnLeuGlnHisPheProSerSer 530
QY      13689 CTAGCTTTCTAAATCTTACACAGAAATGACTTTCCTGTATCTTGATGAAACACAGATTC 13748
Db      531  LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysTrpCysGlnHisGlnSerPhe 550
QY      13749 CTGCATATGATCAAGACACAGAGCAGCTCTTGAGTGAAGTTGAACGAATGGAATGCA 13808
Db      551  LeuGlnTrpIleIleValAspGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAla 570
QY      13809 ACACCTTCAGATTAAGACAGGAGGATGCTGTGTGAGTTGAATATCACCTTCAGATGAT 13868
Db      571  ThrProSerAspIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 590
QY      13869 AAGACATCATTTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13928
Db      591  LysThrIleIleGlnValSerValLeuSerValLeuValIleSerValAlaValLeu 610
QY      13929 GTCTATTAAGTTCTATTTTCACTGATGCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 13988
Db      611  ValTyrIleSerPheTyrPheHisIleuMetLeuAlaGlnCysIleIleTyrGlnArgGly 630
QY      13989 GAAAAATCTATGATGATGCTTGTATCTTACTCAAGCCAGATGAGAGATGCGGTGAAGAT 14048
Db      631  GluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTrpValArgAsn 650
QY      14049 GAGCTATTAAGATTTTGAAGAAGAGGGGCTCCATTTCACTGCTGTGCTTCACTACAGA 14108
Db      651  GluLeuValIleValAsnLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 670
QY      14109 GACTTATTCCTCCGGTGTGGCCATGCTGCGCAATCATCATGAAAGTTTCCATAAAGC 14168
Db      671  AspHepIleProGlnValAlaAlaAlaAsnIleIleHisGlnGlnPheHisIleYSer 690
QY      14169 CGAAAGGTGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 14228
Db      691  ArgIleValIleValValIleValSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 710
QY      14229 TATGAGATTTGCTGACAGCTTGCACTTCTGAGCAGTGTGTGTGTATCATTTGATGTC 14288
Db      711  TyrGlnIleLeuIleGlnTrpGlnPheLeuSerSerArgIleGlnIleIlePheIleVal 730
QY      14289 CTGCAGAAAGGTGAGAGAGACCTGCTCAGGAGAGAGGTGAGGCTTCCGCTTCTCAGC 14348
Db      731  LeuGlnIleValIleGlnIleValIleValIleValIleValIleValIleValIleVal 750
QY      14349 AGGAACAATTACCTGAGAGTGGAGAGACAGTGTCTCTGGGCGGCGACATCTTCTGAGAGA 14408
Db      751  ArgAsnThrTyrLeuGlnIleTrpGlnAspSerValLeuGlnArgHisIleIlePheTrpArg 770
QY      14409 CTGAGAAAAGCCCTGCTGAGATGTAATCATGGAATCCAGAGAGACAGTGGGTACAGA 14468
Db      771  LeuArgIleValIleLeuAspGlnIleYleSerTrpAsnProGlnGlnIleValIleThrGly 790
QY      14469 TGCAATTGGAGAGAGAGACATCTATC 14495
Db      791  CysAsnTrpGlnGlnIleAlaHisSerIle 799

```

RESULT 7
AAE16093

```

ID      AAE16093 standard; protein; 799 AA.
XX
AC      AAE16093;
XX
DT      26-MAR-2002 (first entry)
XX
DE      Human DNAX Toll like receptor (DTLR) 4 #1.
XX
KW      Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KW      interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS      Homo sapiens.
XX
PN      WO200190151-A2.
XX
PD      29-NOV-2001.
XX
PF      23-MAY-2001; 2001WO-US016766.
XX
PR      25-MAY-2000; 2000US-0207558P.
XX
PA      (SCHE ) SCHERING CORP.
XX
PI      Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX      WPI; 2002-083085/11.
XX      N-PSDB; AAD26283.
XX
PT      New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT      conditions exhibiting abnormal expression of the receptors of their
PT      ligands, particularly abnormalities manifested by immunological
PT      disorders.
XX
PS      Claim 1; Page 35; 297pp; English.
XX
XX
CC      The invention relates to mammalian receptor proteins, e.g., primate,
CC      human DNAX Toll like receptor (DTLR) protein and their corresponding
CC      nucleic acids. The DTLR is useful for treating conditions exhibiting
CC      abnormal expression of the receptors of their ligands. Such abnormality
CC      is manifested by immunological disorders. In particular, the DTLR is
CC      useful for treating various disease or disorders associated with abnormal
CC      expression or abnormal triggering of response to a ligand. The DTLR is
CC      also useful for the production of antisera or antibodies
CC      specific, e.g. capable of distinguishing between other interleukin (IL)-1
CC      receptor family members, for the DTLR or its various fragments. The
CC      purified DTLR can be used to screen monoclonal antibodies or antigen-
CC      binding fragments. The antibodies are useful for screening expression
CC      libraries for particular expression products. These are useful for
CC      detecting or diagnosing various immunological conditions related to
CC      expression of DTLR or cells that express it. The present sequence is
CC      human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33
XX
SQ      Sequence 799 AA;
XX
Alignment Scores:
Pred. No.: 0 length: 799
Score: 3903.50 Matches: 757
Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Gaps: 9
DB: 5 Indels: 1
US-09-396-985b-47 (1-18989) x AAE16093 (1-799)
QY      12216 TCAATGCTTTTATTTATTC-----TGTAGTGTGGAATC 12248
Db      31 SerTyrSerPhePheSerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIle 50
QY      12249 CAGACAAATTAAGATGGGGCATATTCAGAGCTTAAGCAGCCTCTCTACTTAAATATTGACA 12308
Db      51 GlnThrIleGlnAspGlnAlaTyrGlnIleSerLeuSerHisIleSerThrLeuIleLeuThr 70
QY      12309 GGAAGCCCATTCAGAGATTAGCCCTGGAGAGCTTTTCTGCACTATCAAGTTTACAGAG 12368

```

Db 71 GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIly 90
QY 12369 CTGGTGGCTGTGGAGAGCAATCTAGACATCTCTAGAGAACTTCCCATTTGACATCTCA 12428
Db 91 LeuValAlaValAlaGlnThrAsnLeuAlaSerLeuGlnAsnProIleGlyHisLeuIly 110
QY 12429 ACCTTGAAGAAGCTTAATGAGGCTCAACATCTTAATCAATCTTCAAAATTAACGTAGTAT 12488
Db 111 ThrLeuIlyGlnLeuAsnValAlaHisAsnLeuIleGlnSerPheIlyLeuProGlnIly 130
QY 12489 TTTTCTAATCTGACCAATCTAGAGCACTTGACCTTTCAGCAACAAGATTCAAGTAT 12548
Db 131 PheSerLeuLeuThrAsnLeuGlnHisLeuAsnLeuSerSerAsnIlyIleGlnSerIle 150
QY 12549 TATTGCGACAGACTTGGGGTTCATACAAATGCCCCCTACTCAATCTCTCTTAGACCTG 12608
Db 151 TyrCysThrAsnLeuAlaGValIleuHisGlnMetProLeuLeuAsnLeuSerLeuAsnLeu 170
QY 12609 TCCCTGAACCTTAATGAATCTTAATCCAAACAGGTGCAATTTAAAGAAATTAGGCTTCA 12668
Db 171 SerLeuAsnProMetAsnProIleGlnProGlyAlaPheIlyGlnIleArgLeuHisIly 190
QY 12669 CTGACTTTAAGAAATTAATTTGATAGTTAAATGTAATGAAAACTTGATTTCAAGGTCTG 12728
Db 191 LeuThrLeuAsnArgAsnAsnPheAsnSerLeuAsnValIleIlySerThrCysIleGlnGlyLeu 210
QY 12729 GCTGGTTTAAAGTCCATCGTTTGGTCTGGAGAAATTTAGAAATGAAGAACTTGAA 12788
Db 211 AlaGlyLeuGlnValHisArgLeuValLeuGlyGlnPheArgAsnGlnIlyAsnLeuGln 230
QY 12789 AAGTTTGAACAATGTGCTCTAGAGGCGCTGCAATTTGACCAATGAAGATTCCGATTA 12848
Db 231 LysPheAsnIlySerAlaLeuGlnIlyLeuCysAsnLeuThrIleGlnIlyLysPheAlaGlyLeu 250
QY 12849 GCATACTTAAAGTACTACCTCGATGATATTAATGACTTAATTTAATTTGACAATGTT 12908
Db 251 AlaIlyrLeuAsnProIlyrIlyrIlyLeuAsnProIleIleAsnProIleAsnProIleThrAsnVal 270
QY 12909 TCTTCATTTTCCCTGGGAGAGTGATGATTAATGAAGGTAAGGCTTTCTTAATATTC 12968
Db 271 SerSerPheSerLeuValIleSerValThrIleGlnArgValIlyAsnProIleSerIlyAsnPro 290
QY 12969 GGAATGGCAACATTTAGATTAGTTAAGTGAATTTGAGAGGTTCCCACTTGAATCTC 13028
Db 291 GlnIlyrPheGlnHisLeuGlnLeuValAsnCysIlyPheGlnIlyPheProIleIlyLeuIlyLeu 310
QY 13029 AAATCTCTCAAAAGGCTTAATCTTCACTTCCAAACAAGGTGGAAATGCTTTTTCAGAAAT 13088
Db 311 LysSerLeuIlyAsnArgLeuThrPheThrSerAsnIlyGlnIlyAsnAlaPheSerGlnVal 330
QY 13089 GATCTACCAAGCCTTGAAGTTTCTAGATCTCACTGTAAGAAATGCTTGAAGTTTCAAGGTTC 13148
Db 331 AsnLeuProSerLeuGlnPheLeuAsnProIleSerArgAsnGlnIlyLeuSerPheIlyGlyCys 350
QY 13149 TGTCTCAAGATGATTTTGGGCAACAGGCTTAAGTATTTAGATCTGAGCTTCAAGGT 13208
Db 351 CysSerGlnSerAsnProIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 370
QY 13209 GTTATTCATGATGATTTCAATCTTGGGCTTAGAAACAATGAAACAATCTGATTTTCAG 13268
Db 371 ValIleThrMetSerSerAsnPheLeuGlnIlyLeuGlnIlyLeuGlnIlyHisLeuAsnProIle 390
QY 13269 CATTCGAATTTGAAACAATAGAGTATTTCAAGTATCTTATCACTCAGAACTTCAAT 13328
Db 391 HisSerAsnLeuIlyGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIle 410
QY 13329 TACCTTGAATTTCTCAATCTCAGACCAAGGATTTGATTTCAATGAGATTTTAAAGGCTTG 13388
Db 411 TyrLeuAsnProIleSerHisIleThrIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 430
QY 13389 TCCAGTCTCAAGTCTTGAAGAAATGGCTGGCAATTTCTTTCAGAAACTTCTCCAGAT 13448

Db 431 SerSerLeuGlnValLeuIlySweAlaGlyAsnSerPheGlnGlnAsnPheLeuProAsn 450
QY 13449 ATCTTCAGAGGTGAGAAACTTGAACCTTCTGAGACCTCTCAAGTCAATGAGAGCAG 13508
Db 451 IlePheThrGlnLeuAsnArgAsnLeuThrPheLeuAsnProIleSerGlnCysGlnLeuGlnIly 470
QY 13509 TTGTCTCAACAAGCATTTTAATCACTCTCAGTCTTTCAGGTATCAATAATGAGCCCAAC 13568
Db 471 LeuSerProIleThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
QY 13569 AACTTTTCTTTCATGATATCGTTTCTTAAAGTGTCTGAATCTCCCTCCAGGTTCTTGAT 13628
Db 491 AsnPhePheSerLeuAsnProIlePheProIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 510
QY 13629 TACAGTCAATCAATCAATTAATGACTTCCAAAAACAGAACTACAGCAATTTTCCAAAGTAT 13688
Db 511 TyrSerLeuAsnHisIleMetThrSerIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 530
QY 13689 CTAGCTTTCTTAAATCTTACTCAGAAATGACTTGTGTTGATCTTGTGAACACAGAGTTTC 13748
Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAsnProIleCysThrCysGlnHisGlnSerPhe 550
QY 13749 CTGCAATGATCAAGACCAAGAGGCGCTCTGTGGTGAAGTTGAACGAATGAAATGTGCA 13808
Db 551 LeuGlnIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 570
QY 13809 ACACCTTCAGATTAAGAGGAGGCAATGCTGTGCTGAGTTTGAATTCACCTTCAGATGAAT 13868
Db 571 ThrProSerAsnProIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 590
QY 13869 AAGACCATCATTTGGTGTGTGCTGCTCAAGTGTGCTTGTATGATCTGTTAGAGAGTTCTG 13928
Db 591 LysThrIleIleGlyAlaSerValIleuSerValIleuValIleuSerValIleuValIleu 610
QY 13929 GTCTTAATGATTTCAATTTTCACTGATGCTTCTTGGTGTGCTGCTTAAGTATGATAGCT 13988
Db 611 ValIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 630
QY 13989 GAAACATCATGATGCTTGTATCTACTCAAGCAGAGATGAGAGCTGGTGAAGAT 14048
Db 631 GlnAsnIleIlyrAsnAlaPheValIleIlyrSerSerGlnAsnProIlyrIlyrIlyrIlyr 650
QY 14049 GAGCTAGTAAAGATTTAGAAAGAGGAGGCTCCATTTCAAGCTTGCCTTCACTACAGA 14108
Db 651 GlnLeuValIlyrAsnLeuGlnIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 670
QY 14109 GACTTAATTTCCGGTGTGGCATTTGCTGCCAACAATCACTGAAGGTTTCCATAAAGC 14168
Db 671 AspPheIleProIlyrAlaIleAlaIleAlaIleAlaIleIleIleGlnIlyPheHisIlySer 690
QY 14169 CGAAGGTGATTTGTTGGTGTGCCAGCACTTCAATCCAGAGCGCTGTATCTTGA 14228
Db 691 ArgIlyrValIleValIleValIleValIleSerGlnHisPheIleGlnSerArgIlyrIlyrIlyr 710
QY 14229 TATGAGATTTGCTGAGCTTGGAGGATTTCTGAGAGTGTGCTGTATCATCTTCAATGTC 14288
Db 711 TyrGlnIleAlaGlnIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 730
QY 14289 CTGCAAGAGGTGAGAAAGACCTTGTCTCAGCAGCAGAGGTGAGGCTTTCAGCCTTTCAGC 14348
Db 731 LeuGlnIlyrValIleGlnIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 750
QY 14449 AGGAACACTTAACCTGAGTGGAGGAGCAGGTGCTTGGAGGAGGACATCTTCTGAGAGCA 14408
Db 751 ArgAsnThrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 770
QY 14409 CTCAGAAAAGCCTGTGATGATGATTAATCACTGAAATCAGAAAGAACAGTGGGTACAG 14468
Db 771 LeuArgIlyrAlaLeuLeuAsnProIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 790
QY 14469 TGCATTTGCAAGAGCAACATCTTATC 14495
Db 791 CysAsnIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyrIlyr 799


```

QY 13449 ATCTTCACAGAGCTGAGAACTTGAACCTTCTCTGAGACCTCTCTCACTGTCACATGAGACAG 13508
DB 451 TLebheThrGluLeuAArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 470
QY 13509 TTGCTCCACAGACATTTAACTCACTCTCCAGCTTTCAGAGTACTTAATTAAGAGCCACAC 13568
DB 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
QY 13569 AACTCTTTTCATTGAGTACGCTTTCTTATTAAGTGTCTGAACCTCCCTCCAGAGTTCTTGAT 13628
DB 491 AsnPheSerSerLeuAspThrPheProTyrCysLeuAsnSerLeuGlnValLeuAsp 510
QY 13629 TACAGTCTCAATCACTTAAGACCTTCCAAAAAAGAGAACATCAACGACATTTTCCAGTAGT 13688
DB 511 TysSerLeuAsnHisIleMetThrSerLysGlnGluLeuGlnHisPheProSerSer 530
QY 13689 CTAGCTTTCTTAATTTAACTTCAAGATGACTTTGCTGTACTTGTGAACACAGAGTTTC 13748
DB 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisLeuSerPhe 550
QY 13749 CTGCAATGATCAAGACACAGAGGACGCTTGTGAGAGTTGAACGAATGGAATGTGCA 13808
DB 551 LeuGlnTrpIleLysAspGlnArgGlnLeuValGlnValGlnArgMetGlnCysAla 570
QY 13809 ACACCTTCAGATTAAGACGAGGACGCTGCTGAGTTGAATATCACTGACAGATGAAT 13868
DB 571 ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 590
QY 13869 AAGACATCATATGCTGTGCTCGAGTCTCAAGTGTGCTGATGATGCTGTGAGACAGTTCTG 13928
DB 591 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValValAlaValLeu 610
QY 13929 GTCTAAAGTTCTAATTTTCACTGATGCTTGTGCTGCTGACATTAAGATGATGATGAGT 13988
DB 611 ValTyrLysPheThrGlnPheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGly 630
QY 13989 GAAACATCTATGATGCTTGTGCTTGTATCTCAAGCCAGGATGAGATGAGATGAGAT 14048
DB 631 GlnAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTrpValArgAsn 650
QY 14049 GAGCTAGTAAGATTTTGAAGAAGGGGTGCTCATTTGAGCTGTGCTGCTCACTACAGA 14108
DB 651 GlnLeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrArg 670
QY 14109 GACTTATTTCCGGGTGAGCAATGCTGCTCCAAATCATCAATGAAGTTTCCATTAAGC 14168
DB 671 AspPheIleProGlyValAlaIleAlaAlaAsnIleIleHisGlnGlyPheHisLysSer 690
QY 14169 CGAAAGGTGATTTGTTGGTGTCTCCAGACCTTCAAGACCCGCTGATCTTGA 14228
DB 691 ArgLysValIleValValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 710
QY 14229 TATGAGATTGCTCAGACCTGACAGTTTCTGAGAGTCTGTGATCATCTTCAATGTC 14288
DB 711 TyrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 730
QY 14289 CTGCAAGAGGTGAGAGAGACCTGCTCAGGACAGAGGTGAGCTGATCCGCTTCTCAGC 14348
DB 731 LeuGlnLysValIleGlnLysThrLeuLeuArgGlnValGlnLeuTyrArgLeuLeuSer 750
QY 14349 AGGAACATTTACCTGAGAGTGGAGAGAGAGTGTCCGAGGGGCGGACATTTCTGAGAGCA 14408
DB 751 ArgAsnThrTyrLeuGlnTrpGlnAspSerValLeuGlyArgHisIlePheTrpArgArg 770
QY 14409 CTCGAAAAGCCCTGCTGATGTAAATCATGAGATCCAGAGAGACAGTGGTACAGA 14468
DB 771 LeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlyThrValGlyThrcly 790
QY 14469 TGCATTTGGCAGAGAGCAACATCTATC 14495
DB 791 CysAsnTrpGlnGlnAlaThrSerIle 799

```

```

RESULT 9
ABR42963
ID ABR42963 standard; protein; 799 AA.
XX
AC ABR42963;
XX
DT 08-SEP-2003 (first entry)
XX
DE Human Toll-like receptor 4.
XX
KM Human; Toll-like receptor 4; receptor; antiinflammatory; immunomodulator.
XX
OS Homo sapiens.
XX
PN M02003044163-A2.
XX
PD 30-MAY-2003.
XX
PF 14-NOV-2002; 2002MO-US036390.
XX
PR 19-NOV-2001; 2001US-00001863.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Karas JG, Koller E;
XX
PI WPI; 2003-468766/44.
XX
DR N-PSDB; ACC83601.
XX
PT New antisense oligonucleotides for modulating Toll-like receptor 4 gene
PT expression, particularly useful for preventing, delaying or treating e.g.
PT inflammatory disorders, or conditions involving Th1 or Th2 immune
PT responses.
XX
PS Example 14; Page 100-104; 110pp; English.
XX
CC The present sequence is the protein sequence human Toll-like receptor 4.
CC The invention provides chimeric phosphorothioate oligonucleotides (see
CC ACC8361-98) targeted to human Toll-like receptor 4 mRNA. Such antisense
CC oligonucleotides inhibit the expression of human Toll-like receptor 4 and
CC are useful for treating or preventing a disease or condition associated
CC with Toll-like receptor 4, e.g. an inflammatory disorder or a condition
CC involving an immune response, particularly Th1 or Th2 responses
XX
SQ Sequence 799 AA;
XX
Alignment Scores:
Pred. No.: 0
Score: 3903.50
Percent Similarity: 98.57%
Best Local Similarity: 98.44%
Query Match: 11.81%
DB: 6
Gaps: 1
US-09-396-985b-47 (1-18989) x ABR42963 (1-799)
QY 12216 TCAATGCTTTTATTTCC-----TGTAGTGTGGAATC 12248
DB 31 SerTyrSerPhePheSerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIle 50
QY 12249 CAGCAATTAAGATGGGAGCATATCAGAGCTTAAGCACCTCTCACTTAATATTGACA 12308
DB 51 GlnThrIleGlnAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThr 70
QY 12309 GGAACCCCATCCAGAGATTAGCCCTGGAGACCTTTTCTGAGATATCAAGTTTACAGAG 12368
DB 71 GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys 90
QY 12369 CTGATGCTGTGAGAGCAAAATTTAGCATCTCTAGAGAACTTCCCATTTGAGACATCTCAA 12428
DB 91 LeuValAlaValGlnThrAsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuLys 110
QY 12429 ACTTGAAAGAACTTAATGTGGCTCAACAATCTTATCAATCTTCAATTAATCACTGAGTAT 12488

```


Db 111 ThrLeuysGIuLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluLysr 130
 QY 12489 TTTTCTATCTGACCAATCTGAGACACTTGACCTTCCACACAAATTCGAAGTAT 12548
 Db 131 PheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIle 150
 QY 12549 TATTCACAGACTTGCGGGTCTACATCAATGCCCCCTCAATCTCTCTTGAAGCTG 12608
 Db 151 TyrCysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 170
 QY 12609 TCCCTGAACCTTATGACCTTTATCCACAGGTCGATTTAAGAAATTAAGGCTTCATAG 12668
 Db 171 SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLys 190
 QY 12669 CTGACTTTAAGAAATTAATTTGATAGTTAAATGTAAGAAACTTGATTCAGAGTCTG 12728
 Db 191 LeuThrLeuArgAsnAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeu 210
 QY 12729 GCTGGTTTGAAGTCCATCGTTGGTCTGGAGAAATTTAGAAATGAAGAACTTGAA 12788
 Db 211 AlaGlyLeuGlnValHisArgLeuValLeuGlyGlnPheArgAsnGluGlyAsnLeuGln 230
 QY 12789 AAGTTTGAACAATCTGCTCTAGAGGCGCTGCAATTTGACCAITGAAAGATTCGATTA 12848
 Db 231 LysPheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGlnPheArgLeu 250
 QY 12849 GCATACCTTAGACTACTACTCTGATGATTTATTTGACTTATTTAATTTGTTGACAAATGTT 12908
 Db 251 AlaTyrLeuAspTyrTyrLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnVal 270
 QY 12909 TCTTCATTTTCCCTGGAGAGTGAGTACTTGAAGGGAAGAACTTTCTTATATTTTC 12968
 Db 271 SerSerPheSerLeuValSerValThrIleGlnLysValLysAspPheSerTyrAsnPhe 290
 QY 12969 GGATGGCAACATTTAGAAATTAATTAAGTAAATTTGACAGTTTCCCACTGAAATCTC 13028
 Db 291 GlyTyrGlnHisLeuGlnLeuValAsnCysLysPheGlyGlnPheProThrLeuLysLeu 310
 QY 13029 AAACTCTCAAAAAGGCTTACTTCACTTCCACAAAGGTGGGAATGCTTTTTCGAAGTT 13088
 Db 311 LysSerLeuLysArgLeuThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGlnVal 330
 QY 13089 GATCTACCAAGCTTGAAGTTCTAGATCTCAGTGAAGATGGCTTGAAGTTCAAGGTTC 13148
 Db 331 AspLeuProSerLeuGlnPheLeuAspLeuSerArgAsnGlyLysLeuSerPheLysGlyCys 350
 QY 13149 TGTTCGAAAGTGAATTTTGGGACAAACAGCTTAAAGATTTAGATCTGAGCTTCAATGCT 13208
 Db 351 CysSerGlnSerArgPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGly 370
 QY 13209 GTTATTACATGAGTTCAAACTTTGTGGGCTTGAACAACAATGATCTGATTTTCAG 13268
 Db 371 ValIleThrMetSerSerAsnPheLeuGlyLeuGlnGlnLeuGlnHisLeuAspPheGln 390
 QY 13269 CATTCGAATTTGAACAAATAGAGGATTTTCAATTTCTATCTCAGTCAAGAACTCTGAT 13328
 Db 391 HisSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuAsnLeuIle 410
 QY 13329 TACCTTGAACATTTCTACTACACACAGAGTTGCTTCAATGAGCATTTCAATGCTTG 13388
 Db 411 TyrLeuAspIleSerHisIleThrHisIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 430
 QY 13389 TCCAGTCTCGAAGCTTGAAGATGGCTGGCAATTTCTTCCAGAAACTTCTCTTCAGAT 13448
 Db 431 SerSerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAsp 450
 QY 13449 ATCTTCACAGAGCTGAGAAATTTGACCTTCTGAGACCTCTCAGTGTCAACTGAGACAG 13508
 Db 451 IlePheThrGlnLeuAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnGln 470
 QY 13509 TTGTCTCAACAGCAATTTAACTCACTCTCAGTCTTCAAGTACTTAATATAGCCACAC 13568

Db 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
 QY 13569 AACTCTTTTCATTTGATAGTTTCTTATTAAGTGTGAACTCCCTCCAGGTTCTGAT 13628
 Db 491 AsnPheSerSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAsp 510
 QY 13629 TACAGTCTCAATCAATTAAGACTTCCAAAAACAGAACACTACAGACTTTTCCAGTAGT 13688
 Db 511 TyrSerLeuAsnHisIleMetThrSerLysLysGlnGlnLeuGlnHisPheProSerSer 530
 QY 13689 CTAGCTTTCTTAAATCTTACTCAGATGACTTTGCTGTGATCTTGTGAACACAGAGTTTC 13748
 Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe 550
 QY 13749 CTGCAATGATCAAGACACAGAGCACTTGTGTGAAGATTTGAACGAATGGAATGGCA 13808
 Db 551 LeuGlnThrPyrLysArgGlnArgGlnLeuValGlnValGlnArgMetGlnCysAla 570
 QY 13809 ACACTTCAGATTAAGCAGGCAATGCTGTGCTGAGTTGAATATCACCTGTCAAGTAAAT 13868
 Db 571 ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 590
 QY 13869 AAGACATCATTTGGTGTGTGCTGCTCAGTGTGCTGTGATATCTGTTGAGCAGTTCTG 13928
 Db 591 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaValLeu 610
 QY 13929 GTCTATAGTTCTTATTTTCACTGATGCTTCTTGTGCTGCTGCTGATAAAGTATGGTAGGT 13988
 Db 611 ValTyrLysPheTyrPheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGly 630
 QY 13989 GAAAAACATCATGATGCTTGTATATCTACTCAAGACAGAGATGAGCACTGGTGAAGAT 14048
 Db 631 GlnAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspThrValArgAsn 650
 QY 14049 GAGCTAGTAAAGATTTAGAAAGAGGCTCTCCATTTGACTTGCCTTCACTACAGACA 14108
 Db 651 GlnLeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrArg 670
 QY 14109 GACTTATTTCCCGGTGGGCAATTTGCTGCCAATCATCATGAAGTTTCCATTAAGC 14168
 Db 671 AspPheIleProGlyAlaAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSer 690
 QY 14169 CGAAAGGTGAATTTGGTGGTGTCCAGCACTTATCATCCAGAGCGCTGTATCTTGA 14228
 Db 691 ArgLysValIleValValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGln 710
 QY 14229 TATGAGATTTGCTGAGCTTGGAGATTTCTGAGCATGCTGCTGATCATTTCAATGTC 14288
 Db 711 TyrGlnIleHisGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 730
 QY 14289 CTGCAAGAGGTGGAAGAACCTTGTCTCAGGACAGAGGTGAGCTGTACCGCTTCTCAGC 14348
 Db 731 LeuGlnLysValAlaLysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSer 750
 QY 14349 AGGAACACTTACCTGGAGTGGAGGACAGGTGCTCGAGGAGGAGCAATCTTCTGAGACGA 14408
 Db 751 ArgAsnThrTyrLeuGlnThrTrpGlnAspSerValLeuGlnArgHisIlePheThrArgArg 770
 QY 14409 CTGAGAAAGCCCTGTGATGTGTAATCATGTGAATCCAGAAAGAACAGTGGGTACAGGA 14468
 Db 771 LeuArgLysAlaLeuLeuAspGlyLysSerTyrAsnProGlnGlyHisValGlyThrGly 790
 QY 14469 TGCATTTGGCAGAGACACATCTTATC 14495
 Db 791 CysAsnThrPyrGlnGlnAlaThrSerIle 799
 RESULT 10
 ADB39121 standard; protein; 799 AA.
 ID ADB39121
 AC ADB39121;
 XX
 DT 04-DEC-2003 (first entry)

XX Human toll-like receptor (TLR) -4 protein amino acid sequence.
 DE
 XX
 KM vascular disease; Toll-like receptor-4 inhibitor; TLR-4 inhibitor;
 KM atherosclerosis; restenosis; inflammation; vasotropic;
 KM atherosclerosis; thrombotic; cardiatic; antiinflammatory;
 KM antiense therapy; gene therapy; transplant atherosclerosis;
 KM vein-graft atherosclerosis; thrombosis; stent restenosis;
 KM angioplasty restenosis; heart disease; human.
 XX
 OS Homo sapiens.
 PN
 XX US2003072729-A1.
 PD
 XX 24-APR-2003.
 PE 23-APR-2002; 2002US-00128166.
 XX
 PR 24-OCT-2001; 2001US-0315637P.
 PR 17-DEC-2001; 2001US-0341359P.
 XX
 PA (CEDA-) CEDARS SINAI MEDICAL CENT.
 PI
 XX Arditi M, Rajavashisth T, Shah PK;
 DR WPI: 2003-615986/58.
 DR N-PSDB; ADB39120.
 XX
 PT Treating a vascular disease, particularly atherosclerosis, thrombosis,
 PT restenosis, stent restenosis or angioplasty restenosis, by administering
 PT a Toll-like receptor-4 (TLR-4) inhibitor to a mammal.
 XX
 PS Disclosure; Page 13-15; 21pp; English.
 XX
 CC This invention relates to a novel method for the treatment of a vascular
 CC disease through the administration of a Toll-like receptor-4 (TLR-4)
 CC inhibitor to a mammal. The TLR-4 protein has been linked to several
 CC disease such as atherosclerosis, restenosis, inflammation and other
 CC vascular diseases. Compounds which inhibit the activity of TLR-4, through
 CC the inhibition of its receptor, may have vasotropic,
 CC antiatherosclerotic, thrombolytic, cardiac and antiinflammatory
 CC activities. This may also be achieved through antisense therapy or gene
 CC therapy. The method or the system of the invention may therefore be
 CC useful for inhibiting or treating a vascular disease, for example
 CC atherosclerosis, transplant atherosclerosis, vein-graft atherosclerosis,
 CC thrombosis, restenosis, stent restenosis, angioplasty restenosis, or
 CC inflammation and other heart disease. The present sequence is the amino
 CC acid sequence of the human TLR-4 protein which was the target receptor
 CC for inhibitory compounds in the method of the invention.
 CC
 XX
 SQ Sequence 799 AA:
 Alignment Scores:
 Pred. No.: 0 Length: 799
 Score: 3903.50 Matches: 757
 Percent Similarity: 98.57% Conservative: 1
 Best Local Similarity: 98.44% Mismatches: 2
 Query Match: 11.81% Indels: 9
 DB: 7 Gaps: 1
 US-09-396-985B-47 (1-18989) x ADB39121 (1-799)
 QY 12216 TCATGCTTTTATTC-----TGNAGTGTGAATC 12248
 DB 31 SerTySerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIle 50
 QY 12249 GAGCAATTGAAGATGGGCGATATCAGAGCCTTCTACTATATTTGACA 12308
 DB 51 GlnThrIleGluAspGlyAlaIleGlnSerLeuSerHisLeuSerThrLeuIleLeuThr 70
 QY 12309 GGAAGCCCATCCAGAGTTTGAAGCCCTGGAGCCTTTTCTGACATCAATCAAGTTTACAGAG 12368
 DB 71 GlyenProIleGlnSerIleuAlaLeuGlyAlaPheSerGlyLeuSerSerIleuGlnIlys 90

QY 12369 CTGGTGGCTGGAGAGCAAAATCTAGCATCTAGAGAACTTCCCATTTGACATCTCAAA 12428
 DB 91 LeuValAlaValGluThrAsnLeuAlaSerIleuGluAsnPheProIleGlyIleuLys 110
 QY 12429 ACTTTGAAGAACTTAATGTGGCTCACAATCTTATTCAAATCTTTCAAAATTTACTGGAT 12488
 DB 111 ThrLeuLysGluIleuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTy 130
 QY 12489 TTTTCTAACTGACCAATCTAGAGCACTTGGACCTTCCAGCAAGAAATTCAGAGTAT 12548
 DB 131 PheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIle 150
 QY 12549 TATTGACAGACTTGGGGGTTCTACATCAAAATGCCCTTACTCAATCTCTTTAGACTTG 12608
 DB 151 TyrCysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 170
 QY 12609 TCCCTGAACCTTATGAACTTTATCCAAACGAGTGCAATTTAAGAAATTAAGCTTCATAG 12668
 DB 171 SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLys 190
 QY 12669 CTGACTTTAAGAAATATTTTGAATAGTTTAAATGAAACTTGATTCAGAGGCTTG 12728
 DB 191 LeuThrLeuArgAsnAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeu 210
 QY 12729 GCTGGTTTGAAGATCCATCGTTTGGTCTGGAGAAATTTAGAATGAAGAACTTGAA 12788
 DB 211 AlaGlyLeuGlnValHisArgLeuValIleuGlyGluPheArgAsnGluIleAsnLeuGlu 230
 QY 12789 AAGTTTGACAAATCTGCTCTAGAGGCGCTGTGCAATTTGACATTTGAAGAAATTCGATTA 12848
 DB 231 LysPheAspLysSerIleuGlnGluGlyLeuCysAsnLeuThrIleGluGluPheArgLeu 250
 QY 12849 GCATCTTGAACACACACACCTCGATATTAATGACTTATTAATGTTTGAACAAATGTT 12908
 DB 251 AlaTyrLeuAspLysTyrTyrLeuAspAspIleIleAspLeuPheAsnLysLeuThrAsnVal 270
 QY 12909 TCTTCAATTTTCCCTGGTGAAGTGATGACTATTTGAAGGTTAAGGCTTTTCTTAATTTTC 12968
 DB 271 SerSerPheSerIleuValSerValThrIleGluArgValLysAspPheSerTyrAsnPhe 290
 QY 12969 GAGTGGCAACATTTAGAAATTAAGTTAACTGTAATTTTGGACAGTTTCCACATTTGAACTC 13028
 DB 291 GlyTyrGlnHisLeuGlnIleuValIleuValAsnCysLysPheGlyGlnIlePheProThrLeuLys 310
 QY 13029 AAATCTCTCAAAAGGCTTACTTCACTTCCAAAGAGTGGGAAGCTTTTTCAGAAAGTT 13088
 DB 311 LysSerLeuLysArgLeuThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGluVal 330
 QY 13089 GATCTACCAAGCCTTGAGTTTCTAGATCTCAGTAGAAATGGCTTGAGTTTCAAGGTTGC 13148
 DB 331 AspLeuProSerIleuGlnPheLeuAspLeuSerHisArgAsnLysLeuSerPheLysGlyCys 350
 QY 13149 TGTTCCTCAAGATATTTGGGACCAACGCTTAAAGTATTTAGATCTGAGCTTCAATGTT 13208
 DB 351 CysSerGlnSerAspPheGlyThrThrSerIleuLysTyrLeuAspLeuSerPheAsnGly 370
 QY 13209 GTTATTCATGATGATTAACTTCTGGGCTTGAACAATACTTAACAATCTCGAATTTCCAG 13268
 DB 371 ValIleThrMetSerSerAsnPheLeuGlyLeuGlnIleuGlnHisLeuAspPheGln 390
 QY 13269 CATTCGAATTTGAACCAATGAGTGAAGTTTTCAGTATCTTATCACTCAGAAACCTGATT 13328
 DB 391 HisSerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuAsnLeuIle 410
 QY 13329 TACCTTGCAATTTCTCACTACTCACACGAGTTCCTTCAATGAGCTTCAATGAGCTTG 13388
 DB 411 TyrLeuAspLysSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 430
 QY 13389 TCCAGTCTGCAAGCTTGAAGAAATGGCTGGCAATTTCTTCCAGAGAAACCTTCCAGAT 13448
 DB 431 SerSerIleuGlnValLeuLysMetAlaGlyAsnSerPheGlnGluAsnPheLeuProAsp 450

QY 13449 ATCTTCACAGAGCTGAGAACTTGACCTTCTCTGAGCTCTCTGAGTGTCAACGTGAGAG 13508
 Db 451 ILePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 470
 QY 13509 TTGTCTCCAAAGAGATTAACTCACTCTCCAGTCTTCCAGTACTTAAATATGAGCCACAC 13568
 Db 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
 QY 13569 AACTCTTTTTCATTGATACGTTTCCTTATTAAGTGTGAACTCCCTCCAGCTTCTTGAT 13628
 Db 491 AsnPhePheSerLeuAspThrPheProTyrCysLeuAsnSerLeuGlnValLeuAsp 510
 QY 13629 TACAGTCTCAATCACTATAGTCTTCCAAAAACAGAACTACAGCATTTTCCAGTAGT 13688
 Db 511 TyrSerLeuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPheProSerSer 530
 QY 13689 CTAGCTTTCTTAATCTTACTCAAGATGACTTTGCTGTACTGTGAACACCAAGATTTC 13748
 Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisLeuSerPhe 550
 QY 13749 CTGCATATGATCAAGAGACCAAGGAGAGCTTGGGAGAGTTGAACGAATGAATGTGCA 13808
 Db 551 LeuGlnThrPheLysAspGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAla 570
 QY 13809 ACACCTTCAGATTAAGCAGGAGCATGCTGTGCTGAGTTGAATATCACCTTCAGATGAT 13868
 Db 571 ThrProSerAspLysGlnGlnLysMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 590
 QY 13869 AAGACATCATTTGCTGTGCTGCTCTCAAGTGTGCTGTGATGATCTGTGATGCAAGTTCTG 13928
 Db 591 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaValLeu 610
 QY 13929 GTCTATTAAGTCTTATTTTCACTGATGCTTCTGCTGGCGCAATTAAGTATGATGAGT 13988
 Db 611 ValTyrLysPheTyrPheHisLeuMetLeuAsnGlyCysIleLysTyrGlyArgGly 630
 QY 13989 GAAACATCTATGATGCTTGTATCTTACTCAAGCAGATGAGATGAGATGAGATGAGAT 14048
 Db 631 GluAsnIleTyrAlaPheAlaPheValIleTyrSerSerGlnAspGlnAspThrValArgAsn 650
 QY 14049 GAGCTAGTAAAGATTTTAAAGAAAGGGGCTGCTCAATTTCACTGCTGCTTCACTACAGA 14108
 Db 651 GluLeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrArg 670
 QY 14109 GACTTTATCCCGGTGGGACATGCTGCCAATCATCATCAATGAAGTTTCCATAAAGC 14168
 Db 671 AspPheIleProGlyValAlaIleAlaIleAsnIleIleHisGlnGlyPheHisLysSer 690
 QY 14169 CGAAGGTGATTTGTTGTGTGTCCACAGACTTTCACAGAGCCGCTGATCTTGA 14228
 Db 691 ArgLysValIleValValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGln 710
 QY 14229 TATGAGATTGCTGACCTGGAGCTTTCAGAGCTGCTGCTGATCATCTTCAATGTC 14288
 Db 711 TyrGlnIleIleGlnIleThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 730
 QY 14289 CTGAGAGAGGTGAGAGAGACCTGCTGAGAGAGAGTGAAGCTGATCCGCTTCTACG 14348
 Db 731 LeuGlnIlyValGlnLysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSer 750
 QY 14349 AGGAACACTTACCTGAGTGGAGAGAGAGTCTCTGGGGCGGACATCTTCTGAGAGCA 14408
 Db 751 ArgAsnThrTyrLeuGlnIlyThrGlnAspSerValLeuLysArgHisIlePheThrPArgArg 770
 QY 14409 CTGAGAAAGCCCTGCTGATGTAAATCATGGAATCCAGAAAGAGAGAGTGGGTACAGA 14468
 Db 771 LeuArgLysAlaLeuLeuAspGlyLysSerThrPAsnProGlnGlyThrValGlyThrGly 790
 QY 14469 TGCAATTGGAGAGAGAGACATCTATC 14495
 Db 791 CysAsnThrGlnGlnAlaIleMetSerIle 799

ADP56656
 ID ADP56656 standard; protein; 799 AA.
 XX
 AC ADP56656;
 XX
 DT 09-SEP-2004 (first entry)
 XX
 DE Human Toll-like receptor (TLR)-related protein - SEQ ID 8.
 XX
 KM expression system; Toll-like receptor; TLR; immune response modifier;
 KM IRM; cancer; gene therapy; human; receptor.
 XX
 OS Homo sapiens.
 XX
 PN MO2004053057-A2.
 XX
 PD 24-JUN-2004.
 XX
 PF 31-OCT-2003; 2003MO-US034563.
 XX
 PR 11-DEC-2002; 2002US-0432651P.
 XX
 PA (MINN) 3M INNOVATIVE PROPERTIES CO.
 XX
 PI Gupta SK, Ghosh TK, Fink JR;
 XX
 DR WPI; 2004-468833/44.
 DR N-PSDB; ADP56655.
 XX
 PT New expression system comprising a first nucleic acid sequence that
 PT encodes a Toll-like receptor (TLR), useful for preparing a composition
 PT comprising TLR agonist for treating e.g., cancer.
 XX
 PS Claim 4; SEQ ID NO 8; 699p; English.
 XX
 CC The invention relates to a novel expression system comprising a first
 CC nucleic acid sequence that encodes a Toll-like receptor (TLR) operably
 CC linked to a first expression control sequence and a second nucleic acid
 CC sequence that encodes a reporter. TLRs are immune response modifiers
 CC (IRMs). The expression system of the invention may be useful for
 CC preparing a composition comprising the TLR agonist for treating cancer,
 CC possibly via gene therapy. The current sequence is that of the human Toll
 CC -like receptor (TLR)-related protein (SEQ ID 8) of the invention.
 XX
 SQ Sequence 799 AA.
 Alignment Scores:
 Pred. No.: 0 Length: 799
 Score: 3903.50 Matches: 757
 Percent Similarity: 98.57% Conservative: 1
 Best Local Similarity: 98.44% Mismatches: 2
 Query Match: 11.81% Indels: 9
 DB: 8 Gaps: 1
 US-09-396-985b-47 (1-18989) x ADP56656 (1-799)
 QY 12216 TCATGCTTTTATTC-----TGTAGTGTGAATC 12248
 Db 31 SerTyrSerPhePheSerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIle 50
 QY 12249 CAGACATTAAGATGAGGGGATATCAGAGCCTAAGCCACTTCACTTAATATTGACA 12308
 Db 51 GlnThrIleGlnAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThr 70
 QY 12309 GGAACCCCATCCAGATTAGCCCTGGAGACCTTTTCTGAGTATCAAGTTTACAGAG 12368
 Db 71 GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerClyLeuSerSerLeuGlnLys 90
 QY 12369 CTGTGGCTGTGAGAGCAATCTAGCATCTCTAGAGAACTTCCCATTTGAGCATCTCAGAA 12428
 Db 91 LeuValAlaValGlnThrAsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuLys 110
 QY 12429 ACTTGAAGAAGACTAATGCTGCTCAACAATCTTATCCAAATTACTGAGTAT 12488

|||||
Db 111 Thrleuysgluleuasnvalalanhiasnleuileglnserpheylsleuproglnlyr 130
Qy 12489 TTTTCTAATCGACCAATCTAGACACTGTGGACCTTCCAGCAACAAGATTCAAAAGATT 12548
Db 131 Pheaserbnleuthraenleuglnhisleuabpserleuasnlysllelnserlle 150
Qy 12549 TATGCAAGACTGGGGTCTACATCAATGCCCTACTCAATCTCTTTAGACTG 12608
Db 151 TyrcysrthrleuabpvalleuuhleuileglnmerProleuenuenleuaserleuabp 170
Qy 12609 TCCCTGAACCTTGAACCTTATATCCAACAGGTGCATTTAAAGAAATTTAGGCTTCATAG 12668
Db 171 SerleuabpPromeleasnphelleglnProglialaheylsguilleargleuhislys 190
Qy 12669 CTGACTTTAAGAAATTAATTTGATAGTTTAAATGTAATGAATACTGTATTCAGAGCTG 12728
Db 191 Leuthrleuabpaganasnpheserleuasnvalaileuylslnrcyslileglnlyeu 210
Qy 12729 GCTGGTTTAGAAGTCAATCGTTTGTCTGGAGAAATTTAGAAATGAAGAACTTGAAA 12788
Db 211 Aleglileuenglualhisargleuvalleuuglylunhearaganugllyasnleu 230
Qy 12789 AAGTTTGAACAATGTGCTCTAGAGGGCTGTGCATTTGACCATTTGAAGAAATTCGATTA 12848
Db 231 LysheabpLysSerAlaleuuglnlyeuCysasnleuthrileglnlunpheargleu 250
Qy 12849 GCATCTTAGACTCTACCTCGATGATATTAATGACTTATTAATTTGAGCAAAAGTT 12908
Db 251 AlalatyreuabpTyrltyrleuabpAspilleleasnleupheasnCybleuthrahsval 270
Qy 12909 TCTTCATTTCCCTGAGTGTGATGACTATTTGAAGGGTAAAGACTTTCTTATATTTTC 12968
Db 271 SererPheaserleuvalserValthrileglunargllysaapPheaserTyraasnph 290
Qy 12969 GGATGGCAACATTTAGAAATTAAGTTAACTGTAAATTTGGACAGTTTCCACATTTAAATCTC 13028
Db 291 GlylrpnlhisleuuglnleuvalaasnCylysbphegllynPheProthrleuylsleu 310
Qy 13029 AAATCTCCAAAAGGCTTACTTTCATCTCCAAAGAGTGGAGATGCTTTTTCAGAGTT 13088
Db 311 LysserleuylsaargleuthrPheThrserasnlysglylaasnAlaPheSerGlual 330
Qy 13089 GATCTACCAAGCTTGAAGTTCTAGATCTCAGTGAATAAGCTTGAAGTTCAAGAGTTGC 13148
Db 331 AspleuProserleuuglnpheuabpseraraganlyleuSerPheylslyCys 350
Qy 13149 TGTCTCAAGATGATTTTGGACAACAGCCTAAAGTATTTAGATCTGAGCTTCAATGCT 13208
Db 351 CysserglinserserphegllyThrThrserleuylsTyrlleuabpLeuSerPheasnly 370
Qy 13209 GTTATTCACAGAGTCAAACTTCTTGGCTTAGAACAACATGAACATCTGATTTCCAG 13268
Db 371 ValillethlmetSerSerasnphelueuglyleuuglnleuuglnhisleuabpPhe 390
Qy 13269 CATTCATTTGAAAACAATAGAGTGAAGTTTCAAGTATCTATGACTCAGAAAACCTCAT 13328
Db 391 HisserasnleuylslnmetSerGlunpheSerValPheleuSerleuabpAsnleuile 410
Qy 13329 TACCTTGACATTTCTCATATCTCACACAGAGTTGCTTCAATGGCATTTCAATGGCTTG 13388
Db 411 TyrlleuabpRilleSerHisethrHisethrargValAlaPheasnlyllePheAsnlyleu 430
Qy 13389 TCCAGTCTCGAAGCTTGAAGAAATGCTGGCAATTTCTTCCAGAAAATTTCTTCCAGAT 13448
Db 431 SerSerleuuglnualleuylsMetAlaGlyasnSerPheglnglnuasnPheleuProasp 450
Qy 13449 ATCTTCACAGAGCTGAGAAACTTGAACCTTCTGGAACCTCTCAGTGTCAACTGAGAG 13508
Db 451 IlePheThrGlnleuabpAsnleuthrPheleuabpLysSerGlnCysglinsleuugln 470
Qy 13509 TTGTTCTCAACAGCATTTAACTCACTCCAGTCTTCAGGTACTAAATATAGAGCCACAAC 13568
|||||

Db 471 LeuSerProthrAlaPheasnserleuSerSerleuuglnValleuabpMetSerHisasn 490
Qy 13569 AACTCTTTTCAATGGATAGCTTTCTTAAAGTGTCTGAACCTCCAGAGTTCTTGAT 13628
Db 491 AsnpheserleuabpThrPheProTyrlsCybleuabpSerleuuglnValleuabp 510
Qy 13629 TACAGTCTCAATCAATATGACTTCCAAAACAGGAACTACAGCATTTTCCAGTAGT 13688
Db 511 TySerleuabpHisilleMetThrSerlyslsGlnGlnleuuglnhisPheProSerSer 530
Qy 13689 CTAGCTTTCTTAAATCTCTACAGATGACTTTGCTGTGATCTGTGAACAACAGAGTTTC 13748
Db 531 LeuAlaPheleuasnleuthrGlnasnAspPheAlaCysThrCysglinslnserPhe 550
Qy 13749 CTGCAATGATCAAGAGCAAGAGGAGCTCTTGGTGAAGTTGAAGAAATGAGTGC 13808
Db 551 LeuGlnThrPrlleuabpGlnarglnleuValGlnValGlnargmetGlnCysAla 570
Qy 13809 ACACTTCAGATTAAGAGGAGATGCTGTGCTGAGATTGAATATCACTGTCAATGAAT 13868
Db 571 ThrProSerabpLysglnglnMetProValleuSerleuabpnlleThrCysglinsMetasn 590
Qy 13869 AAGACCATCATTTGGTGTGCTGCTCAAGTGTGCTGTAGTATCTGTGAGAGTTTC 13928
Db 591 LysThrillelellyalserValleuSerValleuValserValAlaAlaVal 610
Qy 13929 GTCTATAGTTCTAATTTTCACTGATGCTTCTTGTGCTGTGATTAAGTATGATAGGT 13988
Db 611 ValTyrlsPheTyrlrhehisleuMetleuAlaGlyCysrileylsTyrlsArgly 630
Qy 13989 GAAAACATCTAGATGCTTTGTATCTACTCAAGCCAGATGAGAGATCTGGTAAAGAT 14048
Db 631 GluasnIleTyraapAlaPheValIleTyserSerGlnAspGlnAspTrValArgasn 650
Qy 14049 GACCTAGTAAAGATTTAGAAAGAGGGGCTCCATTTCAAGTCTGCTCACTACAG 14108
Db 651 GlnleuValIlysaasnleuuglnuglyValaProPheGlnleuCybleuHisTyArg 670
Qy 14109 GACTTATTCCTCGGTGGCCATTTGCTGCCACATCATCATGAAGTTCCTCAATAAAGC 14168
Db 671 AspPheilleProgllyAlaAlaileAlaAlaasnIlelehisGlnuglyPhehislybser 690
Qy 14169 CGAAGGTGATGTGTGTGTGCCAGACACTTCATCCAGACGCGTGTGTATCTTTGAA 14228
Db 691 ArglyValAlleValValIserGlnHisPheilleGlnserArgTrpCysIlePheGln 710
Qy 14229 TATGAGATTTCTCAGACTGGCAGTTTCTGAGAGATCGTGTATCATCTTCAATGTC 14288
Db 711 TyrlGlnilleAlaGlnThrTrpGlnPheleuSerSerArgAlaGlyIleillePheilleVal 730
Qy 14289 CTGCAAGAGGTGAGAAAGACCTGTGCTCAGGACAGGATGAGCTGTACCGCTTCTCAGC 14348
Db 731 LeuGlnIlysaIgluylsThrleuabpArglnGlnValGlnleuTyraargleuLeuSer 750
Qy 14349 AGAACACTTACCTGAGTGGAGAGACAGTGTCTGGGGCGGCAATCTTCTGAGACGA 14408
Db 751 ArgasnThrTyrlleuuglnTrpGlnAspSerValleuGlyArgHisIlePheTrpArgArg 770
Qy 14409 CTCAGAAAACCTGTCTGATGTGTAAATCATGGAATCCAAAGAAACAGTGGGATCAAGA 14468
Db 771 LeuArglysaAlaLeuLeuabpGlyLysSerTrpAspProglnglnThrValGlyThrGly 790
Qy 14469 TGCATATGCGCAGGAAGCAATCATATC 14495
Db 791 CysasnTrpGlnGlnAlaThrSerlle 799
RESULT 12
ADP48597
ID ADP48597 standard; protein; 799 AA.
AC ADP48597;
XX
DT 09-SEP-2004 (first entry)

XX Human Toll-like receptor protein SEQ ID NO:8.
 DE Toll-like receptor; TLR; human; detection; identification; TLR agonist;
 KM TLR antagonist.
 KW TLR antagonist.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO2004053452-A2.
 XX WO2004053452-A2.
 PD 24-JUN-2004.
 XX 31-OCT-2003; 2003WO-US034554.
 PF 31-OCT-2003; 2003WO-US034554.
 XX 11-DEC-2002; 2002US-0432650P.
 PR 11-DEC-2002; 2002US-0432650P.
 XX (MINN) 3M INNOVATIVE PROPERTIES CO.
 PA (MINN) 3M INNOVATIVE PROPERTIES CO.
 PI Gupta SK, Ghosh TK, Fink JR;
 PI WPI: 2004-468955/44.
 DR N-PSDB; ADP48596.
 DR N-PSDB; ADP48596.
 XX
 PS Claim 8; SEQ ID NO 8; 78pp; English.
 XX
 CC The present invention describes a method for detecting activation of a
 CC Toll-like receptor (TLR) in a cell. The method comprises: (a) providing a
 CC cell culture comprising cells transfected with a nucleic acid sequence
 CC that encodes a reporter that (i) generates a detectable signal when the
 CC reporter is expressed and the cell is exposed to conditions for
 CC generating the detectable signal, and (ii) is operably linked to an
 CC expression control sequence that is induced by activation of a TLR and
 CC comprises a cytokine promoter, a chemokine promoter, a co-stimulatory
 CC marker promoter, or a defense promoter; (b) exposing the cell culture to
 CC a compound that activates a TLR; (c) providing conditions for generating
 CC the detectable signal; and (d) detecting the detectable signal. Also
 CC described: (1) a method of identifying a TLR agonist or antagonist; (2) a
 CC TLR agonist or antagonist identified by the method of (1); and (3) a
 CC pharmaceutical composition comprising a TLR agonist or antagonist
 CC identified by the method of (1) and a pharmaceutical salt. The methods
 CC are useful for detecting activation of a TLR in a cell and for
 CC identifying TLR agonist or antagonist. The present sequence represents a
 CC human TLR which is used in the exemplification of the present invention.
 XX
 SQ Sequence 799 AA;
 Alignment Scores:
 Pred. No.: 0 Length: 799
 Score: 3903.50 Matches: 757
 Percent Similarity: 98.57% Conservative: 1
 Best Local Similarity: 98.44% Mismatches: 2
 Query Match: 11.81% Indels: 9
 DB: 8 Gaps: 1
 US-09-396-985B-47 (1-18989) x ADP48597 (1-799)
 QY 12216 TCAATGCTCTTTTATTC-----TGAAGTGAATC 12248
 Db 31 SerYrserPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGlnIle 50
 QY 12249 CAGACAAATGGAAGTGGGGCTATCAGAGCTTAAGCACTCTTACTTAATATGACA 12308
 Db 51 GlnThrIleGluAspGlyAlaItyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThr 70
 QY 12309 GGAAGCCCATCCAGAGTTTGACCTGGAGACCTTTTCTGACATCATCAAGTTTACAGAG 12368
 Db 71 GlnAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIlys 90
 QY 12369 CTGTGGCTGTGAGACAAATCTAGCATCTCTAGAGAACTTCCCATGTGACATCTCAA 12428

Db 91 LeuValAlaValGluThrAsnLeuAlaSerLeuGluAsnPheProIleGlyHisLeuIlys 110
 QY 12429 ACTTTGAAGAACTTAATGAGGCTCAACAATCTTATCCATCTTTCAATTAACCGAGAT 12488
 Db 111 ThrLeuGlyGluAsnValAlaHisAsnLeuIleGlnSerPheIysLeuProGluItyr 130
 QY 12489 TTTTCTAATCTGACCAATCTAGAGACCTTGACCTTCCAGCAACAAGATTCAGATAT 12548
 Db 131 PheSerAsnLeuThrAsnLeuGluHisLeuAspLeuSerSerAsnIysIleGlnSerIle 150
 QY 12549 TATTGACAGACTTGGGGTTCTATCATCAATGCCCCCTACTCAATCTCTCTTAGACCTG 12608
 Db 151 TyrCysThrAspLeuArgValIleuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 170
 QY 12609 TCCCTGAACCTTAATGAACTTATCCAAACGAGGTCATTTAAAGAAATTAGGCTCATAG 12668
 Db 171 SerLeuAsnProIleAsnPheIleGlnProGlyAlaPheIysGluIleArgLeuHisIlys 190
 QY 12669 CTGACTTAAAGAAATATTTTGTAGTATTAATGTAATGAAACTTGTATTCAGAGTCTG 12728
 Db 191 LeuThrLeuArgAsnAsnPheAspSerLeuAsnValMetIysThrCysIleGlnGlyLeu 210
 QY 12729 GCTGGTTTGAAGTCATCGTTGGTTCTGGGGAATTTAGAAATGAGAAACTTGAA 12788
 Db 211 AlaGlyLeuGluValHisArgLeuValIleuGlyGluPheArgGlnGlyAsnLeuGlu 230
 QY 12789 AAGTTTACAAATCTGTCTAGAGGCGCTTCGACATTTGACATTTGAAGAAATCCGATTA 12848
 Db 231 LysPheAspIysSerAlaIleuGluGlyLeuCysAsnLeuThrIleGluGluPheArgLeu 250
 QY 12849 GCATTAATTAAGTACTACTCGATGATATTAATTAATTAATTAATTAATTAATTAATTA 12908
 Db 251 AlaTyrLeuAspItyrTyrLeuAspPheIleIleAspLeuPheAsnIysLeuThrAsnVal 270
 QY 12909 TCTTCATTTTCCCTGGAGTGTGATCTATTGAAAGGTTAAAGACTTTCTTATTAATTC 12968
 Db 271 SerSerPheSerLeuValSerValThrIleGluArgValIysAspPheSerTyrAsnIle 290
 QY 12969 GATGGCAATTTAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 13028
 Db 291 GlyTyrPheIleHisLeuGluValAsnIysLeuPheIleGlnIlePheProIleLeuIle 310
 QY 13029 AAATCTCTGAAAGGCTTACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 13088
 Db 311 LysSerLeuIysArgLeuThrPheThrSerAsnIysGlyValAsnAlaPheSerGlyVal 330
 QY 13089 GATCTACCAAGCTTGAAGTTCTAGATCTGATGAGAAATGAGCTTGAAGTTCAAGTTGC 13148
 Db 331 AspLeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheIysGlyCys 350
 QY 13149 TGTTCCTCAAGATATTTGGGACACACGCTTAAGATTTAGATCTGACCTCAATGCT 13208
 Db 351 CysSerIleAsnIysPheGlyThrThrSerLeuIysTyrLeuAspLeuSerPheAsnGly 370
 QY 13209 GTTATTACAGTGAAGTCAAACTTCTGGGCTTGAACAATAGTGAACATCTGAAATTCAG 13268
 Db 371 ValIleThrCysSerSerAsnPheLeuGlyLeuGluIleuGluIleuGluIleuAspPheGln 390
 QY 13269 CATTTCAATTTGAACAATAGTGAAGTTTTCAGATTTCTCATCTCAAGAACTGAT 13328
 Db 391 HisSerAsnLeuIysGlnMetSerGluPheSerValPheLeuSerLeuAlaGlnLeuIle 410
 QY 13329 TACCTTGACATTTCTCATCTACACACAGAGTTCCTTCAATGACATCTTCAATGCTTG 13388
 Db 411 TyrLeuAspIleSerHisIleThrHisIleArgValAlaPheAsnGlyIlePheAsnGlyLeu 430
 QY 13389 TCCAGTCTGAAGCTTGAAGAAAGGCTGGAATTTCTTCAAGGAAACTCTTCCAGAT 13448
 Db 431 SerSerLeuIleValLeuIysMetAlaGlyAsnSerPheGlnGluAsnPheLeuProAsp 450
 QY 13449 ATCTTCAAGAGCTGAAGAACTTGAACCTTCTGAGACTCTCTGATGCTCAATGAGACAG 13508

Db 451 IlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 470
 QY 13509 TTGCTCCAAAGAGATTAACTCACTCCAGCTTCCAGGACTTAATATGAGCCAAAC 13568
 Db 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
 QY 13569 AACTCTTTTCATTGGATACGTTTCCTTATAGTGTGAATCCCTCCAGGTTCTTGAT 13628
 Db 491 AsnPheSerLeuAspThrPheProTyrLeuCysLeuAsnSerLeuGlnValLeuAsp 510
 QY 13629 TACAGTCTCAATCAATCAATGACTTCCAAAAACAGAACTACAGCAATTTTCCAGTAGT 13688
 Db 511 TyrSerLeuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPheProSerSer 530
 QY 13689 CTGAGCTTTTAATCTTAATCAAGATGACTTGTCTGTGATCTGTGAACCCAGAGTTTC 13748
 Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe 550
 QY 13749 CTGCATATGATCAAGACACAGAGCCAGCTCTTGAGTGAAGTTGAACGAATGGAATGTGA 13808
 Db 551 LeuGlnTrpTyrLeuAspGlnAspGlnLeuLeuValGlnValGlnAspMetGlnCysAla 570
 QY 13809 ACACCTTCAGATAAGACAGGGGACCTGTGTGCTGAGTTGAATATCACCCTGCAGATGAAT 13868
 Db 571 ThrProSerAspLysGlnGlnLysMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 590
 QY 13869 AAGACCATCATTTGGTGTGTGCTGCTCAGTGTGCTGAGTGAATGTTGTAGAGAGTTCTG 13928
 Db 591 LysThrIleIleGlyValSerValLeuSerValLeuValSerValAlaValLeu 610
 QY 13929 GTCTATAGTGTCTATTTTTCACCTGATGCTTCTGCTGCTGCTCATGAATGATGATAGAGT 13988
 Db 611 ValTyrLysPheTyrPheHisIleMetLeuLeuAlaGlyCysIleLysTyrGlnArgGly 630
 QY 13989 GAAACATCTATGATGCTTTGTTATCTCAAGCCAGATGAGATGAGATGAGATGAGAT 14048
 Db 631 GluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTyrValArgAsn 650
 QY 14049 GAGCTAGTAAGATTTTAAAGAGAGGGGCTCATTTGAGCTGTGCTTCAATACAGA 14108
 Db 651 GluLeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuCysValHisTyrArg 670
 QY 14109 GACTTTATTTCCCGGTGTGGACATTTGCTGCCAAATCATTCATGAAGTTTCCATAAAGC 14168
 Db 671 AspHelleProGlnValAlaIleAlaHisIleIleHisGlnGlnPheHisLysSer 690
 QY 14169 CGAAAGTGATTTGTGTGTGTGTCCAGACATTCATCCAGACCCCTGTGTATTTGAA 14228
 Db 691 ArgLysValIleValIleValSerGlnHisPheIleGlnSerArgTyrCysIlePheGln 710
 QY 14229 TATGAGATTTGCTGAGCTGTGCACTTTCTGAGCAGTGTGTGTGATCATTTGATGTC 14288
 Db 711 TyrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 730
 QY 14289 CTGCAGAAAGTGTGAGAAAGACCTGCTCAGCAGCAGTGTGAGTATCCGCTTCTCAGC 14348
 Db 731 LeuGlnLysValGlnLysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSer 750
 QY 14349 AGGAACACTTACCTGTGAGTGTGAGAGCAGTGTCTGTGGGCGGCAATTTTGTGAGAGCA 14408
 Db 751 ArgAsnThrTyrLeuGlnLysTrpGlnAspSerValLeuGlnArgHisIlePheThrArgArg 770
 QY 14409 CTCGAGAAAAGCCCTGCTGAGTGTGATATCATGGAATCCAGAAAGAAACAGTGGGTATCAGCA 14468
 Db 771 LeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlnTyrThrValGlnThrGly 790
 QY 14469 TGCATTGGCAGGAGAAACATCTATC 14495
 Db 791 CysAsnTrpGlnGlnAlaThrSerIle 799
 RESULT 13
 AAW86361
 ID AAW86361 standard; protein; 837 AA.

XX AC AAW86361;
 XX 15-MAR-1999 (first entry)
 DT 15-MAR-1999 (first entry)
 DE Human DNAX toll-like receptor DTLR4.
 XX DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
 KW interleukin 1 receptor; phosphate metabolism; innate immunity response;
 KW modulate inflammatory function; morphological effect;
 KW immunological disorder.
 OS Homo sapiens.
 XX NC
 PN W09850547-A2.
 PD 12-NOV-1998.
 XX 07-MAY-1998; 98MO-US008979.
 PF 07-MAY-1997; 97US-0044293P.
 PR 22-JAN-1998; 98US-0072212P.
 PR 05-MAR-1998; 98US-0076947P.
 XX (SCHE) SCHERING CORP.
 PA
 PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
 XX WPI; 1999-059670/05.
 DR N-PSDB; AAW8675.
 XX
 PT Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate
 PT metabolism, modulate inflammatory function or innate immunity responses.
 XX
 PS Claim 3, Page 147-149, 171pp; English.
 XX
 CC The present invention specifically describes human DNAX toll-like
 CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
 CC in the present invention. Also described are: (1) a fusion protein
 CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
 CC an antibody or antibody fragment which specifically binds to a DTLR
 CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
 CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
 CC host cell comprising the vector of (4). The host cell of (5) can be used
 CC to produce the DTLR proteins. The DTLR proteins can be used to alter
 CC phosphate metabolism, to modulate inflammatory function, innate immunity
 CC responses or morphological effects. The DTLR proteins can be used in the
 CC treatment of conditions exhibiting abnormal expression of the receptors
 CC of their ligands. These abnormalities are typically manifested by
 CC immunological disorders
 CC
 SO Sequence 837 AA;
 XX
 Alignment Scores:
 Pred. No.: 0 Length: 837
 Score: 3903.50 Matches: 757
 Percent Similarity: 98.57% Conservative: 1
 Best Local Similarity: 98.44% Mismatches: 2
 Query Match: 11.81% Indels: 9
 DB: 2 Gaps: 1
 US-09-396-985b-47 (1-18989) x AAW86361 (1-837)
 QY 12216 TCAATGCTTTTATATTC-----TGTAGTGTGAATC 12248
 Db 69 SerTyrSerPhePheSerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIle 88
 QY 12249 CAGCAATTAAGATGGGGATATCAGAGCCTAAGCAGCCTCTACTTAATATTGACA 12308
 Db 89 GlnThrIleGlnAspGlnAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThr 108
 QY 12309 GGAACCCCATCCAGATTAGCCCTGGAGACCTTTTCTGAGACTATCAGATTACAGAG 12368

Db 109 GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuLys 128
 Qy 12369 CTGGTGGCTGTGGAGACAATCTAGACATCTTAGAGAACTTCCCATGGACATCTCAAA 12428
 Db 129 LeuValAlaValGluThrAsnLeuAlaSerLeuGluAsnProIleGlyHisLeuLys 148
 Qy 12429 ACTTGAAAGAACTTAATGTGGCTCAACAATCTTATCCAACTTTGAAATTAACCTGATAT 12488
 Db 149 ThrLeuLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLeuProIleLys 168
 Qy 12489 TTTTCTAATCTGACCAATCTAGAGACATGGACCTTCCAGAACAAATTCAAAGTAT 12548
 Db 169 PheSerAsnLeuThrAsnLeuGlnHisLeuAsnLeuSerSerAsnLysIleGlnSerIle 188
 Qy 12549 TATTGACAGACTTGGGGTCTCATCATCAAAATGCCCTACTCAATCTCTCTTAGACCTG 12608
 Db 189 TyrCysThrAspLeuAsnArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAsnLeu 208
 Qy 12609 TCCCTGAACCTTAGAACCTTTATCCAACAGGTGATTTAAAGAAATTTAGGCTTCATAG 12668
 Db 209 SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLys 228
 Qy 12669 CTGACTTTAAGAAATTAATTTTATGATTTTAAATGTAATGAAATCTTGATTCAGGCTTG 12728
 Db 229 LeuThrLeuAsnArgAsnAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeu 248
 Qy 12729 GCTGGTTTGAAGTCCATCGTTGGTCTGGAGAGAAATTTAGAAATGAAAGAACTTGGA 12788
 Db 249 AlaGlyLeuGluValHisArgLeuValLeuGlyGluPheAsnArgGluGlyAsnLeuGlu 268
 Qy 12789 AAGTTTGACAATCTGCTCTAGAGGGCTGTGCAATTTGACATTTGAGAAATTCGATTA 12848
 Db 269 LysPheAspLysSerAlaLeuGluGlyLeuCysAsnLeuThrIleGluGluPheArgLeu 288
 Qy 12849 GCATTAATTAAGCTACTACCTGATGATATTTATGACTTAATTTATTTGTTGACAAATGTT 12908
 Db 289 AlaTyrLeuAspTyrTyrLeuAsnAspIleIleAspLeuPheAsnCysLeuThrAsnVal 308
 Qy 12909 TCTTCATTTTCCCTGGTAGAGTGTGACTTATGAAAGGTTAAAGACTTTTCTTAAATTC 12968
 Db 309 SerSerPheSerLeuValSerValThrIleGluArgValLysAspPheSerTyrAsnPhe 328
 Qy 12969 GGATGGCAACATTTAGAAATTAATTAATCTGTAATTTGACAGTTTCCCAATGAAATC 13028
 Db 329 GlyTyrGlnHisLeuGluLeuValAsnCysLysPheGlyGlnPheProThrLeuLysLeu 348
 Qy 13029 AAATCTCCAAAGAGCTTACTTCACTTCCAAAGAGTGGAAATGCTTTTTCGAAGTT 13088
 Db 349 LysSerLeuLysAsnArgLeuThrPheThrSerAsnLysGlyAlaAsnAlaPheSerGluVal 368
 Qy 13089 GATCTACCAAGCTTAGAGTTCTAGATCTAGTGAATGAGCTTAGTTTCAAGTTGC 13148
 Db 369 AspLeuProSerLeuGluPheLeuAsnAspLeuSerArgAsnGlyLeuSerPheLysGlyCys 388
 Qy 13149 TGTTCCTCAAGATTTTGGAGCAACAGCTTAAGATTAATTAATCTGAGCTTCATAGT 13208
 Db 389 CysSerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAsnLeuSerPheAsnGly 408
 Qy 13209 GTTATTCACATGATTTCAAACTTTGGGGCTTAAGAACTAGAACTCTGAGATTTCCAG 13268
 Db 409 ValIleThrMetSerSerAsnPheLeuGlyLeuGlnGlnLeuGlnHisLeuAspPheGln 428
 Qy 13269 CATTCCAATTTGAACAATAGAGTGTTCAGTATTTCCATATCTCATGACCTCAAT 13328
 Db 429 HisSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuAsnArgAsnLeuIle 448
 Qy 13329 TACCTGACATTTCTCACTACTCACACAGAGTTCTTTCAATGGCATCTTCAATGCTTG 13388
 Db 449 TyrLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 468
 Qy 13389 TCCAGTCTCAAGCTTGAAGAAATGGCTGGCAATCTTTCCAGGAAATCTCTTCCGAT 13448
 Db 469 SerSerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAsp 488
 Qy 13449 ATCTTCACAGAGCTGAGAAATTTGACCTTCCCTGAGACCTCTCTGAGTGTCAATGAGAG 13508
 Db 489 IlePheThrGluLeuAsnArgAsnLeuThrPheLeuAsnLeuSerGlnCysGlnLeuGlnGlu 508
 Qy 13509 TTGTCTCCAAACAGCATTTAACTCACTCTCCAGTCTTCCAGTACTTAAATATGAGCCACAAC 13568
 Db 509 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 528
 Qy 13569 AACTCTTTTTCATTGATAGTGTTCCTTATTAAGTGTCTGAATCTCCCTCAGGTTCTTGAT 13628
 Db 529 AsnPheSerLeuAsnProThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAsp 548
 Qy 13629 TACAGTCCATCATCATTAATGACTTCCAAAAACAGAACTACAGCAATTTCCAAATGAT 13688
 Db 549 TyrSerLeuAsnHisIleMetThrSerLysLysGlnGluLeuGlnHisPheProSerSer 568
 Qy 13689 CTAGCTTTCTTAAATCTTACTCAGAAATGACTTGTGTACTTGTGAACACAGAGTTTC 13748
 Db 569 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGluHisGlnSerPhe 588
 Qy 13749 CTGCAATGATCAAGAGACACAGAGCAGCTTGTGGTGAAGTTGACGAATGGAATGTGCA 13808
 Db 589 LeuGlnThrPheLysAspGlnArgGlnLeuLeuValGluValGluArgMetGluCysAla 608
 Qy 13809 ACACCTTCAGATTAAGCAGGAGCAGCTGTGCTGAGTTGTAATATCACCTGTCAGATGAT 13868
 Db 609 ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnLysIleThrCysGlnMetAsn 628
 Qy 13869 AAGACATCATTTGGTGTGTGTGCTCTCAGTGTGCTGTGATATCTGTTTGAAGAGTTCTG 13928
 Db 629 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaValLeu 648
 Qy 13929 GTCTATAAGTTCTAATTTTTCACCTGATGCTTCTGCTGCTGCAATAAGTATGCTAGAGT 13988
 Db 649 ValTyrLysPheTyrPheHisLeuMetLeuAlaGlyCysIleLysTyrGlyArgGly 668
 Qy 13989 GAAAAACATCATGATGCTTGTGTTATCTATCTCAAGACAGAGATGAGAGCTGGATTAAGGAT 14048
 Db 669 GluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTyrPheValArgAsn 688
 Qy 14049 GAGCTAGTAAAGATTTAGAAAGAGGGTGCCTCCATTTGAGCTGTGCTTCACTACAGA 14108
 Db 689 GluLeuValLysAsnLeuGlnGluGlyValProProPheGlnLeuCysLeuHisTyrArg 708
 Qy 14109 GACTTAATTTCCGGTGTGCTGCTGCTGCTGCCAATCATATCATAAGGTTTCCATTAAGC 14168
 Db 709 AspPheIleProGlyAlaAlaIleAlaIleAsnIleIleHisGluGlyPheHisLysSer 728
 Qy 14169 CGAAAGGTGATTTGTGGGTGTCGCCAGCACTTATCAGAGCGGCTGGTATCTTTGAA 14228
 Db 729 ArgLysValIleValAlaValSerGlnHisPheIleGlnSerArgTyrCysIlePheGln 748
 Qy 14229 TATGAGATTTGCTCAGACTGTGAGCTTCTGAGCAGTGTGCTGTGATCATCTTCAATGTC 14288
 Db 749 TyrGluIleIleGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 768
 Qy 14289 CTGCAAGAGGTGAGAAAGACCTGTCTCAGGACAGAGGTGAGCTGTACCGCTTCTCAGC 14348
 Db 769 LeuGlnLysValGluLysThrLeuLeuArgGlnGlnValGluLeuTyrArgLeuLeuSer 788
 Qy 14349 AGGAAACATTAAGCTGAGAGTGGAGAGCAGGTGCTGTGGGGGGGAGCAATCTTGGAGAACGA 14408
 Db 789 ArgAsnThrTyrLeuGluLysTrpGluAspSerValLeuGlyArgHisIlePheTrpArgArg 808
 Qy 14409 CTCAGAAAAGCCCTGTGATGAGTAAATCATGATGATCCAGAAAGAAACAGTGGGTACAGCA 14468
 Db 809 LeuArgLysAlaLeuLeuAsnAspGlyLysSerTrpAsnProGlnGlyThrValGlyThrGly 828
 Qy 14469 TCGAATTTGGCAGAGAACCAATCTTATC 14495
 Db 829 CysAsnTrpGlnGluAlaThrSerIle 837

RESULT 14
AAE16102
ID AAE16102 standard; protein: 837 AA.
XX
AC AAE16102;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX Toll like receptor (DTRLR) 4 #2.
XX
KW Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KM Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS Homo sapiens.
XX
PN MO200190151-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;
XX
DR WPI, 2002-083085/11.
XX
DR N-PSDB; AAD26292.
XX
PT New DNAX Toll like receptor (DTRLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
XX
PS Claim 3; Page 41; 297p; English.
XX
CC The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTRLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g., capable of distinguishing between other Interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
CC Note: The present sequence SEQ ID NO 26 is stated to be similar to the
CC sequence shown in page 240-243 (AAE16116). However these sequences differ
CC at several locations
CC
XX
SQ Sequence 837 AA;
XX
Alignment Scores:
Pred. No.: 0 Length: 837
Score: 3903.50 Matches: 757
Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Indels: 9
DB: 5 Gaps: 1
US-09-396-985B-47 (1-18989) x AAE16102 (1-837)
QY 12216 TGAATGCTTTTATTC-----TGAGGTGCAATTC 12248
DB 69 SerTyrSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIle 88

QY 12249 CAGACAATTGAGATGGGCGATATCAGAGCCTTACAGCACCCTCTCACTTAATTATGACA 12308
DB 89 GlnThrIleGluaspGlyAlaTyrGlnSerLeuSerHisLeuSerThrIleLeuThr 108
QY 12309 GGAACCCCATCCAGAGTTTACGCCCTGGAGCCTTTCTGGACTATTCAGAGAG 12368
DB 109 GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys 128
QY 12369 CTGGTGCTGTGGAGCAAAATCTAGACATCTCTAGAGAACTTCCCATTTGACATCTCAA 12428
DB 129 LeuValAlaValGlnThrAsnLeuAlaSerLeuGluAsnProIleGlyHisLeuLys 148
QY 12429 ACTTGAAGAACTTAATGAGCTCAACATCTTATCCAACTTTCAATTAAGCTGATAT 12488
DB 149 ThrLeuaspGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyr 168
QY 12489 TTTTCTAATCTGACCAATCTAGAGCACTTGGACCTTTCCAGCAACAAGATTCAAAGTAT 12548
DB 169 PheSerAsnLeuThrAsnLeuGluHisLeuAspLeuSerAsnLysIleGlnSerIle 188
QY 12549 TATTGACAGACTTGGGGGTTCTTACATCAAAATGCCCTACTCAATCTCTTTAGACCTG 12608
DB 189 TyrCysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 208
QY 12609 TCCCTGAACCCCTATGAACTTATCCAAACAGGTGACTTTAAAGAAATTAGGCTTCATAG 12668
DB 209 SerLeuAsnProMetAsnProIleGlnProGlyAlaPheaspGluIleArgLeuHisLys 228
QY 12669 CTGACTTTAAGAAATATTTTGAATAGTTTAAATGTAATGAAACTTGTATTCAGAGCTGTG 12728
DB 229 LeuThrLeuArgAsnAsnProPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeu 248
QY 12729 GCTGGTTTAAAGTCATCGTTGGTTTGGTTCGGGGAATTTGAATGAAAGAACTTGGAA 12788
DB 249 AlaGlyLeuGluValHisArgLeuValLeuGlyGluPheArgAsnGluLysAsnGlu 268
QY 12789 AAGTTGACAAATCTGCTCTTAGAGGGCTGTGCAATTTGACATGGAAGATTCAGATTA 12848
DB 269 LysPheAspLysSerAlaLeuGluGlyLeuCysAsnLeuThrIleGluGluPheArgLeu 288
QY 12849 GCATCTTAACTACATCACTTCGATGATATTTATTTATTTATTTGACAAATGTT 12908
DB 289 AlaTyrLeuAspTyrTyrLeuAspAspIleIleAspLeuAsnCysLeuThrAsnVal 308
QY 12909 TCTTCATTTCCCTCGGAGTGTGACATTTGAAGAGGTAAAGCTTTCTTAAATTC 12968
DB 309 SerSerPheSerLeuValSerValThrIleGluArgValLysAspPheSerTyrAsnPhe 328
QY 12969 GSATGCAACATTTAGATTAAGTTAACTGTAAATTTGACAGGTTCCACATTTGAAATCTC 13028
DB 329 GlyTyrGlnHisLeuGluValLeuValAsnCysLysPheGlyGlnPheProThrLeuLysLeu 348
QY 13029 AAATCTCTCAAAAGGCTTACTTTCACCTTCCAAACAAGGTGGGAATGCTTTTTCAGAACTT 13088
DB 349 LysSerLeuLysArgLeuThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGluVal 368
QY 13089 GATCTACCAAGCCTTGAGTTTCTAGATCTAGTAGAAGAGGCTTGAAGTTTCAAGGTTGC 13148
DB 369 AspLeuProSerLeuGluPheLeuAspLeuSerArgAsnLysLeuSerPheLysGlyCys 388
QY 13149 TGTTCTCAAGATGTTTGGGACAAACCAAGCTTAAAGTATTAGATCTGAGCTTCAATGCT 13208
DB 389 CysSerIleThrAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGly 408
QY 13209 GTTATTACATGAGTTCAAACTTCTGGGCTTGAACAACATCTAGAACTCTGGATTTCCAG 13268
DB 409 ValIleThrMetSerSerAsnPheLeuGlyLeuGluGlnLeuGluHisLeuAspPheGln 428
QY 13269 CATTCGAATTTGAAACAATGAGAGGATTTTCAATCTCTCAATCACTCAAGAACTCATAT 13328
DB 429 HisSerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuAsnLeuIle 448
QY 13329 TACCTTGACATTTCTCACTACTACACACAGAGTTGCTTCAATGGCATCTTCAATGCTTG 13388


```

Db      449  TyrLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnIleu 468
QY      13389  TCCAGTCTCGAAGCTTTGAAAATGGCTGCAATCTTTCCAGAAACCTTCCTCCAAAT 13448
Db      469  SerSerLeuGluValLeuIleuMetAlaGlyAsnSerPheGlnGlnAspPheIleuTrpAsp 488
QY      13449  ATCTTCACAGAGCTGAGAAACTTGAACCTTCTGACCTCTGACCTCTGACCTGTCACCTGAGCAG 13508
Db      489  IlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnIleuGluIn 508
QY      13509  TTGTCTCAACAGCATTTAACTCACTCTCCAGCTTTCAGGTCCTAAATATGACCCACAC 13568
Db      509  LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 528
QY      13569  AACTCTCTTTCATGATGATACGTTTCTTAAATAGTCTGAACTCCCTCCAGCTTCTTAT 13628
Db      529  AsnPhePheSerLeuAspThrPheProTyrIleCysLeuAsnSerLeuGlnValLeuAsp 548
QY      13629  TACAGTCTCAATGACATATGATGATCTTCAAAAAACAGAACTACAGCATTTTCCAACTAGT 13688
Db      549  TyrSerLeuAsnHisIleMetThrSerIleGlnIleuGlnIlePheProSerSer 568
QY      13689  CTAGCTTCTTAAATCTTAACTCAAGATGACTTGTGCTTGTGATCTTGAACACAGAGTTTC 13748
Db      569  LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe 588
QY      13749  CTGGAATGATCAACAGAACCAAGGAGCTCTTGGTGAAGTTGAACCAATGAAATGTGCA 13808
Db      589  LeuGlnTrpIleIleValAspGlnArgGlnLeuLeuValGluValGluMetGlnCysAla 608
QY      13809  ACACCTTCAGATTAAGCAGGAGGAGCTGCTGCTGATTTGAATATCACCTTCAGATGAT 13868
Db      609  ThrProSerAspIleGlnGlnIleMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 628
QY      13869  AAGACCATCATTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 13928
Db      629  LysThrIleIleGlnValSerValLeuSerValLeuValValSerValAlaValLeu 648
QY      13929  GTCTTAAGTCTTAAATCTTAACTCACTGATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 13988
Db      649  ValTyrIlePheThrPheHisLeuMetLeuLeuAlaGlyCysIleLeuGlyArgGly 668
QY      13989  GAAACATCTATGATGCTTGTGCTTGTATCTCAAGCCAGATGAGATGAGGATTAAGGAT 14048
Db      669  GluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTrpValArgAsn 688
QY      14049  GAGCTAGTAAAGAAATTTAGAAAGGAGGCTGCTCAATTCAGCTCTGCTTCACTACAGA 14108
Db      689  GluLeuValIleAsnLeuGluGluGlyValProProPheGlnIleuCysLeuHisIleTyrArg 708
QY      14109  GACTTTATCCCGGTGGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14168
Db      709  AspPheIleProGlyValAlaAlaIleAlaAsnIleIleHisGlnGlyPheHisIleuSer 728
QY      14169  CGAAAGGATGTTGTGGTGTCCAGACATCTTCCAGACCCCTGCTGATCTTGAATTTGAA 14228
Db      729  ArgValValIleValValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 748
QY      14229  TATGAGATGCTGACCTGACCTGACCTTCTGACAGCTGCTGCTGCTGCTGCTGCTGCTGCT 14288
Db      749  TyrIleIleAlaGlnTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 768
QY      14289  CTGCAAGAAAGTGGAGAAAGACCTCTGCTGACGACAGGCTGACGCTGACCTTCTGAC 14348
Db      769  LeuGlnIleValGlnIleValThrLeuLeuArgGlnGlnIleValGluLeuTyrArgLeuLeuSer 788
QY      14349  AGGAACACTTACCTGAGTGGAGAGACAGTCTCCGGGGGGGAGCATCTTCTGAGAGCA 14408
Db      789  ArgAsnThrTyrLeuGluTrpGlnAspSerValLeuGlnIleArgHisIlePheTrpArgArg 808
QY      14409  CTCAGAAAAGCCCTGCTGATGATTAATCATGAGATCCAGAAAGAACAGTGGGTACAGCA 14468

```

```

Db      809  LeuArgIleValAlaLeuLeuAspGlyIleuSerTrpAsnProGlnGlyThrValGlyThrGly 828
QY      14469  TGCATATGGCAGAGAACATCATATC 14495
Db      829  CysAsnTrpGlnGlnAlaThrSerIle 837
RESULT 15
ABU04776
ID  ABU04776 standard; protein; 837 AA.
AC  ABU04776;
DE  29-JAN-2003 (first entry)
DE  Human expressed protein tag (EPT) #1442.
KW  Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW  protease; protease inhibitor; transporter; cytoskeletal protein;
KW  receptor; transcription factor; cancer; MHC;
KW  major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW  adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
OS  Homo sapiens.
PN  WC200278524-A2.
PD  10-OCT-2002.
PE  28-MAR-2002; 2002WC0-US009671.
PF  28-MAR-2001; 2001US-0279495P.
PR  21-MAY-2001; 2001US-0292544P.
PR  08-AUG-2001; 2001US-0310801P.
PR  01-OCT-2001; 2001US-0326370P.
PR  04-DEC-2001; 2001US-0336780P.
PR  20-FEB-2002; 2002US-0358985P.
PA  (ZYCO-) ZYCO5 INC.
PI  Chicz RM, Tomlinson AJ, Urban RG;
DR  WPI; 2003-040607/03.
XX  PT  New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT  cytoskeletal proteins, receptors or transcription factors), useful for
PT  treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT  leukemia.
XX  PS  Example 2; SEQ ID NO 1442; 134pp; English.
XX  CC  The invention describes a purified polypeptide, which comprises a
CC  fragment of a kinase, phosphatase, protease, protease inhibitor,
CC  transporter, cytoskeletal protein, receptor or transcription factor. The
CC  polypeptide is useful as an immunogenic composition for eliciting in a
CC  mammal an immunogenic response directed against any of the purified
CC  polypeptide. The purified polypeptide, or the antibody that binds to this
CC  polypeptide, is useful for treating cancer. The polypeptide is also
CC  useful for identifying compounds that binds to a naturally processed
CC  class I or class II MHC-binding polypeptide. The polypeptides and
CC  polynucleotides are particularly useful for treating or preventing
CC  myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC  lymphoma or leukaemia. These are also useful for screening agents for
CC  treating the above mentioned diseases. This sequence represents an
CC  expressed protein tag (EPT) isolated from human tissue for translational
CC  profiling. Note: This sequence does not appear in the printed
CC  specification but was obtained in electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
SO  Sequence 837 AA.
Alignment Scores: 0 Length: 837
Pred. No.: 3903.50 Matches: 757
Score:

```

Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Indels: 9
DB: 6 Gaps: 1
US-09-396-985b-47 (1-18989) x AB004776 (1-837)
12216 TCAATGCTTTTATTC-----TGAGGTGGAATC 12248
||| |||||
Db SerIySerPheSerPheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIle 88
12249 CAGCAATGAGATGGGCGATATCAGAGCCTTAAGCCACTCTTACCTTAATATGACA 12308
||| |||||
Db GlnThrIleGluAspGlyAlaTyrgInSerLeuSerHisLeuSerThrIleLeuThr 108
12309 GGAAGCCCATCCAGATTTAGCCCTGGAGCCCTTTCTGGACATCAAGTTTACAGAG 12368
||| |||||
Db GlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys 128
12369 CTGGTGGCTGGAGCAAACTTCAAGCATCTTCAAGAACTTCCCATTTGACATCTGAAA 12428
||| |||||
Db LeuValAlaValGluThrAsnLeuAlaSerLeuGlnUbsnProIleGlyHisLeuLys 148
12429 ACTTGAAGAACTTAATGTGGCTCAGAACTTATTCGAATCTTCAATCTTCAATTAAGTAT 12488
||| |||||
Db ThrIeuLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyx 168
12489 TTTTCTAATCTGACCAATCTTGAGCACTTGGACCTTTTCAGACAAGATTTCAAGTAT 12548
||| |||||
Db PheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIle 188
12549 TATTGACAGACTGGCGGTCTCATCAAAATGCCCTTCAATCTCTTTAGACCTG 12608
||| |||||
Db TyrgSerHisAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 208
12609 TCCCTGAACCTTAATGAATTTATCCAAACAGTGCATTTAAAGAAATTAAGCTTCATAG 12668
||| |||||
Db SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLys 228
12669 CTGACTTAAGAAATTAATTTGATAGTTAAATGAAGAACTTGAATTCAGAGCTG 12728
||| |||||
Db LeuThrLeuAsnArgAsnAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeu 248
12729 GCTGATTTAGAAAGTCCATCGTTTGTTCTGGAGAAATTTAGAAATGAAGAACTTGAA 12788
||| |||||
Db AlaGlyLeuGlnValHisArgLeuValLeuGlyGlnPheArgAsnGlyLysAsnLeuGln 268
249 AlaGlyLeuGlnValHisArgLeuValLeuGlyGlnPheArgAsnGlyLysAsnLeuGln 268
12789 AAGTTTGCAAAATCTGCTCTAGAGGGCTGTGCAATTTGACCATTTGAAGAAATTCGATTA 12848
||| |||||
Db LysPheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGluPheArgLeu 288
12849 GCATTAATTAAGTACTACTCTGATGATATTATGACTTAATTTAATTTGTTGACAAATGTT 12908
||| |||||
Db AlaTyrgLeuAspTyrgTyrgLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnVal 308
12909 TCTTCATTTTCCCTGGAGTGTGACTATTAAGAGGCTAAAGAACTTTCTTAATATTC 12968
||| |||||
Db SerSerPheSerLeuValSerValThrIleGlnArgValLysAspPheSerTyrgAsnPhe 328
12969 GGATGGCAAACTTTAGAAATTTAGTTAACTGTAATTTGACAGTTTCCACATTTGAACTC 13028
||| |||||
Db GlnTyrgGlnHisLeuGlnLeuValAsnCysLysPheGlnGlnPheProThrLeuLysLeu 348
13029 AAATCTCAAAAGGCTTAATCTTCACTTCCAAAGAGTGGAAATGCTTTTTCAGAAATT 13088
||| |||||
Db LysSerLeuLysArgLeuThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGlyVal 368
13089 GATTCACAAAGCTTGAATTTAGTCTCAGTACAGTAAATGGCTGAGTTTCAAGAGTGC 13148
||| |||||
Db AsnLeuProSerLeuGlnPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCys 388
13149 TGTTCCTCAAAAGTATTTTGGCAACACAGCCTAAAGTATTTAGATCTGAGCTTCATGAT 13208
||| |||||

Db CysSerGlnSerAspPheGlyThrThrSerLeuLysTyrgLeuAspLeuSerPheAsnGly 408
13209 GTTATTAACCATGAGTTCAAACTTCTGGCTTGAACAACATGACATCTGATTTCCAG 13268
||| |||||
Db ValIleThrMetSerSerAsnPheLeuGlyLeuGlnGlnLeuGlnHisLeuAspPheGln 428
409 ValIleThrMetSerSerAsnPheLeuGlyLeuGlnGlnLeuGlnHisLeuAspPheGln 428
13269 CATTCGAATTTGAACAAATGAGTGAATTTTCAGTATTCCTTCACTCAGAAACCTTCATT 13328
||| |||||
Db HisSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIle 448
429 HisSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIle 448
13329 TACCTTGACATTTCTCACTACTCACACAGAGTGGCTTTCAATGGCATCTTCAATGGCTTG 13388
||| |||||
Db TyrgLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 468
449 TyrgLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 468
13389 TCCAGTCTGGAATCTTGAAGAAAGGCTGGCAATCTTTCAGAGAAACCTTCTTCAGAT 13448
||| |||||
Db SerSerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAsp 488
469 SerSerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAsp 488
13449 ATCTTCACAGAGCTGAGAACTTGAACCTTCTGGAACCTCTCTCAGTGTCAACTGAGACAG 13508
||| |||||
Db IlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 508
489 IlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 508
13509 TTGTCTCAACAGCATTTAACTCACTCTCCAGTCTTCAGGTACTAAATATGACCCACAC 13568
||| |||||
Db LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 528
509 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 528
13569 AACTCTTTTCAATGGATAGTTTCTTAAAGTGTCTGAACCTCCCTCAGTGTCTGAT 13628
||| |||||
Db AsnPheSerSerLeuAsnProThrPheProTyrgCysLeuAsnSerLeuGlnValLeuAsp 548
529 AsnPheSerSerLeuAsnProThrPheProTyrgCysLeuAsnSerLeuGlnValLeuAsp 548
13629 TACAGTCTCAATCACAATTAAGTCTTCCAAAAACAGAACTACAGCATTTTCCAGTATG 13688
||| |||||
Db TyrgSerLeuAsnHisIleMetThrSerTyrgGlnGlnLeuGlnHisPheProSerSer 568
549 TyrgSerLeuAsnHisIleMetThrSerTyrgGlnGlnLeuGlnHisPheProSerSer 568
13689 CTGACTTTCTTAATCTTACTCAGAAATGACTTTTGCTTGTACTTGTGAACACAGAGTTTC 13748
||| |||||
Db LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnLysGlnSerPhe 588
569 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnLysGlnSerPhe 588
13749 CTGCAATGATCAAGAGCAGAGGAGCTTGTGGTGAAGTTGAACGAATGAATGATGCA 13808
||| |||||
Db LeuGlnThrIleLysAspGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAla 608
589 LeuGlnThrIleLysAspGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAla 608
13809 ACACTTCAGATTAAGCAGGCGATGCTGTGCTGATGTTGAATACCTTGCAGATGAAT 13868
||| |||||
Db ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 628
609 ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 628
13869 AAGACCATCAATGGTGTGTGCTCTCAAGTGTGCTTGTATGATCTGTTGACAGATTCG 13928
||| |||||
Db LysThrIleIleGlyValSerValLeuSerValLeuValAlaSerValAlaAlaValLeu 648
629 LysThrIleIleGlyValSerValLeuSerValLeuValAlaSerValAlaAlaValLeu 648
13929 GTCATTAAGTTCTATTTTCACTGATGCTCTTGTGCTGCTGATTAAGTATGGTAGAGT 13988
||| |||||
Db ValTyrgLysPheTyrgPheHisLeuMetLeuLeuAlaLysLysIleTyrgIleTyrgGly 668
649 ValTyrgLysPheTyrgPheHisLeuMetLeuLeuAlaLysLysIleTyrgIleTyrgGly 668
13989 GAAAACATCTATGATGCTTGTATCTACTCAAGCCAGATGAGACGTGGTAAAGAAAT 14048
||| |||||
Db GlnAsnIleTyrgAspAlaPheValIleTyrgSerSerGlnAspGlnAspTrpValArgAsn 688
669 GlnAsnIleTyrgAspAlaPheValIleTyrgSerSerGlnAspGlnAspTrpValArgAsn 688
14049 GAGCTAGTAAAGAAATTTAGAAAGAGGCTGCTCAATTTGACCTGTGCTTCACTACAGA 14108
||| |||||
Db GlnLeuValLysAsnLeuGlnGlnGlyValArgProThrGlnLeuCysLeuHisTyrgArg 708
689 GlnLeuValLysAsnLeuGlnGlnGlyValArgProThrGlnLeuCysLeuHisTyrgArg 708
14109 GACTTAATCCCGGTGGCGCATTTGCTGCGCAACATCAATCAAGTGAAGGTTTCCATTAAGC 14168
||| |||||
Db AspPheIleProGlyValAlaIleAlaAlaAsnIleIleHisGlnGlyPheHisLysSer 728
709 AspPheIleProGlyValAlaIleAlaAlaAsnIleIleHisGlnGlyPheHisLysSer 728
14169 GAAAGGTGATTTGTGTGTGTCCACAGCATTTCAACAGCCGCTGTATCTTTGAA 14228
||| |||||
Db ArgLysValIleValValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 748
729 ArgLysValIleValValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 748
14229 TATGAGATGTGCTCAGACCTGGCAGTTTCTGACAGTGTGTGTATCATCTTCAATGTC 14288
||| |||||
Db TyrgIleIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 768
749 TyrgIleIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 768

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 14:31:58 ; Search time 153 Seconds
(without alignments)
18529.557 Million cell updates/sec

Title: US-09-396-985B-47
Perfect score: 33065
Sequence: 1 tccctactcttcacatc.....catgaabdcabdcabdc 18989

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_n2p -model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09396985/runat_28032005_155744_21170/app_query.fasta_1.85098
-DB=Issued_Patents_AA -OPMT=fastan -SOPFX=rai -MINMATCH=0.1 -LOOPLC=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USR=US09396985 @CGN 1.1 732 @runat_28032005_155744_21170 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.dep:*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.dep:*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.dep:*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.dep:*
5: /cgn2_6/ptodata/1/iaa/PTUS.COMB.dep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.dep:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3903.5	11.8	844	4	US-09-949-016-9438
2	557.5	1.7	784	4	US-09-982-308B-23
3	529	1.6	661	1	US-08-514-014-4
4	497	1.5	661	2	US-08-833-823-4
5	457	0.9	775	4	US-09-949-016-8799
6	287.5	0.9	1112	3	US-09-353-585-3
7	282.5	0.9	1112	3	US-09-353-585-2
8	267.5	0.8	863	2	US-08-666-271-2
9	267	0.8	605	3	US-09-063-950-5
10	267	0.8	1874	4	US-09-331-403-2
11	263.5	0.8	1166	4	US-10-101-464A-900
12	262.5	0.8	907	4	US-09-170-496D-264

13	262.5	0.8	907	4	US-09-170-496D-278	Sequence 278, App
14	258	0.8	605	1	US-08-190-802A-49	Sequence 49, App1
15	258	0.8	605	1	US-08-477-346-49	Sequence 49, App1
16	258	0.8	605	3	US-08-473-089-49	Sequence 49, App1
17	258	0.8	605	4	US-08-487-072A-49	Sequence 49, App1
18	258	0.8	605	4	US-09-538-092-1087	Sequence 1087, App
19	258	0.8	623	4	US-09-949-016-10995	Sequence 10995, A
20	253	0.8	102	4	US-09-513-999C-8144	Sequence 8144, App
21	251.5	0.8	603	1	US-08-190-802A-50	Sequence 50, App1
22	251.5	0.8	603	3	US-08-477-346-50	Sequence 50, App1
23	251.5	0.8	603	3	US-08-473-089-50	Sequence 50, App1
24	251.5	0.8	603	4	US-08-487-072A-50	Sequence 50, App1
25	249	0.8	1529	4	US-09-312-283C-396	Sequence 396, App
26	246.5	0.7	806	3	US-08-945-983-2	Sequence 2, App1
27	246	0.7	391	4	US-09-270-767-43901	Sequence 43901, A
28	246	0.7	968	3	US-09-180-439-3	Sequence 3, App1
29	246	0.7	968	3	US-09-180-439-4	Sequence 4, App1
30	246	0.7	1119	4	US-09-907-794A-294	Sequence 294, App
31	246	0.7	1119	4	US-09-905-125A-294	Sequence 294, App
32	246	0.7	1119	4	US-09-902-775A-294	Sequence 294, App
33	246	0.7	1119	4	US-09-906-700-294	Sequence 294, App
34	246	0.7	1119	4	US-09-903-603A-294	Sequence 294, App
35	246	0.7	1119	4	US-09-904-920A-294	Sequence 294, App
36	246	0.7	1119	4	US-09-909-064-294	Sequence 294, App
37	246	0.7	1119	4	US-09-905-381A-294	Sequence 294, App
38	246	0.7	1119	4	US-09-906-618-294	Sequence 294, App
39	245.5	0.7	1059	4	US-09-907-794A-290	Sequence 290, App
40	245.5	0.7	1059	4	US-09-905-125A-290	Sequence 290, App
41	245.5	0.7	1059	4	US-09-902-775A-290	Sequence 290, App
42	245.5	0.7	1059	4	US-09-906-700-290	Sequence 290, App
43	245.5	0.7	1059	4	US-09-903-603A-290	Sequence 290, App
44	245.5	0.7	1059	4	US-09-904-920A-290	Sequence 290, App
45	245.5	0.7	1059	4	US-09-909-064-290	Sequence 290, App

ALIGNMENTS

RESULT 1
US-09-949-016-9438
Sequence 9438, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTUR, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9438
LENGTH: 844
TYPE: PRT
ORGANISM: Human
US-09-949-016-9438

Alignment Scores:
Pred. No.: 0
Score: 3903.50
Percent Similarity: 98.57%
Best Local Similarity: 98.44%
Query Match: 11.81%
DB: 4
Gaps: 1

US-09-396-985B-47 (1-18989) x US-09-949-016-9438 (1-844)
12216 TCAATGCTTTTATTC-----TGTAAGTGAATC 12248

|||||
Db SerIysSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIle 95
12249 CAGCAATTGAAGATGGGGCATATCAAGACCTTAAGCCACTCTTACTTAAATTGACA 12308
Db GlnThrIleGluAspGlyAlaTyrglnSerLeuSerHisLeuSerThrIleLeuThr 115
12309 GGAACCCCATCCGAGGTTTAGCCCTGGAGCCCTTTCTGGACTATGAAAGTTTACAGAG 12368
Db GlnAsnProIleGlnSerLeuAlaLeuGlnAlaPheSerGlyLeuSerSerLeuGlnIys 135
12369 CTGGTGGCTGTGAGACAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTGAA 12428
Db LeuValAlaValGluThrAsnLeuAlaSerLeuGluAsnPheProIleGlyHisLeuIys 155
12429 ACTTTGAAGAAGCTTAATGTGGCTCAATCTTATCCAACTTTCCAAATTACCTGAGAT 12488
Db ThrLeuIysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheIysLeuProGluTyx 175
12489 TTTTCTATCTGACCAATCTAGACACTTGGACCTTTCCAGACAAAGATTCAAGTAT 12548
Db PheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnIysIleGlnSerIle 195
12549 TATTGACAGACTTGGGGGTTCTACATCAAAATGCCCTACTCAATCTCTTTAGACCTG 12608
Db TyrCysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 215
12609 TCCCTGAACCTTATGAACTTTATGCAACAGAGTGCATTTAAAGAAATTAGCTTCATAG 12668
Db SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheIysGluIleArgLeuHisIlys 235
12669 CTGACTTAAGAATAATTTTGTAGTATTAATGAATGAAGAACTTGATTCAGAGCTTG 12728
Db LeuThrLeuAspGlnAsnPheAspSerLeuAsnValIleCysIleGlnGlyLeu 255
12729 GCTGATTTGAAGTCATCGTTGGTTCTGGAGAAATTTAGAAAATGAAGAACTTGGAA 12788
Db AlaGlyLeuGlnValHisArgLeuValLeuGlyGlnPheArgAsnGlnGlyAsnLeuGln 275
12789 AAGTTTGCAAAATGCTCTCTAGAGGGCTGTGCAATTTGACATTTGAAGAATTCGATTA 12848
Db LysPheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGlnPheArgLeu 295
12849 GCATACTAGACTACTACCTGAGATGATTTATGACTTATTAATTTGTTGACAAATGTT 12908
Db AlaTyrlsLeuAspTyrlsLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnVal 315
12909 TCTTCATTTTCCCTGGTGAAGTGTGACTATTTGAAGGATAAAGACTTTTCTTATTAATTC 12968
Db SerSerPheSerLeuValSerValThrIleGlnArgValLysAspPheSerTyrlsAsnIle 335
12969 GGAATGGCAACTTTAGAAATTAAGTAACTGTAAATTTGGACAGTTTCCCAATGAACTC 13028
Db GlnTyrlsGlnHisLeuGlnLeuValAsnCysLysPheGlnGlnPheProThrLeuIysLeu 355
13029 AAATCTCCAAAAGCTTACTTCACTTCCAAAGAGGTGGAAATGCTTTTTCAGAACTT 13088
Db LysSerLeuLysAspGlyLeuThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGlnVal 375
13089 GATCTACCAAGCTTGAAGTTTCTAGATCTCAGTAGAAATGGCTTGAGTTTCAAGGTTC 13148
Db AspLeuProSerLeuGlnPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCys 395
13149 TGTTCGAAAGTATTTGGGCAACACAGCTTAAGTATTTAGATCTGAGCTTCATGCT 13208
Db CysSerGlnSerAspPheGlyThrThrSerLeuLysTyrlsLeuAspLeuSerPheAsnIly 415
13209 GTTATACAGAGTTTCAAACTTCTGGGCTTGAACAAGTAAAGTCTGAGATTTCCAG 13268
Db ValIleThrMetSerSerAsnPheLeuGlnLeuGlnLeuGlnHisLeuAspPheGln 435
13269 CATTCCAATTTGAACAATAGATGATTTTCAAGTATCTATCACTGAGAACTCTCAT 13328

436 HisSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIle 455
13329 TACCTTGACATTTCTGATCTGACACAGAGTTGCTTTCAATGCAATCTTCAATGGCTTG 13388
Db TyrLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 475
13389 TCCAGTCTCGAAGCTTGAAGAAATGGCTGGCAATCTTTCACAGAAAATCTCTTCAGAT 13448
Db SerSerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAsp 495
13449 ATCTTGACAGAGCTTGAGAACTTGAACCTTCTGGAGCTCTCTCAAGTGTCAATGGAGCG 13508
Db IlePheThrGlnLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnGln 515
13509 TTGTCGCCAACAGACTTTAACTCACTCCAGCTTCAGGCTTCAAGTAAATGAGCCCAAC 13568
Db LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 535
13569 AACTCTTTTCAATGGATACGTTTCTTATTAAGTGTCTGAATCCCTCCAGGTTCTTGAT 13628
Db AsnPheSerLeuAspThrPheProTyrlsCysLeuAsnSerLeuGlnValLeuAsp 555
13629 TACAGTCTCAATACATATGACTTCCAAAAACAGAACTTACAGCAATTTCCAGTAT 13688
Db TyrSerLeuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPheProSerSer 575
13689 CTAGCTTCTTAATCTTACTGAGAATGACTTGTGCTTGTACTTGTGAAACACAGAGTTTC 13748
Db LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe 595
13749 CTGCAATGATCAAGACACAGAGGACGCTTGTGGAGATTGAACGAATGAAATGTGCA 13808
Db LeuGlnThrIleLysAspGlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAla 615
13809 ACACCTTGACATTAAGCAGGGCAATGCTGTGCTGAGTTTGAATTCACCTTGACATGAT 13868
Db ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 635
13869 AAGCACTCATGAGTGTGTGTCGCTCAGAGTGTCTTGATCTGTGTAGAGAGTTCTG 13928
Db LysThrIleIleGlyAlaSerValLeuSerValLeuValAlaSerValAlaAlaValLeu 655
13929 GTCTATAGTCTTATTTTCACTGATGCTTCTTGCTGGCTGCAATAAGTATGGTAGAGT 13988
Db ValTyrlsPhePheTyrlsPheHisLeuMetLeuLeuAlaGlyCysIleLysTyrglyArgGly 675
13989 GAAAACATCTAGATGCTTGTGATTAATCTTCAAGCCAGATGAGATCGGGTAAAGAT 14048
Db GlnAsnIleTyrlsAspAlaPheValIleTyrlsSerSerGlnAspGlnAspTyrlsValArgAsn 695
14049 GAGCTACTAAGAAATTTAGAAAGAGGGTGCCTCCATTTGAGCTGTGCTCTCACTACAGA 14108
Db GlnLeuValLysAsnLeuGlnGlnGlyValaProProPheGlnLeuCysLeuHisTyrlsArg 715
14109 GACTTATTTCCCGGTGGCCATTTGCTGCCAATCATCCATGAAGGTTTCCATAAAGC 14168
Db AspPheIleProGlyValAlaIleAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSer 735
14169 CGAAAGGTGATTTGTGTGTGTCCAGCACTTCACTCAAGCCGCTGTGTATTTTGA 14228
Db ArgLysValIleValAlaValaIleSerGlnHisPheIleGlnSerArgTyrlsPheGln 755
14229 TATGAGATGCTGACACTGGCACTTTCTAGACAGTGTGTGTGTATCATTTCACTGTC 14288
Db TyrlsIleIleAlaGlnThrTyrlsGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 775
14289 CTGCAAGAGGTGAGAAAGACCTGTCTCAGCAGAGGCTGGAGCTGTACCGCTTCTCAGC 14348
Db LeuGlnLysValaGlnLysThrLeuLeuArgGlnGlnAlaGlnLeuTyrlsArgLeuLeuSer 795
14349 AGAACACTTACCTGAGTGGAGAGACAGTGTCTCGGGCGGCACTTCTTGAGACGA 14408
Db ArgAsnThrTyrlsLeuGlnIuTyrlsGlnAspSerValLeuGlnTyrlsHisIlePheTyrlsArg 815

```

QY      14409 CTCAGAAAGCCCTGCTGATGTAATCATGGAATCAGAGAAAGAGGAGGATACAGA 14468
      |||
Db      816 LeuArglySalaleuLeuAspGlyLysSerTrpAsnProGluGlyThrValGlyThrGly 835
      |||

QY      14469 TGCATTTGGCAGAGCAACATCTATC 14495
      |||
Db      836 CysAsnTrpGlnGluAlaThrSerIle 844
      |||

RESULT 2
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
; APPLICANT: Daille, Barbara
; APPLICANT: Fan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tan, Jimmy C.
; APPLICANT: Zavadny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: J06010C
; CURRENT APPLICATION NUMBER: US/09/982,308B
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-982-308B-23

Alignment Scores:
Pred. No.: 3.64e-52 Length: 784
Score: 557.50 Matches: 220
Percent Similarity: 41.59% Conservative: 121
Best Local Similarity: 26.83% Mismatches: 260
Query Match: 1.69% Indels: 219
DB: 4 Gaps: 38

US-09-396-985B-47 (1-18989) x US-09-982-308B-23 (1-784)
QY      12246 ATCCAGACAATTGAGATGGGAGCATATCAGAGCCCACTCTCTACTTATATATG 12305
      |||
Db      88 IleAsnThrIleGluGluAspSerPheSerSerLeuGlySerLeuGluHisLeuAspLeu 107
      |||

QY      12306 ACAGAAAACCCCATCCAGAGTTTAAAGCCCTGGAGCCCTTTTCTGAGCTATCAAGTTTACAG 12365
      |||
Db      108 SerTyrAsnTyrLeuSerAsnLeuSerSerSerTrpPheLysProLeuSerSerLeuThr 127
      |||

QY      12366 AAGTCG-----GTGGCTGTGGAGCACAAT 12389
      |||
Db      128 PheIuAsnLeuLeuGlyAsnProTyrLysThrLeuGlyLuhTrSerLeuPheSerHis 147
      |||

QY      12390 CTAGACATCTAGAGAACTTCCCATTTGACATCTCAAAACT-----12431
      |||
Db      148 LeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIleGlnArg 167
      |||

QY      12432 -----TTGAAAGACTTAAATGTGGCTCACCAATCTTATCCAA 12467
      |||
Db      168 LysAspPheAlaGlyLeuThrPheLeuGlnGluLeuGluIleAspAlaSerAspLeuGln 187
      |||

QY      12468 TCTTTCAATTAATCTGAGTATTTTCTAATCTGACCAATCTAGAGCACTTGGACCTTCC 12527
      |||
Db      188 SerTyrGlu--ProLysSerLeuLysSerIleGlnAsnValSerHisLeuIleLeuHis 206
      |||

QY      12528 AGCAACAAG-----ATTCAAAAGTATTTATGTC 12554
      |||

```

```

Db      207 MetLysGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerValGluCys 226
      |||
QY      12555 ACAGACTTGGGGGTCTTACATCAAAATGCCCTACTCAATCTCTTTAGACCTGCTCCTG 12614
      |||
Db      227 LeuGluLeuLys-----AspThrAspLeu 234
      |||

QY      12615 AACCCCTATGAACTT-----ATCCAACAGAGTCATTTAAAGAAATTAAGGCTTCATTAAG 12668
      |||
Db      235 AspThrPheHisPheSerGluLeuSerThrGlyLuhTrAsnSerLeu---IleLysLys 253
      |||

QY      12669 CTGACTTTAAGAAAT-----AATTTGATAGTTTA---AATGTAATGAAACCTTGT 12716
      |||
Db      254 PheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMetLysLeuLeu 273
      |||

QY      12717 -----ATTCAAGTCTGGCTGCTTTGAGAGTCATGCTGTTGCTCG-----CGA 12761
      |||
Db      274 AsnGlnIleSerGlyLeuGluGluLeuGluPheAspCysThrLeuAsnGlyValGly 293
      |||

QY      12762 GAATTGAAATGAAAGAACTTGAAAGATTGACAAATCTGCTCTAGAGGGCTGTGC 12821
      |||
Db      294 AsnPheArgAlaSerAspAsnAspArgValIleAspProGlyLysValGlu-----310
      |||

QY      12822 AATTTGACCATTTGAAGAAATTCGATTAACA-----TACTTGACTACTACCTTGATGAT 12875
      |||
Db      311 ThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyr-----Asp 327
      |||

QY      12876 ATTTATGACTTATTTAATTTGTTGACAAAGTTTCTTCATTTCCCTGCGACGTGACT 12935
      |||
Db      328 LeuSerThrLeuLysSerLeuThrGluArgValLys-----ArgIleThr 342
      |||

QY      12936 ATTGAAGAGGTAAAGACTTTTCTTATATTTGGATGCGAACATTTAGATTGATTAAAC 12995
      |||
Db      343 ValGluAsnSerLysValPhe-----LeuValPro 352
      |||

QY      12996 TGTAAATTTGACAGATTTCACCATTTGAAACCTCAATCTCTCAAAAGCTTACTTCACT 13055
      |||
Db      353 CysLeuLeuSerGln-----357
      |||

QY      13056 TCCAACAAAGGTGGAAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAAGTTTCTAGAT 13115
      |||
Db      358 -----HisLeuLysSerLeuGluTyrLeuAsp 366
      |||

QY      13116 CTCAGTAGAAAT-----GGCTTGAGTTCAAGAGTCTGTTCCAAGT 13160
      |||
Db      367 LeuSerGluAsnLeuMetValGluGluTyrLeuLysAsnSerAlaCys-----382
      |||

QY      13161 GATTTTGGGACCAACAGACCTTAAAGTATTTAGATCTGAGCTTCAATGCTTATTAACATG 13220
      |||
Db      383 GluAspAlaTrpProSerLeuGlnThrLeuIleLeuArgGlnAsn-----397
      |||

QY      13221 AGTTCAAACTTCTTGGCTTGAACAACTGAAACATCTGCAATTTCCAGCATTTG 13280
      |||
Db      398 -----HisLeu-----AlaSerLeu 402
      |||

QY      13281 AAACAAATGATGAGTTTTCAGATTTCTATCACTGCAAGAAACCTTATTAACCTTGACATT 13340
      |||
Db      403 GluLysThrGlyGlu-----ThrLeuLeuThrLeuLysAsnLeuThrAsnIleAspIle 420
      |||

QY      13341 TCTCATATCAGACACAGAGTGTGCTTTCATGAGCATCTTCAATGGCTTGCAGTCTCGAA 13400
      |||
Db      421 SerLys-----422
      |||

QY      13401 GTCTTGAATAATGGCTGCAATTTCTTTCCAGAGAAACCTTCTTCCAGATATCTTACAGAG 13460
      |||
Db      423 -----AsnSerPheHisSer-----MetProGluThrCysGlnTrp 434
      |||

QY      13461 CTGAGAAACTGGAACCTTCCGAGCTCTCAGTGCACTGAGAGAGTGTGCT-----13514
      |||
Db      435 ProGluLysMetLysTyrLeuAsnLeuSerSerThrArgIleHisSerValIleGlyCys 454
      |||

QY      13515 ---CCAAAGCATTTAACTCACTCTCCAGTCTTCAAGTACTTAAATATGAGCCCAAC--13568
      |||

```

455 IlePro-----LysThrLeuGluIleLeuAspValSerAsnAsn 468
QY 13569 ----ACCTCTTTTCATTGAT----- 13586
DB 469 LeuAsnLeuPheSerLeuAsnLeuProGluLeuGluLeuTyrIleSerArgAsnLys 488
QY 13587 ----ACGTTTCTCT--TTAAAGTGTCTGAACCTCCAGGTTCTTGAATTACAGTCTC 13637
DB 489 LeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValIleSerArg 508
QY 13638 AATCACAATAATGACTTCCAAAAACAGAACTACAGACTTTCCAAAGTACTTACGTTTC 13697
DB 509 AsnAlaIleThrThrPheSerLysGluGluIleLeuAspSerPhe--HisThrLeuLysThr 527
QY 13698 TTAAATCTTACTCAGATGACTTGTCTTGTACTGTGAACCCAGACTTTCTCCATCG 13757
DB 528 LeuGluIleGlyGlyAsnAsnPheIleCysSerCysGluPheLeuSerPheThrGln-- 546
QY 13758 ATCAGAGACGACGAGCTCTGTGGAAAGT-----GAAAGAAATGAAA 13802
DB 547 -----GluGlnGlnAlaLeuAlaLysValIleLeuIleAspTrpProAlaAsnTyrLeu 563
QY 13803 TGTGCAACACCTTCAGATTAACGAGGCAATGCTGTGCTGACTTGAATATACG----- 13856
DB 564 CysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSerValSer 583
QY 13857 ----TGTCAATGATTAAGACATCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 13913
DB 584 GluCysHisArgIleAlaLeuValSerIleMetCysAlaLeuPheLeuIleLeu 603
QY 13914 GTTGTAGACGTTTGTCTTAATGATTTCTA-----TTTCACTGATGCTTCTGTGAGC 13967
DB 604 LeuThrGlyValIleCysHisArgPheHisGlyLeuTyrIleMetLysMetMetTrpAla 623
QY 13968 TGCATTAAGTATGTAGA-----GCTGAAAATC--TATGATGCC 14006
DB 624 TrpLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTyrAspAla 643
QY 14007 TTTTGTATCTTCTCAGACGAGATGAGACTGGGTGAAGATGAGCTAATGAATTTA 14066
DB 644 PheValSerTyrSerGluArgAspAlaTyrTrpValGluAsnLeuMetValGlnGluLeu 663
QY 14067 GAAGAAGGGGTGCTCCATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 14126
DB 664 GluAsnPheAsnProProPheLysLeuCysLeuHisLysArgAspPheIleProGlyLys 683
QY 14127 GCCATGTGTCGAATCATCATCATGATGATGATGATGATGATGATGATGATGATG 14186
DB 684 TrpIleIleAspAsnIleIle--AspSerIleGluLysSerHisLysThrValPheVal 702
QY 14187 GTGTCCCAAGCACTTCATCCAGACCGCTGGGTATCTTTGAATATGATGATGCTCAGACC 14246
DB 703 LeuSerGluAsnPheValLysSerIleTyrCysLysTyrGluLeuAspPheSerHisPhe 722
QY 14247 TGGAGATTCTGAGACGCTGCTGTATCATCTTCATCTTCATCTTCATCTTCATCTTC 14306
DB 723 ArgLeuPheAspGluAsnAsnAspAlaAlaIleLeuIleLeuGluProIleGluLys 742
QY 14307 ACCCTGCTCAGCAGCAG--GTGAGCTGTACCGCTTCTCAGCAGAACATTTACTGT 14363
DB 743 LysAlaIleProGlnArgPheCysIleLeuArgLysIleMetAsnThrLysThrLeu 762
QY 14364 GAGTGGAGGAGACGCTCTGGGGGAGCACTTTCTGAGACGACTCAGAAAAAGCCCTG 14423
DB 763 GluTrpProMetAspGluAlaGlnArgGluGlyPheTrpValAsnLeuArgAlaAlaIle 782

APPLICANT: Kelleher, Kerry
APPLICANT: Carlin, McKeough
TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
TITLE OF INVENTION: ENCODED THEREBY
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
STREET: 87 CambridgePark Drive
City: Cambridge
STATE: Massachusetts
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/514,014
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G16000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 488-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-514-014-4
Alignment Scores:
Pred. No.: 5e-49 Length: 661
Score: 529.00 Matches: 183
Percent Similarity: 44.83% Conservative: 103
Best Local Similarity: 28.68% Mismatches: 254
Query Match: 1.60% Indels: 98
Gaps: 26
US-09-396-985b-47 (1-18989) x US-08-514-014-4 (1-661)
QY 12171 TTAAATATTATTTTAAAGTTCTTA-----TTGACAGAAATATT 12209
DB 58 LeuGluPheSerPheAsnPheLeuProThrIleHisAsnArgThrPheSerArgLeuMet 77
QY 12210 AGATTAATCATATGCTTTTATTTC--TGTAGGTGGAATCCAGAACTTGAAGATGG 12266
DB 78 ----AsnLeuThrPheLeuAspLeuThrArgCysGlnIleAsnTrpIleHisGluAsp 95
QY 12267 GCATTAAGAGCCCTAAGCCACTCTTACCTTAATATTGACAGAAACCCATCCAGAT 12326
DB 96 ThrPheGlnSerHisHisGlnLeuSerThrLeuValLeuThrGlyAsnProLeuIlePhe 115
QY 12327 TTAGCCCTGGAGCCTTTTCTGACATATCAAGTTTACAGAACTGTGCTGTGAGACA 12386
DB 116 MetAlaGluThrSerLeuAsnGlyProLysSerLeuLysHisLeuPheLeuIleGlnThr 135
QY 12387 AATTAAGACTCTCAGGAACCTTCCCATTTGACATCTCAAACTTTGAAGAATTAAAT 12446
DB 136 GlyIleSerAsnLeuGluPheIleProValHisAsnLeuGluAsnLeuGluSerLeuTyr 155
QY 12447 GTGCTCACAATCTTATCCATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCTT 12506
DB 156 LeuGlySerHisHisIleSerSerIleLysPheTrpLysAspPhePro--AlaArgAsn 174
QY 12507 CTAGAGACTTGAACCTTTCCAGCAGCAAGATTCAAAGTATTATTTATTCACAGACTTCGG 12566
DB 175 LeuLysValLeuAspPheGlnAsnAsnAlaIleHisTyrIleSerArgGluAspMetArg 194

Alignment Scores:

Pred. No.: 5e-49 Length: 661
 Score: 529.00 Matches: 183
 Percent Similarity: 44.83% Conservative: 103
 Best Local Similarity: 28.68% Mismatches: 254
 Query Match: 1.60% Indels: 98
 DB: 2 Gaps: 26

US-09-396-985b-47 (1-18989) x US-08-833-823-4 (1-661)

```

QY 12171 TTAATATCTAATTTTAAAGTTCTTA-----TTCAAGCAGAAATAT 12209
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 58 LeuGIuPheserPheAsnPhelEuProThrlIehIsAnrghThrPheSerArgLeuMet 77
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12210 AGATATCAATGCTTTTATTCC---GTNAGGTGAAATCCAGACATTTGAAGATGG 12266
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 78 -----AsnLeuThrPheLeuAspLeuThrArgCysGlnIleAsnTrpIleHisGluAsp 95
    : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 12267 GCATATCAGAGCCCTAACGCCCTCTCACTTATATGACAGAAACCCCATCCAGAGT 12326
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 96 ThrheGlnSerHisSHsGlnLeuSerThrLeuValLeuThrGlyAsnProLeuIlePhe 115
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12327 TTACCCCTGGAGGCTTTTCTGACCTATCAAGTTTACAGAGCTGTGGCTGAGACACA 12386
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 116 MetValGluThrSerLeuAsnGlyProIySerLeuIySHsIleuPheLeuIleGlnThr 135
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12387 AATTCAGATCTTCAGAGACTTCCCATTCGACATCTCAAAACTTTGAAAGACTTAAT 12446
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 136 GlyIleSerAsnLeuGluPheIleProValHisAsnLeuGluAsnLeuGluSerLeuIyr 155
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12447 GTGCCTCAACATCTTATCCAACTTTCAAATTCAGATGATTTTCTTAATCTGACCAAT 12506
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 156 LeuGlySerAsnHisIleSerSerIleIySpherProIyAspPhePro---AlaArgAsn 174
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12507 CTAGAGCACTTGAACCTTTCCAGACACAAGATTCAAAGTATTTATTCACAGACTTGGG 12566
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 175 LeuIyValIleuAspPheGlnAsnAsnAlaIleHisTrpIleSerArgGluAspMetArg 194
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12567 GTTTCATCAATCAATGCCCTCACTCAATCTCTTTAGACCTGTCCTCGAACCTCATGAC 12626
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 195 SerLeuGluGln-----AlaIleAsnLeuSerLeuAsnPheAsnGlyAsnAsnValIys 212
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12627 TTTATCCAACAGGCGATTTAAAGAAATTAAGGCTTCAATAGCTATTAAAGAAATAT 12686
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 213 GlyIleGluLeuGlyAlaPheAspSerThrValPheGlnSerLeu-----Asn 228
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12687 TTTGATAGTTTAAATGTATGAAAACTGTATTCAGAGCTGTGGCTGTTAGAAGTCCAT 12746
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 229 PheGlyGlyThrProAsnLeuSerValIlePheAsnGlyLeuGlnAsnSerThrThcGln 248
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12747 CGTTTGGCTTCGGAGAAATTTAGAAATGAGAAACTTGAAGAACTTTGACAAATCTGCT 12806
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 249 SerLeuTrpLeuGlyThrPheGluAspIleAspAsp---GluAspIleSerSerAlaMet 267
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12807 CTAGAGGCGCTGTGAATTTGACATTCAGAGAAATTCGATTAAGCTACTTAAGCTATCAC 12866
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 268 LeuIySGlyLeuCysGluMetSerValGluSerLeuAsnLeuGln-----GluHisArg 285
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12867 CTCGATGATATTAATGAC---TTATTAATGTGTTGACAAATGTTTCTTCAATTTCCCTG 12923
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 286 PheSerAspIleSerSerThrThrPheGlnCysPheThrGlnLeuGlnGluLeuAspLeu 305
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12924 GTGAGTGTGACTATTGAAAGGTAAGAAAGCTTTTCTTAATTTGGATGGCAACATTTA 12983
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 306 ThrIleThrHisLeuIySGlyLeuProSer-----GlyMetIleSGlyLeu 320
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 12984 GAATTAAGTTAAC-----TGTAATATT--- 13004
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 321 AsnLeuLeuIySGlyLeuValLeuSerValAsnHisPheAspGlnLeuCysGlnIleSer 340
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13005 ---GGACAGTTTCCACATTTG-----AACTCAAAATCTCTCAAA 13040
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
```

```

DB 341 AlaIleAsnPheProSerLeuThrHisLeuTrpIleArgGlyAsnValIySGlyLeuHis 360
QY 13041 AGGCTTACTTTGACTTCCAAAGAGTGGAAATGTTTTTTCAGAAAGTTGATCATCAAGC 13100
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 361 LeuGlyValGlyCysLeuGluIySGlyAsn----- 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13101 CTTCAGTTTCTTACATCTCAGTAAAGAAATGCGCTTGAAGTTTCAMAGTTCTGTCTCAAAAGT 13160
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 372 LeuGlnThrLeuAspLeuSerHisAsnAspIleGluAlaSerAspCysCysSerLeuGln 391
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13161 GATTTTGGACACACAGCTTAAGTATTTAGATTCAGCTTCAATGCGTTATATACCATG 13220
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 392 LeuIyAsnLeuSerHisLeuGlnThrLeuAsnLeuSerHisAsnGluProLeuGlyLeu 411
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13221 AGTTCAAC---TTCTTGGGCTTAGAACCTAGAACATCTGAGATTTCCAG----- 13268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 412 GlnSerGlnAlaPheIySGlyCysProGlnLeuGlnLeuLeuAspLeuAlaPheThrArg 431
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13269 ---CATTCCAATTTGAAACCAATAGTAGTACTTTCA-----GTATTCCTATGACCTCAGA 13319
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 432 LeuHisIleAsnAlaProGln---SerProPheGlnAsnLeuHisPheLeuGlnValLeu 450
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13320 AACCTCAATTAAC---CTTGACATTTCTCAATACCTCACACAGAGTGTCTTCATATGC 13373
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 451 AsnLeuThrIyCysPheLeuAspThrSerAsnGlnHis----- 463
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13374 ATCTCAATGCGCTTGCACAGCTCTGAAAGCTTGAAGAAATGCGCTGCAATTTTCCAGAA 13433
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 464 LeuLeuAlaGlyLeuProValIleuArgHisLeuAsnLeuIySGlyAsnHisPheGlnAsp 483
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13434 AACTTCCTT-----CCAGATATCTTCACAGAGCTGAGAAACTTGACCTTCTGAGACTTC 13487
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 484 GlyThrIleThrIySThrAsnLeuLeuGlnThrValGlySerLeuGlnValLeuIleLeu 503
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13488 TTCACGTGTCACTGACAGAGCTGTCTCCAAACAGACTTAACTCACTCTCCAGTCTCAG 13547
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 504 SerSerCysGlyLeuLeuSerIleAspGlnAlaPheHisSerLeuGlyIySGlyMetSer 523
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13548 GTACTAAATATGAGCCACACAACTCTTT-----TCATGTGATACGTTTCCCTTAAT--- 13598
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 524 HisValAspLeuSerHisAsnSerLeuThrCysAspSerIleAspSerLeuSerHisLeu 543
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13599 -----AAGTGTCTGAACCTCCCTCAGAGTCTTGATTAACAGTCTCAAT 13640
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 544 IySGlyIleTrpLeuAsnLeuAlaIleAsnSerIleAsnIleIleSerProArgLeuLeu 563
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13641 CACATATGACTTCCAAAAACAGAACTACAGACTTTCCAGATTAAGTACTTCTTCA 13700
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 564 ProIleLeu-----SerGlnGlnSerThrIle 572
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13701 AATCTTACGAAATGACTTGTGCTTGTATCTTGAAACACCAAGATTTCTGCAATGATC 13760
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 573 AsnLeuSerHisAsnProLeuAspCysThrCysSerAsnIleHisPheLeuThrTrpIyr 592
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13761 AAGGACCAAGAGCAGCTCTTGCTGAGAGTTGAAGCAATGAAATGTGCAACCTTCAGAT 13820
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 593 IySGluAsnLeuHisIySGlyLeuGlySerGlnGluIyThrThrCysAlaAsnProProSer 612
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13821 AAGCAGGCGAATGCTGTGCTGAGATTTGAATATACCTGTGAGATGAATTAAGCATGATT 13880
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 613 LeuArgIyValIySGlyLeuSerAspValIyLeuSerCysGlyIle-----ThAlaIle 630
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 13881 GGTGTGTGCGGCTCAGATGTGCTGTGATATCTGTGTAGACAGTTCTGTGTAT 13934
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 631 GlyIlePhePheLeuIleValPheLeuLeu-----LeuLeuAlaIleLeuLeuPhe 647
    : : : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
```

RESULT 5

US-09-949-016-8799
 ; Sequence 8799, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```

: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001307
: CURRENT APPLICATION NUMBER: US/09/949,016
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8799
: LENGTH: 775
: TYPE: PRT
: ORGANISM: Human
: US-09-949-016-8799

Alignment Scores:
Pred. No.: 2,22e-45 Length: 775
Score: 497.00 Matches: 205
Percent Similarity: 40.87% Conservative: 113
Best Local Similarity: 26.35% Mismatches: 242
Query Match: 1.50% Indels: 218
DB: 4 Gaps: 37

US-09-396-985b-47 (1-18989) x US-09-949-016-8799 (1-775)

QY 12446 ATTCAGCAATTTGAAGATGGGCGATATCAGAGCCTTAAGCCACTCTTACTTAAATATG 12305
DB 123 IleasnThrIleGluGluAspSerPheSerLeuGlySerLeuGluHisLeuAspLeu 142
QY 12306 ACAGAAACCCTTCAGAGATTCAGCCCTGGAGCCTTTCTGGACTATCAAGTTTCAG 12365
DB 143 SerThrAsnThrLeuSerAsnLeuSerSerSerThrPheLysProLeuSerSerLeuThr 162
QY 12366 AACCTG-----GTGGCTGTGAGACAAT 12389
DB 163 PheLeuAsnLeuLeuGlyAsnProThrLysThrLeuGlyGluThrSerLeuPheSerHis 182
QY 12390 CTGACATCTTAGAAGAACTTCCCATTTGACATCTCAAACT-----12431
DB 183 LeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIleGlnArg 202
QY 12432 -----TTGAAGAAGTAAATGCGCTCAACATCTTATCA 12467
DB 203 LysAspPheAlaGlyLeuThrPheLeuGluGluLeuGluIleAspAlaSerAspLeuGln 222
QY 12468 TCTTTCAATTAATCTGAGATTTTCTTAATCTGACCAATCTAGACACTTGGACCTTCC 12527
DB 223 SerThrGlu---ProLysSerLeuLysSerIleGlnAsnValSerHisLeuIleLeuHis 241
QY 12528 AGCAACAG-----ATTCAAGTATTTATTGC 12554
DB 242 MetLysGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerValGlyCys 261
QY 12555 ACAGCTGGGGGTTCATCAATCAATGCCCCCTACTCATCTCTTTAGACCTTCCCTG 12614
DB 262 LeuGluLeuArg-----AspThrAspLeu 269
QY 12615 AACCTTAATGAACTT-----ATCCAACAGAGTCATTTAAAGAAATTAAGGCTTCATAG 12668
DB 270 AspThrPheHisPheSerGluLeuSerThrGlyIuThrAsnSerLeu---IleLysLys 288
QY 12669 CTGACTTAAGAAAT-----AATTTGATAGTTTA---AATGTAATGAAAATCTGT 12716
DB 289 PheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMetLysLeuLeu 308
QY 12717 -----ATTCAAGGCTGGCGGTGTTTAGAGTCATGGTTTGCTTG-----GGA 12761
DB 309 AsnGlnIleSerGlyLeuLeuGluLeuPheAspCysThrLeuAsnGlyValGly 328
QY 12762 GAATTTGAATGAAGAACTTGAAAAGTTTGACAAATCTGCTTAGAGGGGCTGTGC 12821

```

```

DB 329 AsnPheArgLaseAspAsnAspArgValIleAspProGlyLysValGlu-----345
QY 12822 AATTGACCAATTTGAAGAAATCCGATTGCA-----TACTAGACTCTACTCGATGAT 12875
DB 346 ThrLeuThrIleArgArgLeuHisIleProArgPheThrLeuPheThr-----Asp 362
QY 12876 ATTATGACTTAATTAATGTTTGAACAATGTTTCTTCAATTTTCCCTGGTGAAGTGCAT 12935
DB 363 LeuSerThrLeuThrLysSerLeuThrGluArgValLys-----ArgIleThr 377
QY 12936 ATTGAAGGTTAAAGACTTTTCTTAATTAATTTGGAATGGCAATTGAATTAAGTTAAC 12995
DB 378 ValGluAsnSerLysValPhe-----LeuValPro 387
QY 12996 TGTAAATTTGACAGCTTTCCACATTTGAACCTCAATCTCTCAAAAGCTTACTTCACT 13055
DB 388 CysLeuLeuSerGln-----392
QY 13056 TCCAACAAGGTGGGAATGCTTTTTCAGAGTTGATCTACACAGCTTGATTTCTAGAT 13115
DB 393 -----HisLeuLysSerLeuGluThrLeuAsp 401
QY 13116 CTCAGTAGAAAT-----GCTTGAGTTTCAAAAGGTGCTGTTCTCAAGT 13160
DB 402 LeuSerGluAsnLeuMetValGluGluThrLeuLysAsnSerAlaCys-----417
QY 13161 GATTTGGGACACACACCTTAAGATTTAGATCTGAGCTTCAATGGTGTATTATCAATG 13220
DB 418 GluAspAlaThrProSerLeuGlnThrLeuIleLeuArgGlnAsn-----432
QY 13221 AGTTCAAACTTGGGCTTAGAAACAATGAAATCATGATTCGATTTCCAGATTCCAATTTG 13280
DB 433 -----HisLeu-----AlaSerLeu 437
QY 13281 AAACAATGAGTAGATTTCAGATTCTATCACTCAAGAAACCTCAATTAACCTGACATT 13340
DB 438 GluLysThrGlyGlu-----ThrLeuThrLeuLysAsnLeuThrAsnIleAspIle 455
QY 13341 TCTCATATCTACACACCAAGTTGCTTCAATGGCATTTCAATGGCTTGCAGTCTGAA 13400
DB 456 SerLys-----457
QY 13401 GTCTTGAAATATGGCTGCAATCTTTCAGAGAAACAATCTCTCCAGATATCTCACAGAG 13460
DB 458 -----AsnSerPheHisSer-----MetProGluThrCysGlnThr 469
QY 13461 CTGAGAAACTTGACCTTCTCTGACCTCTCTCACTGATGCACTGAGACAGTGTCT-----13514
DB 470 ProGluLysMetLysThrLeuAsnLeuSerSerThrArgIleHisSerValThrGlyCys 489
QY 13515 ---CCAAAGCAATTTAACTCACTCTCCAGTCTTCAGTCACTTAATATGAGCCACAC--13568
DB 490 IlePro-----LysThrLeuGluIleLeuAspValSerAsnAsn 503
QY 13569 ---AAGCTTTTCAATGAT-----13586
DB 504 LeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGluLeuThrLysSerArgAsnLys 523
QY 13587 -----ACGTTTCT---TATAAGTGTGAAGTCCCTCCAGGCTTGTGATTACAGTCTC 13637
DB 524 LeuMetThrLeuProAspAlaSerLeuLeuPheMetLeuLeuValLysIleSerArg 543
QY 13638 AATCACTAATGACTTCCAAAAGAGAACTACAGACATTTTCCAACTAGCTTACCTTTC 13697
DB 544 AsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe---HisThrLeuLysThr 562
QY 13698 TTAATCTTACTAGATGACTTGTCTGTGATCTTGGAACAACAGAGATTTCCGCAATGG 13757
DB 563 LeuGluAlaGlyLysAsnAsnPheIleCysSerCysGluPheLeuSerPheThrGln---581
QY 13758 ATCAAGACCAAGAGAGCTCTTGAGTGAAGTT-----GAACGAAATGAA 13802

```

```

Dd      582 -----GUGINGINALALEUALALysValLeuLleAspTrpProAlaSerTyrLeu 598
Qy      13803 TGTCACACCTTCAGATTAAGCAGCGCATCCGTGCTGAATTGAATCAACC----- 13856
Db      599 CysAserPerProSerHisValArgGLYgInGlnIvalGlmsrValArgSueValSer 618
Qy      13857 ---TGTCAGATGAATAAGCACATTCATTGGTGTGCCTGCTCAGTGTGCTTGAGATTC 13913
Db      619 GLucyshiIsargThrAlaLeuValSerGLYMetCySeAlaLeuPheLeuIleLeu 638
Qy      13914 GTTGTACAGTTCTGTGCTATTAAGTTTAT-----TTTCACCTGATGCTTCCTGCTGAC 13967
Db      639 LeuthrGLYValLeuCyshiIsArgPheHisGLYLeuTrpTyrMetLysMetLeuTrrAla 658
Qy      13968 TGCATAAAGTAGTGGTAGA-----GGTGAACAATC---TATGATGCC 14006
Db      659 TrpLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCySerTrrAla 678
Qy      14007 TTGTGTATCTACTACACGAGATGAGGACTGGGTAAAGAATGAGCTAGTAAAGATTTA 14066
Db      679 PheValSerTyrSerGIUAArgAspAlaTyrTrpValGIUbsmLeuMetValGIngluleu 698
Qy      14067 GAAGAAGGGGTGCTCCATTTTCAGCTGCTGCCTTCACATACAGACATTTATCCCCGGTGG 14126
Db      699 GIUsmPheAsnPProPheLysCysLeuHisLysArgAspPheIleProGLYlys 718
Qy      14127 GCCATGTGTCGCAACATCATCATGAGGTTTCCATTAAGCCGAAGGTGATTTGTGG 14186
Db      719 TrpIleIleAspAniIlelle--AspSerIleGLYSerHisLysThrValPheVal 737
Qy      14187 GTGTCCACGACCTTCATCCAGAGCCGCTGGTGTATCTTTGAATATGAGATTGCTCAGACC 14246
Db      738 LeuSerGIUsmPheValLysSerGIUTripCyshiSerTyrGIUlsAspPheSerHisPhe 757
Qy      14247 TGGCAGTTTCAGACAGTCGTCGTGATCATCTTCATTTGCTCCGCAAGAGNG 14300
Db      758 ArgLeuPheAspGIUsmAsnAspAlaAlaIleLeuIleLeuLeuGIUpole 775

RESULT 6
US-09-353-s85-3
; Sequence 3, Application US/09353585
; Patent No. 6287865
; GENERAL INFORMATION:
; APPLICANT: Dixon, Mark S
; Jones, David A
; Jones, Jonathan DG
; TITLE OF INVENTION: Plant pathogen resistance genes and uses thereof
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 6287865th Giebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/353,585
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
; 1/68
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/930,277
; FILING DATE: 27-OCT-1997
; APPLICATION NUMBER: PCT/GB96/00785
; FILING DATE: 01-APR-1996
; APPLICATION NUMBER: GB 9506658.5
; FILING DATE: 31-MAR-1995

```

```

: ATTORNEY/AGENT INFORMATION:
: NAME: Ms Mary J Wilson
: REGISTRATION NUMBER: 32,955
: REFERENCE/DOCKET NUMBER: 620-69
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 816-4000
: TELEFAX: (703) 816-4100
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1112 amino acids
: TYPE: amino acid
: STRANDEDNESS: <Unknown>
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: HYPOTHEICAL: YES
: ORIGINAL SOURCE:
: ORGANISM: Tomato
: STRAIN: Cf2
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-353-585-3

Alignment Scores:
Pred. No.:          9,61e-22      Length:       1112
Score:             287.50         Matches:       132
Percent Similarity: 42.17%        Conservative:   78
Best Local Similarity: 26.51%     Mismatches:   159
Query Match:       0.87%          Indels:       89
DB:                3              Gaps:        20

US-09-396-985B-47 (1-189989) x US-09-353-585-3 (1-1112)

QY      12279 CTAAGCACTCTCTACCTTAAATTATGACAGAAAACCATCCATGCAGATTTCGCCCGGA 12338
           |||||
DB      430 LeuSerSerLeuThrTrpTryLeuAsnLysLeuSerAsnAsnSerIleAsnGlyPheIleProAla 449

QY      12339 GCCCTTTCTGGACGTATCAAGTTAAGAGAGCTGGTGCGTGGAGACAATACTCAGCATCT 12398
           ::::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
DB      450 SerPheGlyAsnMetSerAsnLeuValaPheLeuPheLeuTyArgIubAsnGlnLeuAlaSer 469

QY      12399 CTAGAAGAACTCCCACTGACACTCCAAAACTTTGMAAGAACTTATATGCGCTCACAAT 12458
           |||||
DB      470 SerAlaProgluGluIleGlyTryLeuArgSerLeuAsnValLeuAsnLysSerGluAsn 489

QY      12459 CTATATCCAATCTTTCAAATTAAGTAGAGTATTTTCTAATCTGCACCAATCTTAAGACATTG 12518
           ::|
DB      490 AlaLeuAsnGly---SerIleProAlaSerPheGlyAsnLeuAsnAsnLeuSerArgLeu 508

QY      12519 GACCTTTCCAGAACCAAGATTCAAAAGTATTTATTGACACAGACCTTGGCGGTTCTACATCA 12578
           ::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
DB      509 AsnLeuValAsnAsnGlnLeuSerGlySerIleProgluGluIleGlyTryLeuArgSer 528

QY      12579 ATGCCCCCTACTCATCTCTCTTTAGACCTGCCCCGTAAGCCCTTATATGCCAACCA 12638
           |||||
DB      539 -----LeuAsnVal---LeuAsnLysSerGluAsnAlaLeuAsnGlySerIlePro 544

QY      12639 GGTCGATTTTAAAGAATAATGAGCTTCAATAGCTGACTTTAAGAAATATTTGATAGCTTGA 12698
           :::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |
DB      545 AlaSerPheGlyAsnLeu-----AsnAsnLeuSerArgLeu 556

QY      12699 AATGTAATGAAAACCTGTATATTCAGGCTGGCGGTGTTGAAATGCATGCTTTGGTTCG 12758
           |||||
DB      557 AsnLeuValAsnAsnGlnLeuSerGlySerIleProgluGluIle----- 571

QY      12759 GGAGAATTTTGAAGTAAAGAACTTGGAAGAAATTTGCAAAATCTGCTCTAGAGGCG--- 12815
           |||||
DB      572 GlyTryLeuArgSerLeuAsnAsnLysPhe---GlyLeuSerGluAsnAlaLeuAsnGlySer 590

QY      12816 -----CTGTGCAATTTGACCATTTGAAGAAATTCGGATTAGCATACTTGAATCAC 12863
           |||||
DB      591 IleProAlaSerLeuGlnGlyAsnLeuValAsnAsnLeuSerMetLeuTyryrAsnAsnGln 610

QY      12864 TACCTCGATGATGATTATGACTTATTTAATGTTTGGACAAATGTTCTTCATATTTTCCCTG 12923
           |||

```

```

Db      611 LeuSerGlySerIleProGluGluIleGlyTyrLeuSerSerLeuThrTyrLeuSerIleu 630
QY      12924 GTGAGTGTGACTATTTGAAAGGTAAGACATTTCTTATTAATTCGATGGCAACATTTA 12983
      : : : : :
Db      631 GlyAsnAsnSerLeuAsn----- 636
QY      12984 GAATTAAGTAACGTAAATTTTGGACAGTTTCCACATTGAAATCTCAATCTCGAAAGG 13043
      : : : : :
Db      637 GlyLeuIleProAlaSerPheGly-----AsnMetArgAsnLeuGlnAla 651
QY      13044 CTTCCTTCACTTCCACAAAGAGTGGAGATCTTTTTCAGAGAT----- 13088
      : : : : :
Db      652 LeuIleLeuAsnAspAsn-----AsnLeuIleGlyGluIleProSerSerValCys 668
QY      13089 GATCTACCAAGCTTGTAGTTCTTCTAGATCTCAGTAAATGAGTTTCAAGTTTCAAGTTGC 13148
      : : : : :
Db      669 AsnLeuThrSerLeuGluValLeuTyrMetProArgAsnAsnLeu-----LysGlyLys 686
QY      13149 TGTTCCTCAAGTGAATTTTGGACCAACAGCTTAAAGTATTTTGAATCTGAGCTTCAATGT 13208
      : : : : :
Db      687 ValProGlnCysLeuGlyAsnIleSerAsnLeuGlnValLeuSerMetSerSerAsnSer 706
QY      13209 GTTATT---ACGATGAGTTCAACTTCTTGCGCTTAGAACAACACTAGAACATCTGATTTTC 13265
      : : : : :
Db      707 PheSerGlyGluLeuProSerSerIleSerAsnLeuThrSerLeuGlnIleLeuAspPhe 726
QY      13266 CAGCATTCGCAATTTGAAACAAATGAGTGTTCAGATTTCCATCACTCAGAAACCTC 13325
      : : : : :
Db      727 GlyArgAsnAsnLeuGly----- 733
QY      13326 ATTACCTTGACATTTCTCATCTACACACAGAGTGTCTTCAATGGCATCTTCAATGCGC 13385
      : : : : :
Db      734 -----AlaIleProGlnCysPheGlyAsn 741
QY      13386 TTGTCCAGTCTCGAAGTCTTGAATAATGCGTGGCAATTTCTTCCAGAAATCTCTTCCA 13445
      : : : : :
Db      742 IleSerSerLeuGluValPheAspMetGlnAsnAsnLysLeu---SerGlyThrLeuPro 760
QY      13446 GATATCTTCACAGAGCTGAGAAACTTGACCTTCTGAGACCTCTCTCACTGATCGACGTGAG 13505
      : : : : :
Db      761 ThrAsnPheSerIleGlyCysSerLeuIleSerLeuAsnLeuIleGlyAsnGlnLeuGlu 780
QY      13506 CAGTTGTCTCCACAGAGATTTAACTCACTCCAGCTTCTCACTAATATGATGAGCCAC 13565
      : : : : :
Db      781 AspGluIleProArgSerLeuAspAsnCysLysLysLeuGlnValLeuAspLeuGlyAsp 800
QY      13566 AACACTTCTTTTCATTTGATGATGCTTCT---TATAAGTGTCTGAACCTCCCTCAG 13619
      : : : : :
Db      801 AsnGlnLeu-----AsnAspThrPheProMetTyrLeuGlyThrLeuProGluLeuArg 818
QY      13620 GTTCTGATTAACAGTCTCAATCAGATCA-----ATGACTTCCAAATAACAGAACTA 13670
      : : : : :
Db      819 ValLeuArgLeuThrSerAsnLysLeuIleGlyProIleArgSerSerArgAlaGlnIle 838
QY      13671 CAGCATTTTTCAGATGATCTTCTTAAATCTTCAATCTTCAAGATGATGCTTGTCT 13724
      : : : : :
Db      839 Met---PhePro---AspLeuArgIleIleAspLeuSerArgAsnAlaPheSer 854

```

```

STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-Jul-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB86/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 950658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: CF2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-353-585-2
Alignment Scores:
Pred. No.: 3,5e-21 Length: 1112
Score: 282.50 Matches: 137
Percent Similarity: 40.04% Conservative: 68
Best Local Similarity: 26.76% Mismatches: 208
Query Match: 0.85% Indels: 99
DB: Gaps: 20
US-09-396-985b-47 (1-18989) x US-09-353-585-2 (1-1112)
QY      12276 AGCCTAAGCCACTCTCTACTTAATTAATTAACAGAAACCCATCCAGATTAGCCCTG 12335
      : : : : :
Db      381 AsnLeuAsnAsnLeuSerMetLeuTyrLeuTyrAsnAsnGlnLeuSerGlySerIlePro 400
QY      12336 GAGACCTTTCTGAGCATCAATTAACAGAACTGTGCTGTGAGAGCAAAATCTAGCA 12395
      : : : : :
Db      401 AlaSerLeuGlyAsnLeuAsnAsnLeuSerArgLeuTyrLeuTyrAsnAsnGlnLeuSer 420
QY      12396 TCTCTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAAAGACTTAATGTGGCTCAC 12455
      : : : : :
Db      421 GlySerIleProGluGluIleGlyTyrLeuSerSerLeuThrTyrLeuAspLeuSerAsn 440
QY      12456 AATCTTAATCCATCTTCAAAATTAACGATGATTTTCTTAATCTGACCAATCTAGAGCAC 12515
      : : : : :
Db      441 AsnSerIleAsnGlyPhe---IleProAlaSerPheGlyAsnMetSerAsnLeuAlaPhe 459
QY      12516 TTGACCTTTCCAGCAAGATTTCAAGATTTATTTGACACAGACTTGGGGTTCTACAT 12575
      : : : : :
Db      460 LeuPheLeuTyrGluAsnGlnLeuAlaSerSerValProGluGluIleGlyTyrLeuArg 479
QY      12576 CAATGCCCTACTCATCTCTCTTGAACCTGTCCCTGAACCTTGAACCTTATTCACAA 12635
      : : : : :

```

```

Db 480 Ser-----LeuAsnVal---LeuAspLeuSerGluAsnAlaLeuAsnGlySerIle 495
QY 12636 CCAGGTGATTTAAAGAAATAGGCTTCATAGCTGACTTAAAGAAATATTTTGATAGT 12695
Db 496 ProAlaSerPheGlyAsnLeu-----AsnAsnLeuSerArg 507
QY 12696 TTAATATTAATGAAGAACTTGATTCAGAGTCTGGCTGGTTTGAAGTCCATCGTTGGTT 12755
Db 508 LeuAsnLeuValAsnAsnGlnLeuSerGlySerIleProGluGluIle----- 523
QY 12756 CTGGAGAAATTGAGAAATGAAGAACTTGAGAAAGTTTGACAAATCTGCTAGAGGCG 12815
Db 524 ---GlyIlyrLeuArgSerLeu---AsnValLeuAspLeuSerGluAsnAlaLeuAsnGly 541
QY 12816 CTGTCGATTTGACCATTTGAAGAAATTCGATTCGATTAAGTACTACTGATGATGAT 12875
Db 542 -----Ser 542
QY 12876 ATTAATGACTTAATTAATTTGACAAATGTTTCTTCATTTTCCCTGGTGAAGTGAAT 12935
Db 543 IleProAlaSerPheGlyAsnLeuAsnAsnLeuSerArgLeuAsnLeuValAsn----- 560
QY 12936 ATGAAAGGTTAAAGACTTTTCTTAATTTGCGATGGCAACATTTAAGATTAGTTAAC 12995
Db 561 -----Asn 561
QY 12996 TGTAAATTTGACAGTTTCCACATG-----AACTCAATCTCTCAAAAGGCTTACT 13049
Db 562 GlnLeuSerGlySerIleProGluGluIleGlyIlyrLeuArgSerLeuAsnAspLeuGly 581
QY 13050 TTCACCTTCCAACT-----AAAGTGGGAATCTTTTCAGAAAGTTGATCTACCAAGCTT 13103
Db 582 LeuSerGluAsnAlaLeuAsnGlySerIleProAlaSerLeuGluAsnLeuAsnAsnLeu 601
QY 13104 GAGTTTCTAGATCTCAGTGAATGCGCTTGAGTTTCAAGTTCGCTGCTTCAAAAGTAT 13163
Db 602 SerMetLeuIlyrLeuIyAsnAsnGlnLeuSer-----GlySerIleProGluGluIle 619
QY 13164 TTTGGGACCAACGCTTAAATATTTATGATCTG-----AGTTCAATGGGTATTT 13214
Db 620 GlyIlyrLeuSerSerLeuThrIlyLeuSerLeuGluAsnAsnSerLeuAsnGlyLeuIle 639
QY 13215 ACCATGAGTTCAAACTCTTGGGCTTGAACAACAATGCAATTCGATTTCCAGCATTTCC 13274
Db 640 ProAlaSer-----PheAlaAsnMetArgAsnLeuGlnAlaLeuIleLeuAsnAspAsn 657
QY 13275 AATTGAAACAATGAGTGAAGTTT---TCAGTATTTCTTATGATCTCAAGAACTCATTTAC 13331
Db 658 AsnLeu-----IleGlyGluIleProSerSerValCysAsnLeuThrSerLeuGluVal 675
QY 13332 CTTCGACATTTCTCATCTCACACCGAGATGCTTTCATGCGATCTTCAATGGCTTGC 13391
Db 676 LeuIlyrMetProArgAsnAsnLeuIyAsnValProGlnCysLeuGlyAsnIleSer 695
QY 13392 AGTCTCGAAGCTTGAATAGGCTGGCAATCTTTCCAGAAACTTCTTCCAGATATTC 13451
Db 696 AsnLeuGlnValLeuSerMetSerSerAsnSerPheSerGlyGlu---LeuProSerSer 714
QY 13452 TTCACAGAGCTGAGAACTTGAACCTTCTGAGACTTCTCTCAAGTGTCAACTGAGAGCAT 13511
Db 715 IleSerAsnLeuThrSerLeuGlnIleLeuAspPheGlyArgAsnAsnLeuGluGluVal 734
QY 13512 TCTCCAAAGACTTTAACTCATCTCCAGCTTTCAGATTAATAATAGCAACAAC 13571
Db 735 IleProGlnCysPheGlyAsnIleSerSerLeuGluValPheAspMetGlnAsnAsnIys 754
QY 13572 TTC-----TTTTCATG----- 13583
Db 755 LeuSerGlyThrLeuProThrAsnPheSerIleGlyCysSerLeuIleSerLeuAsnLeu 774
QY 13584 -----GATTAAGTTTCTTATAAGTCTGAGAC-----TCCCTCGAG 13619
Db 775 HisGlyAsnGluLeuGluAspGluIleProArgSerLeuAspAsnCysIlyrLeuGln 794

```

```

QY 13620 GTTCTTGATTACAGTCTCAATCATATGACTTCCAAAAACAGGAAGCTACAGCATTTT 13679
Db 795 ValLeuAspLeuGluIyAspAsnGlnLeuAsnAspThrPheProMetIlyrLeu 814
QY 13680 CCAAGTAGTCTAGCTTTCTTAATCTTACTTACTGAGAAAT 13715
Db 815 Pro---GlnLeuArgValLeuArgLeuThrSerAsn 825

RESULT 8
US-08-666-271-2
; Sequence 2, Application US/08666271
; Patent No. 5920000
; GENERAL INFORMATION:
; APPLICANT: JONES, JONATHAN D
; APPLICANT: HAMMOND-KOSACK, KIM E
; APPLICANT: THOMAS, COLWYN M
; APPLICANT: JONES, DAVID A
; TITLE OF INVENTION: PLANT PATHOGEN RESISTANCE GENES AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,271
; FILING DATE: 19-SEP-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB94/02812
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326428.1
; FILING DATE: 24-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9409363.0
; FILING DATE: 11-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 863 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-666-271-2

Alignment Scores:
Pred. No.: 1,37e-19 Length: 863
Score: 267.50 Matches: 193
Percent Similarity: 37.32% Conservative: 122
Best Local Similarity: 22.87% Mismatches: 309
Query Match: 0.81% Indels: 220
DB: 2 Gaps: 37

US-09-396-985B-47 (1-18989) x US-08-666-271-2 (1-863)
QY 12047 GATTAATCACTAGTCTGTGGGCTTCTTAATTTGCTTAATTCATCATATCATCTGCTGCTTG 12106
|||
::: ||| |||::: |||

```

Db 2 AspCysValIysLeuValPheLeuMetLeuTyThrPheLeuCysGlnLeuAlaLeuSer 21
 QY 12107 ATGTCTTGGCCATGACAAATCATATGACCCATCATCTGTATGAAGAGCTGATGACT 12166
 Db 22 SerSerLeuPro-----HisLeuCysProGlnAspGlnAla-Le 34
 QY 12167 AGATTAATATCTTATTTAGTCTTATTCAGCAAAATATTAATATTAATGATCTTT 12226
 Db 34 userLeuLeu---GlnPheLysAsnMetPheThrIleAsnProGlnAlaSerAspTyCys 53
 QY 12227 TTATTCCTGTAGTGTGAATTCAGACAAATTAAGATGGGCAATTCAGACCTTAAGCA 12286
 Db 53 sTy-----AspIleArgThrTyValAsp-----IleGlnSerTyProArg 67
 QY 12287 CCTCTCTACCTTAATATTAATGACGAAGAACCCATCCAGCTTGAAGCCCTGGAGCCCTTTC 12346
 Db 67 g-----ThrLeuSerTyrAsn-----LysSerThrSerCysCysSerTyrAs 81
 QY 12347 TGAATA-----TCAGATTTCAGAAAGCTGGTGGCTGTGAGACAAATCTAGCATC 12397
 Db 81 pGlyValHisCysAspArgIuThrThrGlyGlnValIleAlaLeuAspLeuArgCysSerG 101
 QY 12398 TCTAGAG-----AACTCCCATTTGACAACTTCGAAACTTTGAAAGAACT 12442
 Db 101 nLeuGlnIlyLysPheHisSerAsnSerSerLeuPheGlnLeuSerAsnLeuLysArgLe 121
 QY 12443 TAATGTGGCTCACTTATTCATCCATCTTGAATTAACCTGATTTTCTTAATCTGAC 12502
 Db 121 uAspLeuSerPheAsnAsnPheThrGlySerLeuIleSerProLysPheGlyGlnPheSe 141
 QY 12503 CAATCTAGACAACTTGAACCTTTCCAGACAAAGATTCAGAACTTTTTCAGACACT 12562
 Db 141 rAsnLeuThrHisLeuAspLeuSerHisSerSerPheThrGlyLeuIleProSerGlnI 161
 QY 12563 GCGGCTTACATCAATGCCCCCTACTCATCTC-----TCTTAAGACCTGTCCCTGAA 12616
 Db 161 eCysHisLeuSerLysLeuHisSvalLeuArgIleCysAspGlnTyGlyLeuSerLeuVa 181
 QY 12617 CCGCTAGAACTTATTCACCAAGCTGATTAAGAAATTAAGCTTCAATAGCTGACT- 12674
 Db 181 lProTyAsnPhe-----GlnLeuLeuLysValAsnLeuThrG 194
 QY 12675 -TTAAGAAAT--AATTTTGAATGTTAAATGTAAGAAACTGTATTAAGAT- 12725
 Db 194 nLeuArgIleuAsnLeuGlnSerValAsnIleSerSerThrIleProSerAsnPheSe 214
 QY 12726 -----CTGAGCTGTATTAAGCTCCATCTGTGGTCTTGAGAGA 12763
 Db 214 rSerHisLeuThrThrLeuGlnLeuSerGlyThrGlnLeuHisGlyIleLeuProGln 234
 QY 12764 ATTTAGAAATGAGAAACTTGGA----- 12788
 Db 234 gValPheHisLeuSerAsnLeuGlnSerLeuHisLeuSerValAsnProGlnLeuThrVa 254
 QY 12789 -----AAGTTGACAAATCTGCT----- 12806
 Db 254 lArgPheProThrThrLysTyrAsnSerSerHisSerLeuMetThrLeuTyValAspSe 274
 QY 12806 ----- 12806
 Db 274 rValAsnIleAlaAspArgIleProLysSerPheSerHisLeuThrSerLeuHisG 294
 QY 12807 -CTAGAGGCGCTGCAATTTGAC-----ATGGAAGA 12838
 Db 294 uTyMetGlyArgCysAsnLeuSerGlyProIleProLysProLeuTyrAsnLeuThrAs 314
 QY 12839 ATTCCGATTAAGCATCTTA--GACTACTACCTCCAGATATATTAATGACTTAATG 12895
 Db 314 nIleValPheLeuHisLeuGlyAspAsnHisLeuGlnIlyProIleSerHisPheThrI 334
 QY 12896 TTTCGAAATGTTTCTTCAATTTCCCTGGTGAAGTGTGACTATTAAGAGGATAAAGACTT 12955
 Db 334 ePheGlnLysLeuLysArgLeuSerLeuValAsnAsnAsnPheAspGlyGlyLeuGlnPh 354

QY 12956 T-----TCTTAATATTTCCGATGGCAACATTTAGAATTA--GTTAACTTAATTTGACA 13009
 Db 354 eLeuSerPheAsnThrGlnLeuGlnArgLeuAspLeuSerSerAsnSerLeuThrGlyPr 374
 QY 13010 GTTTCACCA-----TTGAATCTCAATCTCTCAAAAGGCTTACTTCACTTCCAAACA 13063
 Db 374 oIleProSerAsnIleSerGlyLeuGlnAsnLeuGlnCysLeuTyLeuSerSerAsnHis 394
 QY 13064 A--GCTGGAATGCTTTTTCAGAAAGTT--GATCTACCAAGCCCTGAGTTTCTGATCT 13117
 Db 394 sLeuAsnLysSerIleProSerTyrIlePheSerLeuProSerLeuValGlnLeuAspLe 414
 QY 13118 CAGTAGAATGGCTTGAAGT----- 13136
 Db 414 uSerHisAsnThrPheSerGlyLysIleGlnGlnPheLysSerLysThrLeuSerAlaVa 434
 QY 13137 -----TTCAAGCTTGTCTTCAAAAGTATTTTGGACAAACAG 13177
 Db 434 lThrLeuLysGlnAsnLysLeuLysGlyArgIleProAsnSerLeuLeuAsnGlnLysAs 454
 QY 13178 CTTAAAGTATTAATGATCTGAGCTTCAATGGTGTATTT--ACCAAGACTTCAAACTTCTT 13234
 Db 454 nLeuGlnLeuLeuLeuLeuSerHisAsnAsnIleSerGlyHisIleSerSerAlaIleCy 474
 QY 13235 GGGCTTAGAACAACTAGAACACTTGGATTTCCAGACTTCAATTTGAAACAAATGAGTGA 13294
 Db 474 sAsnLeuLysThrLeuIleLeuLeuAspLeuGlySerHisAsnLeuGlnIlyThrIlePr 494
 QY 13295 GTTTTCAGTATTTCTATCATCTCAGAAACCTCATTTTACCTTGAATTTCTCATCTCAGAC 13354
 Db 494 oGlnCysValValGlnArgAsnGlnTyLeuSerHisLeuAspLeuSerLysAsnArgLe 514
 QY 13355 CAGAGTCTTCAATGAGCATCTTCAATGAGCTGTGCCAGTCTTCCAGACTTGAAGATGAGC 13414
 Db 514 uSerGlyThrIleAsnThrThrPheSerValGlyAsnIleLeuArgValIleSerLeuHis 534
 QY 13415 TGGCAATCTTTCACAGAAACCTTCAGATATCTTTCACAGAGCTGAGAACTTGAC 13474
 Db 534 sGlyAsnLysLeuThrGlyLys--ValProArgSerMetIleAsnCyLysTyLeuThr 553
 QY 13475 CTTCCTGGACCTCTCTCAGTGTCAACTGAGACAGTGTCTCCACAGACATTTAACTCACT 13534
 Db 553 rLeuLeuAspLeuGlyAsnAsnMetLeuAsnAspThrPheProAsnTyrLeuGlyTyLe 573
 QY 13535 CTCAAGTCTTCAAGTATTAATATGAGCCAAACAACATCTTTCATTGATGATACGTTCC 13594
 Db 573 uPheGlnLeuLysIleLeuSerLeuArgSerAsnLysLeuHisGly-----Pr 589
 QY 13595 TTATTAAGTGTGAAATCTC-----CTCAGAGTCTTGTATTAAGT- 13634
 Db 589 oIleLysSerSerGlyAsnThrAsnLeuPheMetGlyLeuGlnIleLeuAspLeuSerSe 609
 QY 13635 -----CTCAATGACATTAATGACTTCCAAAA 13660
 Db 609 rAsnGlyPheSerGlyAsnLeuProGlnArgIleLeuGlnLysAsnLeuGlnThrMetLysG 629
 QY 13661 A--CAGGACTACAGCAATTTTCCAGTATGCTTCACT----- 13694
 Db 629 uIleAspGlnSerThrGlyPheProGlnTyLysIleSerAspProTyAspIleTyTyAs 649
 QY 13694 ----- 13694
 Db 649 nTyLeuThrThrIleSerThrLysGlyGlnAspTyAspSerValArgIleLeuAspSe 669
 QY 13695 -----TTCTTAATCTTACTCAGAAATGACTTGTCTGTATCTTGTGAAC--CAGAG 13744
 Db 669 rAsnMetIleIleLeuAsnSerLysAsnArgPheGln-----GlyHisIleProSe 686
 QY 13745 TTTCCTGAAATGATCAAGACCAAGGACAGCTTGTGTGAAGTGAAGCAAGATGATG 13804
 Db 686 rIleIleGlyAspLeuValGlyLeuArgThrLeuAsnLeuSerHisAsnValLeuGlnG 706


```

Db      519  ArgThrPheThrProGln----- 524:
Qy      1364a ATATGACTTCCAAAAAACAAGAACTACAGCATTTTCCAGAGCTAGCTTCTTAAT 13703
Db      525  -----ProGlnGlyLeuGlnArgLeuTrp 532
Qy      13704 CTTACTCAGAAATGACTTGTCTTGTACTTGTGAACACGAGT----- 13745
Db      533  LeuGlnGlyAanProTrpAspCysSerCysProLeuGlySalLeuArgAspPheAlaLeu 552
Qy      13746 -----TTCTGCAATGATC-----AAGCACCAGAG 13772
Db      553  GlnAsnProSerAlaValProArgPheValGlnAlaIleCysGlnGlyAspAspCysGln 572
Qy      13773 CAGCTCTTGCTGGAAGTGAAGATGGAATGTGCAACCTTGAGATTAACAGGCGATG 13832
Db      573  ProProValIlyrThrTyraAsnAsnIleThrcysAlaSerProProGlnValAlaGlyLeu 592
Qy      13833 CCTGTGCTGAGTTTG 13847
Db      593  AspleuArgAspleu 597

RESULT 10
US-09-331-403-2
; Sequence 2, Application US/09331403
; Patent No. 6489147
;
; GENERAL INFORMATION:
;   APPLICANT: ALTMANN-JOHL, Regula, PHILIPPSEN, Peter; ALTHOFER,
;             Henning; SEULBERGER, Harald.
;   TITLE OF INVENTION: Adenylate cyclase gene, and its use
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;       ADDRESSER: Keil & Weinkauff
;       STREET: 1101 Connecticut Avenue
;       CITY: Washington
;       STATE: D.C.
;       COUNTRY: USA
;       ZIP: 20036
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
;   COMPUTER: IBM AT-compatible, Pentium III processor
;   OPERATING SYSTEM: Windows 95
;   SOFTWARE: Wordperfect version 6.1
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/09/331,403
;       FILING DATE: 21-Jun-1999
;       CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: PCT/EP97/07309
;           FILING DATE: 29-DEC-1997
;           INFORMATION FOR SEQ ID NO: 2:
;               SEQUENCE CHARACTERISTICS:
;                   LENGTH: 1874 amino acids
;                   TYPE: amino acid
;                   STRANDEDNESS: single
;                   TOPOLOGY: linear
;               SEQUENCE DESCRIPTION: SEQ ID NO: 2:
;               US-09-331-403-2

Alignment Scores:
Pred. No.:      2.92e-19      Length:      1874
Score:          267.00      Matches:      187
Percent Similarity: 37.74%      Conservative: 124
Best Local Similarity: 22.69%      Mismatches: 286
Query Match:      0.81%      Indels:      228
DB:              4          Gaps:      36

US-09-396-985B-47 (1-18989) x US-09-331-403-2 (1-1874)
Qy      11652 ACTGCGTCTATCACTGTGTACAGCATTTACTGTGATTAACAGAACTTTCAATATCT 11711
Db      462  ThrsrSerIleHtIsAlaGlnGluLeuGlnuAenAenAepIleGluAspAspLysLeuGln 481

11712  AGTGTCAATGAAACACTTTTTCATTAACATTAAGATATCTGTGCACTTATGTGTAATG 11771
482  His---HisLeuGlnuLySerTyTyraAsnHis----- 490
11772  TTTGATATCTCTGAAATGATATTATTTACAGTATT-----ATCTGGCTACCAAC 11822
491  -----PheSerAepIleAepTyHtIsLeuLySerThrIleArgIlePheAenThrAsp 508
11823  TAAACATATTCATTTATTTCTGTACCAATGATGATGATTAATCAACAATTTTGTGTGAC--- 11879
509  AspThrPheThrThrIleuSerCysArgProGlnuThrThrvAllysGluMetIleProGln 528
11880  ---AGAAATGCGCTAAATGATCCAGGCTATTAC----- 11912
529  IleArgGlySerPheAenValProProGlnAenTyHtGlnValSerLeuLysValGlyLys 548
11913  -----ATGCTTATTAACGTGCACAAATCTTAT 11939
549  LeuSerLysValLeuArgProThrvAlaLysProIleLeuIleGlnIle----- 564
11940  ATATGCAATTAATGATCTTTAATGATTTCCT----- 11972
565  ---ArgLeuLeuLeuPheAenGlyTyTyLysThrsArgLysAenIleMetGly 582
11973  -----TTTATGATTTTCTCCTGCTTATCATGATGATGCC 12008
583  IleGluAspleuSerPheValPheSerPheValPheHisProValIleThrSerGlnLeu 602
12009  TAAATGACAAAMAAAGACCTATATGTCAGCCAGTATGATATATCACTAGTGTGGGCG 12068
603  ThrvGlnGlnGlnGlnArgLeuSerLysGlyGluPheValHisValAspLeuArgAsn 622
12069  TTTCTTATTTGCTTATTCATCATCATCATCTGCTGCTGATGCTTGTGCTTATGACAAATC 12128
623  Met-AspleuThrvIlePro----- 628
12129  ATATGACCCATCATCTGTATGATGAAGAGCTGATGACTAGATTAATATTATTTTAGG 12188
629  -----ProIleIlePheTyHtGlnHisThrSerAspIleGlu----- 640
12189  TTTCTTATTCAGCAAMAAATATTATGATCAATGCTTTTATTTATTCCTGTAGT----- 12240
641  ---SerLeuAspValSerAenAenAlaAsnIlePheLeuProLeuAspPheIleG 658
12241  -----GTGAATCCAGACAATTGAAGATGGGCAATATCAGACCTA----- 12281
658  uSerValIleLysLeuSerSerLeuArgMetValAsnIleArgLaseArgPheProse 678
12282  -----AGCACCTCTTACCTTAATATTGACAGGAACCCATCCAGAG 12325
678  rAsnIleCysGlnuAlaThrvLysLeuIleThrLeuAspLeuGlnuArgAsnPheIleYrAsr 698
12326  TTTAGCCCTGGAGACCTTTTCTGTGACTATCAAGTTTACAGAAAGCTGTGGCTGTGAGAC 12385
698  gValPro-----AspGlnMetSerLysLeuThrsAenLeuThrvIleLeuAenLe 714
12386  AAATTCAGATCTCTAGAGAACTTCCCATTTGCA-----CATTCAAACTTTGAAGA 12439
714  uArgCysAenGlnuLeuAspArgLeuProArgGlyPheLysAspLeuLysSerLeuGlnLe 734
12440  ACTTAATGAGGCTCACATCTTATTCATATCTTTCAATTTCCGAGATTTTCTATCT 12499
734  uLeuAspIleSerSerAsnLysPheAenIleYr-----ProGlnuAlaIleAsnSerCy 752
12500  GACCAATCTAGAGACTTGTGACCTTTCCAGACAACAGATTCAAGATTATTTATTCACAGA 12559
752  sThrsAenLeuGlnuLeuAspLeuSerTyHtAsnLysIleArgSerLeu---ProAspse 771
12560  CTTGCGGCTTCTATCATCAAAATGCCCTACTCATCTCT----- 12599
771  rMetAsnGlnuGlnuLysLeuAlaLysIleAsnLeuSerAsnAsnArgIleThrvHisva 791

```


QY 12315 CCATCCAGATTAGCCCTGGAGCTTTCTGACATA----- 12353
 Db 110 ---ValleuAanleuThrluAanSerPheSerGlylleleProAanGluLeuGlyAs 128
 QY 12353 ----- 12353
 Db 129 LeuAArgleuLysArgleuSerleuLysGlnAanGlnleuLleSerSerlleProGlu 148
 QY 12354 -----TCAAGTTACAGAGCTGAGGCTGGTGGAGACAAATCTACACAT 12398
 Db 149 AlaLeuLysAerCythrSerleuAArgleuAanleuSerHisAanAanleuThrlGly 168
 QY 12399 CTAGAGACTTCCCATTCGACATCTCAAACTTTGAAAGAACTTAATGGCTGACACAT 12458
 Db 169 ThrleProSerGlyleuGlyGlnleuGlnAanleuGlnAanleuSerleuSerPheAan 188
 QY 12459 CTATCCAACTTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTG 12518
 Db 189 GlyleuThrlGly---LysValProGlnThrlPheGlyAanCySerAlaLeuGlnlleu 207
 QY 12519 GACCTTCCAGCAAC----- 12533
 Db 208 GlyleuGlySerAanPheleuSerGlyThrlleProSerHisleuGlyMetleuAlaArg 227
 QY 12534 ---AAGATTCAAGT----- 12548
 Db 228 lleLyslleleuSerleuGlyAArgAanGlnleuSerGlyGlylleProProSerleuLeu 247
 QY 12549 TATTCACACACTTGGGGTCTTACAT----- 12584
 Db 248 AasnCyThrGlnleuAArgGlyleuLysleuThrlGlnAanArgleuThrlGlnllePro 267
 QY 12584 ----- 12584
 Db 268 TrpGlnlleGlyAlaLysleuSerLyslleGlnThrlleuSerleuGlyGlyAanGlnleu 287
 QY 12585 -----CTACTCATCTCTCT-----TTAGCCCTGCTCC 12611
 Db 288 SerGlyGlylleProProSerleuLeuAanCyThrGlnleuSerGlnleuAanleuLys 307
 QY 12612 CTGAACCTTATGAACCTTATCAACCA-----GGTGCATTTAAAGAAATTAAGCTT 12662
 Db 308 GlnAanArgleuThrlGlnlleProTrpGlnlleGlyAla---LysleuSerLyslle 326
 QY 12663 CATAGCTGACTTTAAGAAATAT----- 12686
 Db 327 GlnThrlleuSerleuGlyGlyAanGlnleuSerGlyGlylleProProSerleuLeuAan 346
 QY 12687 -----TTGATAGTTTAAATGATGAATGAACCTTATTCAGAGCTGGCTGTTA 12737
 Db 347 CysThrlGlnleuSerGlnleuAanleuLysAanArgleuThrlGlnlleProTrp 366
 QY 12738 GAA-----GTCCATCGTTTGGTCTGGAGAAATTAAGAAATGA 12776
 Db 367 GlnlleGlyAlaLysleuSerLyslleGlnThrlleuSerleuGlyGlyAanGlnleuSer 386
 QY 12777 GGAACCTTGGAA-----AAGTTGACAA 12800
 Db 387 GlylleProProSerleuLeuAanCyThrGlnleuSerGlnleuGlnleuAanGln 406
 QY 12801 TCTGCTCTAGAGGCTGTGCAATTTGACATTAAGAAATTCGATTAAGCATAC----- 12854
 Db 407 AasnleuThrlGlyGlylleProGlnGlnlleGlyLysleuAArglleuGlnAanPheMet 426
 QY 12855 ---TTAGAC-----TACTACCTGATGATATTAATTAATTAATTAATTTGACA 12902
 Db 427 AasnleuAanPheAanHisleuLysSerGlnleuSerlleSerPhePheGlyAlaLeuSer 446
 QY 12903 AATGTTCTTCAATTTCCCTGCTGAGTGTGACTATTGAAGGGTAAAGAC----- 12953
 Db 447 AasnCyThrAanleuGlnMetleuSerleuSerAanPheLysGlyAanPheLysPro 466

QY 12954 -----TTTCTTAATAATTCGATGCAACATTAAGATTAGTAACTGT 12998
 Db 467 GlySerlleAanPheAanSerGlnAanleu-----leuThrlleuThrlleuGlyLysAan 484
 QY 12999 AATTT---GGACAGTTTCC-----ACATTGAAACTCAAAATCTCAAAAGCTTACT 13049
 Db 485 ArgPheThrlGlyLyslleProGlnGlnMetSerAanleuThrlGlyleuLleleuAanPhe 504
 QY 13050 TTCACTTCCAAC-----AAGGTGGGAATCTTTTTCAGAAAGTTGATCTCAACAGCTT 13103
 Db 505 LeuAanAanPheAanleuLeuSerGlyGlyleuProSerAlaLeuGlyAArgleuSerAlaLeu 524
 QY 13104 GAGTTTCTAGACTCTCAGTAGAATAAGCTTG----- 13133
 Db 525 GlnlleAanleuPheleuSerAArgAanAanleuGlnlleAanlleProCyGlnPheSerGln 544
 QY 13134 -----AGTTTCAAAAGTTGCTGTTCTCA 13157
 Db 545 LeuLysAArgleuThrlAlaLeuGlnleuThrlGlnAanAlaPheSerGlyGlnlleGln 564
 QY 13158 AGTATTTTGGAGACACACAGCTTAAGTATTTAGTCTGAGCTTCAATGCTTATTT--- 13214
 Db 565 ValPheAlaSerleuGlnGlnleuAArgleuAanPheleuSerLysAanLysPheSerGly 584
 QY 13215 ACCATGATTTCAAACTTCTTGGGC---TTAGAACACTAGAACATCTGATTTCCAGCAT 13271
 Db 585 AasnleProAanAanAanPheGlyAanCySerAanleuGlnleuAanPheleuSerLys 604
 QY 13272 TCCAAATTTGAAACAAATGAGTGAAGTTTCAATTTCTATGACTCAAGAACTTC---ATT 13328
 Db 605 AasnGlnleuSerGlyleuMetSerTrpLysAla---AlaSerleuHisAanleuGlnPhe 623
 QY 13329 TACCTTGACATTTTCTTACTACACACAGAGTCTTCAATGAGCATTTCAAGGCTTG 13388
 Db 624 TyrlleAanValSerHisAanAlaLeuThrlAArgValProAlaGlnleuGlyMet 643
 QY 13389 TCCAGTCTGCAAGCTTGAAGAAATGCTGCAATCTTCCAGAAACTCTTCCAGAT 13448
 Db 644 HisMetValGlnAlaIleAanPheleuSerAlaAanAanPheleuSerGlySer---lleProGly 662
 QY 13449 ATCTTCAACAGAGCTGAGAACTTGACCTTCTGAGCTCTTCTGAGTCACTGAGACAG 13508
 Db 663 GlnleuValAanCyAAlaGlnleuAanPheLysleuAanleuSerHisAanSerleuGlnGly 682
 QY 13509 TTGCTTCAACAGAGATTTAACTACTCTCCAGTCTTCAAGTACTTAATATGACACAAAC 13568
 Db 683 ThrleProThrlleuSerlleAanPheGlnValAlaGlyleuGlnAanPheleuSerPheAan 702
 QY 13569 AACTTCTTTTCA---TTGATAGCTTCTTATTAAGTGTGAACTCCCTCCAGGTTCTT 13625
 Db 703 LysleuSerGlyProleuProThr-----SerlleGlnLysleu 715
 QY 13626 GATTACAGTCTCAATCAATATGACTTCCAAAAACAGAACTACAGCAATTTTCCAAGT 13685
 Db 716 Gln---LysleuThrlHisleuAanleuSerLysAanAanPheThrlGlnlleProSer 734
 QY 13686 AGCTTACCTTTC---TTAATCTTACTCAGAAATGACTTTGCTTACTTGTGAACAC 13739
 Db 735 SerGlyAlaPheAArglyleuAanleuThr----- 744
 QY 13740 CAGAGTTTCTG---CAATGATCAAGACACAGAGCAGACTC 13778
 Db 745 ---SerPheleuGlyAanSerGlyleuCyGlyAArgTrpLle----- 757
 QY 13779 TTGGTGAAGTTGAACCAATGAGATGCAACA-----CCTTCAAGTAAACAGAGGC 13829
 Db 758 -----GlnleuProHisCyAlysleuThrlThrlAArgHisHisAanPheSerLysAArg 775
 QY 13830 ATGCTGTGCTGAGTTTGAATATCACTGTCAAGATGATATGACCATATGCTGTGCTGC 13889
 Db 776 ValVallleleuAla-----ThrlSerValGlyleuThr 786
 QY 13890 GTCCCTCAGTGTGCTTATGATGATCTGTTGACAGTTCTGTCTAT 13934


```

QY 13818 GATAGACGAGCATGCTCT----- 13835
Db 545 ProglyProphelysProCygluH1sleuLeuamerglyTrpLeuIleargIleglyVal 564
QY 13836 -----GTCTGAGTTGTAATATCACTGTGCAGATGAATTAAGACCATATTGGTGTGCG 13889
Db 565 TrpThrIleValaIleValaLeuThrCys-----AsnAlaIleValThrSerThrVal 582
QY 13890 GTCTCGAGTGTGCTGTGATATCTGTGTAGACAGTTCGTGCTTAATCTATTATTTCAC 13949
Db 583 PheArgSerProLeuTyrlleSerProIleLysLeuLeuIleGlyValIleAlaIleVal 602
QY 13950 CTGATGCTT-----CTTGCTGCTGTCAATTAAGTAT----- 13979
Db 603 AsnIleLeuThrGlyValaSerSerAlaValaLeuIleGlyValaLeuAlaPheThrPheGly 622
QY 13980 -----GCTAGAGGTGAACATCTATGATGCC 14006
Db 623 SerPheAlaArgH1sGlyAlaTrpTrpGluAsnGlyValaGlyCysH1sValaIleGlyPhe 642
QY 14007 TTTGTATCTACTGACGACGAGATGAGACCTGGGTAAGATGAGCTGTAAAGATTTA 14066
Db 643 LeuSerIlePheAlaSerGluSerSerValaPheLeuLeuThr-----LeuAlaIleLeu 660
QY 14067 GAAGAAGGGG---TGCTCTCATTTGAGCTGTGCTTCACTACAGACATTTATTCGCGT 14123
Db 661 GluArgGlyPheSerValaIlySerAlaIlyPheGluThrIlySala----- 676
QY 14124 GTGGCCATTGCTGCCACATCATTCATGAGGTTTCCATTAAGCCGAAGGTGATTTGT 14183
Db 677 -----ProPheSerSerLeuIlyValIleIle-----Leu 686
QY 14184 GTGGTGTCCACGACCTTATCCAGACCGCTGGTATCTTTG 14226
Db 686 uLeuCysAlaLeuLeuAlaLeuThrMetValaIleValaProLeu 700

RESULT 13
US-09-170-496D-278
; Sequence 278, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339- Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 278
; LENGTH: 907
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-278

Alignment Scores:
Pred. No.: 5,21e-19 Length: 907
Score: 262.50 Matches: 172
Percent Similarity: 38.10% Conservative: 108
Best Local Similarity: 23.40% Mismatches: 249
Query Match: 0.79% Indels: 206
Db: 4 Gaps: 33

US-09-396-985b-47 (1-18989) x US-09-170-496D-278 (1-907)
QY 12276 AGCCTAACCCACCTCTACTTATATATGACAGAAACCCATCCAGATTAGCCTG 12335
Db 88 SerLeuArgPheLeuGluGluLeuArgLeuAlaGlyAsnAlaLeuThrTyrlleProlys 107
QY 12336 GGAGCTTTCTGACATCAAGTTTACAGAAAGCTGTGTGAGACAAATCTATGAC 12395

```

```

Db 108 GlyAlaPheThrGlyLeuTyrlSerLeuIlyValaLeuMetLeuGlnAsnGlnLeuArg 127
QY 12396 TCCTTAGAGAACTTCCCATTTGACATCTGAAAATTGAAAGAACTTAATGGCTTAC 12455
Db 128 HisValProThrGluAlaLeuGlnAsnLeuArgSerLeuGlnSerLeuAlaGlyLeuAspAla 147
QY 12456 AATCTTAATCCAACTTTCAATTAATTAAGTATTTTCTAATCTGACCAATTAAGACAC 12515
Db 148 AsnIleIle---SerTyrlValProProSerCysPheSerGlyLeuH1sSerLeuArgH1s 166
QY 12516 TTGACCTTTCCAGCAACAAAGATTAAGTATTTATTTGACACAGCTTGGGTTCTATC 12575
Db 167 LeuTrpLeuAspAsnAlaLeuThrGluIleProValGlnAlaPheArgSerLeuSer 186
QY 12576 CAATGGCCCTTACATCTCTCTTAGACCTGCTGCAACCTTGAATTTATGCCAA 12635
Db 187 AlaLeuGln-----AlaMetThrLeuAlaLeuAsnIlyIleH1sIlePro 202
QY 12636 CCAGTGCATTTTAAGAAATTT---AGGCTTCATAGCTGACTTTAAGAAATTAAT---TTT 12689
Db 203 AspTyrlAlaPheGlyAsnLeuSerSerLeuValaLeuH1sLeuH1sAsnAsnArgIle 222
QY 12690 GATAGTTTAATGTAATGAATACTGTATTCAGCTGTGCTGTGTTAAGATGCCATCGT 12749
Db 223 HisSerLeuGly-----LysLysCysPheAspGlyLeuH1sSerLeuGluThrLeuAsp 240
QY 12750 TTGGTTTCTGGAGAAATTGAAGAAAGAAAGTGAAGAAAGTTGACAAATCTGCTCTA 12809
Db 241 Leu-----AsnTyrlAsnAsnLeuAspGlyPhe---ProThrAlaIle 253
QY 12810 GAGGCGCTGTGCAATTTGACCATTTGAAGAAATTCGATAGCATTTAGACTACTGCTC 12869
Db 254 ArgThrLeuSerAsn-----LeuLysGluLeuGlyPheH1sSer 266
QY 12870 GATGATATATTTAGCTTA-----TTTAATGTTTGACAAATGTTTCTCATTT 12917
Db 267 AsnAsnIleArgSerIleProGluIlyAlaPhe-----ValGlyAsnPro 281
QY 12918 TCCCTGTGAGCTGAGCATTT---GAAAGGTAAAGACTTTTCTTAATTTGGAGATCG 12974
Db 282 SerLeuIleThrIleH1sPheTyrlAspAsnProIleGlnPheValaGlyArgSerAlaPhe 301
QY 12975 CAACATTTAGAAATTAAGTAACTGTAAATTTGACAGCTTTCCCACTGAAATCAAAATCT 13034
Db 302 GlnH1sLeuPro-----GluLeuArgThrLeuThrLeuAsnGly 314
QY 13035 CTCAAAAGGCTTACTTCACTTCCAAACAAAGGTGGAAATGCTTTTTCAGAAATTGACTA 13094
Db 315 AlaSerGlnIleThr----- 319
QY 13095 CCAAGCTTGAAGTTTCTAGATCTTCAGTAGAAATGGCTTGAAGTTTCAAGTTGCTGTCT 13154
Db 320 -----GluPheProAspLeuThr----- 325
QY 13155 CAAAGTATTTTGGGACACACAGCTTAAGATTTAGATCTGAGCTTCAATGATGTTATT 13214
Db 326 -----GlyThrAlaAsnLeuGlnSerLeuThrLeuThrGlyAlaGlnIleSer 341
QY 13215 ACCATGAGTTCAAACTTCTGGGC---TTAGAACATAGAACATCTGAGATTTCCAGCAT 13271
Db 342 SerLeuProGlnThrValaCysAsnGlnLeuProAsnLeuGlnValaLeuAspLeuSerTyrl 361
QY 13272 TCCAAATTTGAACAAAGAGAGTCTTTCAGTATCTTCATATCTCAAGAAACCTCATTTAC 13331
Db 362 AsnLeuLeuGlnAspLeuProSerPheSerValaCysGlnLysLeuGlnLys----- 378
QY 13332 CTTGACATTTCTCATCTACACACAGAGTGTCTTCAATGACATCTTCAAGCTGTGCC 13391
Db 379 IleAspLeuArgH1s-----AsnGluIleTyrl 387
QY 13392 AGTCTGCAAGTCTTGAAGATGGCTGCAATTTCTTTCAGAGAAACTTCTTCCAGATATC 13451
Db 388 GluIleLysVal-----AspThr 393

```

[illegible]

```

1 GENERAL INFORMATION:
2 APPLICANT: Mochly-Rosen, Daria
3 APPLICANT: Ron, Dorit
4 TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
5 TITLE OF INVENTION: Thereof
6 NUMBER OF SEQUENCES: 265
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Dehlinger & Associates
9 STREET: P.O. Box 60850
10 CITY: Palo Alto
11 STATE: CA
12 COUNTRY: USA
13 ZIP: 94306-0850
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: PatentIn Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/06/190,802A
22 FILING DATE: 01-FEB-1994
23 CLASSIFICATION: 530
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Fabian, Gary R.
26 REGISTRATION NUMBER: 33,875
27 REFERENCE/DOCKET NUMBER: 8600-0139
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (415) 324-0880
30 TELEFAX: (415) 324-0960
31 INFORMATION FOR SEQ ID NO: 49:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 605 amino acids
34 TYPE: amino acid
35 TOPOLOGY: unknown
36 MOLECULE TYPE: protein
37 HYPOTHEetical: NO
38 ANTI-SENSE: NO
39 ORIGINAL SOURCE:
40 INDIVIDUAL ISOLATE: Insulin-like growth factor binding
41 INDIVIDUAL ISOLATE: protein complex, Fig. 32
42
43 US-08-190-802A-49
44
45 Alignment Scores:
46 Pred. No.: 1.2e-18 Length: 605
47 Score: 258.00 Matches: 139
48 Percent Similarity: 39.16% Conservative: 85
49 Best local Similarity: 24.30% Mismatches: 220
50 Query Match: 0.78% Indels: 128
51 DB: 1 Gaps: 23
52
53 US-09-396-985B-47 (1-18989) x US-08-190-802A-49 (1-605)
54
55 QY 12237 AGGNGTGAATTCGACGACAAATTGAAAGATGGGCGATATCAAGGCGTAAAGCCACTCTCTAC 122966
56   ||| :::::::::::::::::::: ||| ::| |:::|
57 Db 131 ArgpanginleuaurgerleuvalaleuglyThrPheAlaHisThrProAlaIeuAlaSer 150
58
59 QY 12297 TTAATATTGACAGAAAACCCCATCCAGAGTTTAAAGCCCTGGAGCCTTTTCTGAGATATCA 123566
60   ||| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
61 Db 151 leuglyleuSerhshnshnhrghleuSerArgleuGluaspGlyleuPheGluGlyleuGly 170
62
63 QY 12357 AGTTTACAGAACTGGTGGCTGTGGAGACAAATCTTGCAATCTCTAGAGAACTTCCCATTT 124166
64   ||| ||| ||| ||| ||| ::| ||| ||| ||| ::|
65 Db 171 SerleuThrpsrleuasnleuGlyTyrPasnSerleuAlaValleuProaspAlaIaphe 190
66
67 QY 12417 GGAATCTCAAAACTTTGAAAGAACTTAATGAGCGTCAACAATCTTAATCCAATCTTCAAA 124766
68   ||| ||| ::| ||| ||| ||| ||| ||| ||| ||| |||
69 Db 191 ArgglyleuGlySerleuAspGluIeuValleuAlaGlyAsnArgleu--AlaTyrIeu 209
70
71 QY 12477 TTAAGTGAATTTTCTAATCTGACCAATCTTAGAGCACTTGGAGCCTTTCCAGACAAG 125366
72   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
73 Db 210 GlmProAlaIeuTheserGlyleuAlaGluIeuAspGluIeuAspIeuSerArgshnAla 229
74
75 QY 12537 ATTCAAGATATTAATGACAGACTTGGGGTTTCAATCAATCAAAATGCCCTCAATCTCATCTC 125966

```

```

Db      230 LeuArgAlaIle-----LysAlaAsnValPheValGlnLeuProArgLeuGln--- 245
Qy      12597 TCCTTAGACCTGTCCCTGACCCATGAACTTTATCCAAACGAGGTCATTAAGAAT 12656
Db      246 LysLeuTyrLeuAspArgAsnLeuLeuAlaValAlaProGlyAlaPheLeuGlyLeu 265
Qy      12657 AGG---CTTCATTAAGCTGACTTTTAAAGAAATATTTGATGTTTAATGTAAGAACT 12713
Db      266 LysAlaLeuArgTyrPheAspLeuSerHisAsn---ArgValAlaGlyLeuLeuGlnAsp 284
Qy      12714 TGATTTCAAGCTCTGCGCTGTTTGAAGTCCATGCTTTGCTTGGGAAATTTAGAAAT 12773
Db      285 ThrPheProGlyLeuLeuGlyLeuArgValLeuArgLeu----- 297
Qy      12774 GAAGAAACTTGAAAAAGTTTGACAAATCTGCTCAGAGGCGCTGTGCATTTGACCAT 12833
Db      298 -----SerHisAsnAlaIleAsnSerLeuArgProArgThrPhe 310
Qy      12834 GAAGAAATTCGATTAGCATACTAGTACTACCTCGATGATATTAATGACTTATTTAAT 12893
Db      311 LysAspLeu-----HisPheLeuGlnGlnLeu----- 319
Qy      12894 TGTTTGACAAATGTTTCTTCAATTTCCCTGCTGAGTGTGACTATTGAAAAGGTAAAGAC 12953
Db      320 -----GlnLeuGlnHisAsnArgIleArgGlnLeuAlaGln 331
Qy      12954 TTTTCTTAATATTCGATGCGCAACTTTAGAAATTAAGTAACTGTAATTTGACAGTTT 13013
Db      332 ArgSerPheGln---GlyLeuGlnGlnLeuGlnValLeuThrLeuAspHisAsnGlnLeu 350
Qy      13014 CCCCATTTGAAGAACTCAATCTCTCAAAAGGCTTACTTCTTCACTTCC-----AACAAAGT 13067
Db      351 GlnGlnVallysalaglyAlaPheLeuGlyLeuThrAsnValAlaValMetAsnLeuSer 370
Qy      13068 GGGAAATGCTTTTTCAGAAATGATCTACCAAGCCTTGAGTTTCAGATCTCAGTAGA--- 13124
Db      371 GlyAsnGlyLeuArg-----AsnLeuProGlnGlnValPheArgGlyLeuGlyLeu 388
Qy      13125 AATGCTTGAATTCAAAGTTGCTGT-----TCTCAAAGTGAATTTGGG 13169
Db      389 HisSerLeuHisLeuGlnGlySerCysLeuGlnValArgIleArgProHisPheThrGly 408
Qy      13170 ACAACGACCCTAAGATTTTATGATCTGAGTTCATGAGTGTATTTACCATGAGTTCAAC 13229
Db      409 LeuSerGlyLeuArgLeuPheLeuHisAspAsnGlyLeuValGlyIleGlnGln 428
Qy      13230 TTCTTG---GGCTTAGAACCACTAGAACATCTGATTTCCAGCATTTCCAAATTTGAAACA 13286
Db      429 SerLeuTyrGlyLeuAlaGlnLeuLeuGlnLeuAspLeuThrSerAsnGlnLeu----- 446
Qy      13287 ATGATGATGTTTCAGATTTCTTACTCACTCAAAACCTCATTTTACCTTGACATTTTCAT 13346
Db      446 ----- 446
Qy      13347 ACTCACACAGAGTTGCTTTCATGAGCATTTCAATGAGCTTGTCCAGTCTGAAAGTCTG 13406
Db      447 ThrHisLeuPro-----HisArgLeuPheGlnGlyLeuGlyLysLeuGlnTyrLeu 463
Qy      13407 AAAATGCTGCGCAATTTCTTCCAGAAAATCTTCTTCCA---GATATCTTCCAGAGCTG 13463
Db      464 LeuLeuSerArgAsnArgLeuAlaGln-----LeuProAlaAspAlaLeuGlyProLeu 481
Qy      13464 AGAACTTGACCTTCTCTGACCTCTCTCAGTGTCACTGAGCAGCTGTCTCCAAACGCA 13523
Db      482 GlnArgAlaPheTyrPheLeuValSerHisAsnArgLeuGlnAlaLeuProAsnSerLeu 501
Qy      13524 TTTAATCACTCTCAGTCTTCAAGTACTAATATGAGCCACAACTTCTTTCATTTG 13583
Db      502 LeuAlaProLeuGlnArgLeuArgTyrLeuSerLeuArgAsnAsn-----SerLeu 518
Qy      13584 GATACGTTTCTTAAAGTGTCTGAACCTCCCTCAGGTTCTTGATTAACAGTCAATCAC 13643

```

```

Db      519 ArgThrPheThrProGln----- 524
Qy      13644 ATAAATGACTTCCAAAAAAGAGAACTACAGACATTTTCCAAAGTACTAGTCTTAAAT 13703
Db      525 -----ProProGlyLeuGlnArgLeuTyr 532
Qy      13704 CTTACTCAGAAATGACTTTGCTTGTACTGTGAACACAGAGTTTCTGCATGATGACAG 13763
Db      533 LeuGlnGlyLeuAsnProTyrPheArgCysGlyCysPro-----LeuLysAlaLeuArg 548
Qy      13764 GAC-----CAGAGCAGCTCTTGTGTGGAAGTTGAACGA 13796
Db      549 AspPheAlaLeuGlnAsnProSerAlaValProArgPheValGlnAlaIleCysGlnGly 568
Qy      13797 ATGGAATGTGCAACCTTCAGATCAATTAAGCAGGCAATGCTGTGCTGAGTTGAATATCAC 13856
Db      569 AspAspCysGlnProProAlaTyrThrTyrAsn-----AsnIleThr 582
Qy      13857 TGTCAGATGAATAGAACATCATTTGCTGTGTGCTC 13892
Db      583 CysAlaSerProProGlnValValGlyLeuAspLeu 594

RESULT 15
US-08-477-346-49
: Sequence 49, Application US/08477346
: Patent No. 6262023
: GENERAL INFORMATION:
: APPLICANT: Mochly-Rosen, Daria
: APPLICANT: Ron, Dorit
: TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
: TITLE OF INVENTION: Theof
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morrison & Foerster
: STREET: 2000 Pennsylvania Avenue, NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/477,346
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/487,072
: FILING DATE: 07-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 2550-0025.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: INFORMATION FOR SEQ ID NO: 49:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 605 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Insulin-like growth factor binding
: INDIVIDUAL ISOLATE: protein complex, Fig. 32
US-08-477-346-49

Alignment Scores: 1.2e-18 Length: 605
Pred. No.:

```

Score: 258.00 Matches: 139
Percent Similarity: 39.16% Conservative: 85
Best Local Similarity: 24.30% Mismatches: 220
Query Match: 0.78% Indels: 128
DB: 3 Gaps: 23

US-09-396-985b-47 (1-18989) x US-08-477-346-49 (1-605)

QY 12237 AGGCTGAATTCAGATTAAGATGGGGGAGGAGCTTACGAGCTTACCTTACC 12296
DB 131 ArgSngInLeuArgSerLeuAlaLeuGlyThrPheAlaHisThrProAlaLeuAlaSer 150
QY 12297 TTAATATTGACAGAAACCCATCCAGATTACCCCTGGAGCCCTTTTCTGACATCA 12356
DB 151 LeuGlyLeuSerHisAsnArgLeuSerArgLeuAlaSerGlyLeuPheGluGlyLeuGly 170
QY 12357 AGTTTACAGAGCTGGCTGGCTGGAGACAAATCTAGCATCTCTAGAAACCTTCCCAT 12416
DB 171 SerLeuThrAspLeuAsnLeuGlyTyrAsnSerLeuAlaValLeuProAspAlaAlaPhe 190
QY 12417 GGCATCTCAAACTTTGAAAGACTTAATGCTGCTCAACATCTTATCCATCTTTGAAA 12476
DB 191 ArgGlyLeuGlySerLeuArgGlnLeuValLeuAlaGlyAsnArgLeu--AlaTyrLeu 209
QY 12477 TTAACCTGAGTATTTTCTTAATCTGACCAATCTAGAGACTTGGACCTTTCAGACAAAG 12536
DB 210 GlnProAlaLeuPheSerGlyLeuAlaGlnLeuArgGlyLeuAspLeuSerArgAsnAla 229
QY 12537 ATTCAAAGTATTTATTTGACAGACTTGGGGTCTCAATCAATGCCCTTACTCAATCTC 12596
DB 230 LeuArgAlaIle-----LysAlaAsnValPheValGlnLeuProArgLeuGln--- 245
QY 12597 TCTTTAAGCTCGTCCCTGAAACCCATAGAACTTTATCCAAACGAGGTGATTAAGAAATT 12656
DB 246 LysLeuTyrLeuAspArgAsnLeuIleAlaValAlaProGlyAlaPheLeuGlyLeu 265
QY 12657 AGG---CTTCATTAAGCTGACTTTAAGAAATTAATTTGATAGTTTAAATGTAATGAAACT 12713
DB 266 LysAlaLeuArgTyrPheLeuAspLeuSerHisAsn---ArgValAlaGlyLeuGlnAsp 284
QY 12714 TGTATTCAGGCTCGGCTGGCTTTGAAAGCTCATGCTTTGGCTTGGAGAAATTTAGAAAT 12773
DB 285 ThrPheProGlyLeuLeuGlyLeuArgValLeuArgLeu----- 297
QY 12774 GAAAGAAACTTGGAAAGTTTGACAAATCTGCTCAGAGGGCTGTGCAATTGACCAT 12833
DB 298 -----SerHisAsnAlaIleAsnSerLeuArgProArgThrPhe 310
QY 12834 GAAAGAAATCCGATTAAGCATTAAGTACTTACTTCCGATGATTAATTTGATTTTAAT 12893
DB 311 LysAspLeu-----HisPheLeuGluGlnLeu----- 319
QY 12894 TGTTTGACAAATGTTTCTTCAATTTTCCCTGGTAGTGACTTATGAAAGGGTAAAGAC 12953
DB 320 -----GlnLeuGlyHisAsnArgGlyLeuArgGlnLeuAlaGln 331
QY 12954 TTTTCTATATTTCCGATGCGCAACATTTAGATTAGTTACTGTAAATTTGACAGTTT 13013
DB 332 ArgSerPheGlu--GlyLeuGlyGlnLeuGlnValLeuThrLeuAspHisAsnGlnLeu 350
QY 13014 CCCCATTTGAAACTCAATCTCTCAAAAAGCTTACTTCACTTCC-----ACAAAAGT 13067
DB 351 GlnGlnValValLysAlaGlyAlaPheLeuGlyLeuThrAsnValAlaValMetAsnLeuSer 370
QY 13068 GGGAAATCTTTTTCAGAAAGTATCTACCAAGCTTGAATTTCTAGATCTCAGTAGA-- 13124
DB 371 GlyAsnCySerLeuArg-----AsnLeuProGlnGlnValPheArgGlyLeuGlyLysLeu 388
QY 13125 AATGCTTGAATTTCAAAAGTTGCTCT-----TCTCAAAAGTATTTGGG 13169
DB 389 HisSerLeuHisLeuGlnGlySerCySerLeuGlyArgIleArgProHisThrPheThrGly 408
QY 13170 ACAACGAGCTTAAAGTATTTAGATCTGCTTCAATGGTGTATTTACCATGAGTTCAAC 13229

DB 409 LeuSerGlyLeuArgArgLeuPheLeuLysAspAsnGlyLeuValGlyIleGluGln 428
QY 13230 TTCTTG---GGCTTAAACAACATCTGAAATCTTGATTTCCAGATTTCCAAATTTGAAACAA 13286
DB 429 SerLeuTyrGlyLeuAlaGlnLeuLeuGlyLeuAspLeuThrSerAsnGlnLeu----- 446
QY 13287 ATGATGATGTTTCAATATCTTATCATCTCAGAAACCTCATTTTACCTTGACATTTCTCAT 13346
DB 446 ----- 446
QY 13347 ACTCACACAGAGTTGCTTTCATATGCAATCTTCAATGCTTGTCCAGTCTCCAAAGCTTG 13406
DB 447 ThrHisLeuPro-----HisArgLeuPheGlnGlyLeuGlyLysLeuGlnTyrLeu 463
QY 13407 AAAATGGCTGGCAATCTTTCCAGGAAACCTTCCCA---GATPACTTTCACAGAGCTG 13463
DB 464 LeuLeuSerArgAsnArgLeuAlaGln-----LeuProAlaAspAlaLeuGlyProLeu 481
QY 13464 AGAACTTGACCTTCTCTGGACCTCTCTCAGTGTCAACTGAGCAGTTGTCTCCAAAGCA 13523
DB 482 GlnArgAlaPheThrLeuAspValSerHisAsnArgLeuGlnAlaLeuProAsnSerLeu 501
QY 13524 TTTAAGTCTCTCCAGTCTTTCAGGTACTTAATATGACCAACAACATTTCTTTGATTG 13583
DB 502 LeuAlaProLeuGlyArgLeuArgTyrLeuSerLeuArgAsnAsn-----SerLeu 518
QY 13584 GATACGTTTCCTTAATAGTGTCTGAATCCTCCAGTCTTGATTTACAGTCTCAATCAC 13643
DB 519 ArgThrPheThrProGln----- 524
QY 13644 ATATGACTTCCAAAAACAGAACTACAGATTTTCCAAAGTACTGATCTTATTAAT 13703
DB 525 -----ProProGlyLeuGlnArgLeuTyr 532
QY 13704 CTTACTCAGAAATGACTTGTGCTTGTACTTGTGAACACCAAGATTCTCGCAATGATCAAG 13763
DB 533 LeuGlnGlyAsnProTyrAspCySerGlyCyPro-----LeuYsAlaLeuArg 548
QY 13764 GAC-----CAGAGGAGCTCTTGGTGAAGTTGAAAGCA 13796
DB 549 AspPheAlaLeuGlnAsnProSerAlaValProArgPheValGlnAlaIleCySerGlnGly 568
QY 13797 ATGAAATGTCAACACCTTTCAGATTAAGCAGGCGCATGCTGTGAGTTTGAATATCAC 13856
DB 569 AspAspCySerGlnProProAlaTyrThrTyrAsn-----AsnIleThr 582
QY 13857 TGTCAATGAATTAAGACATCATTTGTTGTGTGCGTC 13892
DB 583 CyAlaSerProProGlnValValGlyLeuAspLeu 594

Search completed: March 29, 2005, 19:53:21
Job time : 437 secs

1	563.5	1.7	661	2	I56258	RPI05 - mouse
2	474	1.4	786	2	T08664	Toll protein-like
3	441	1.3	1097	2	A29943	Toll protein precu
4	389	1.2	1389	2	T13852	gene wheeler prote
5	377	1.1	1385	2	T13887	tlr protein - frui
6	360	1.1	1280	2	B34087	hypothetical pro
7	355	1.1	712	2	S23650	retrovirus-related
8	348	1.1	1066	2	T15864	hypothetical prote
9	347	1.0	1275	2	S65824	reverse transcript
10	346.5	1.0	275	2	S21348	probable pol poly
11	345	1.0	1275	2	T13858	reverse transcript
12	344	1.0	1275	2	B28096	line-1 protein ORF
13	338	1.0	1259	4	GNNUJ1	retrovirus-related
14	333.5	1.0	1281	1	GNNSLD	retrovirus-related

15	323.5	1.0	1260	4	GNRRL	retrovirus-related
16	320.5	1.0	1134	1	A29344	haoptin precursor
17	310	0.9	603	2	T23115	hypothetical prote
18	287.5	0.9	1112	2	T10504	disease resistance
19	286	0.9	853	2	T17461	disease resistance
20	285.5	0.9	994	2	H96510	probable disease r
21	284	0.9	622	2	JC7973	synlaurin - human
22	282	0.9	855	2	T07015	Cf-44 protein - to
23	278	0.8	855	2	T17460	disease resistance
24	278	0.8	151	2	T42218	slit-1 protein hom
25	276.5	0.8	768	2	T17462	disease resistance
26	276	0.8	845	2	T07039	Hor9-0 protein - t
27	272.5	0.8	143	2	E41925	hypothetical prote
28	271	0.8	1143	2	T10636	hypothetical prote
29	270.5	0.8	890	2	T00800	disease resistance
30	269	0.8	1027	2	B85089	receptor protein k
31	267.5	0.8	863	2	A55173	ci-9 protein precu
32	267	0.8	605	2	JC5239	insulin-like growt
33	266.5	0.8	1019	2	C96519	probable disease r
34	262.5	0.8	907	2	JE0176	orphan G protein-c
35	262.5	0.8	1051	2	T31174	gp150 protein - fr
36	260	0.8	1134	2	T04597	hypothetical prote
37	259	0.8	907	2	JG0193	G protein-coupled
38	258	0.8	605	2	A41915	insulin-like growt
39	256.5	0.8	1784	2	C96615	hypothetical prote
40	256.5	0.8	1839	1	OYBYK	adenylate cyclase
41	254	0.8	771	2	T02565	disease resistance
42	254	0.8	910	2	G84648	probable disease r
43	253	0.8	890	2	C96654	hypothetical prote
44	253	0.8	983	2	H48524	probable disease r
45	251.5	0.8	603	2	JC1282	insulin-like growt

ALIGNMENTS

```

RESULT 1.
156258
RP105 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: 156258
R:Milvake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
J. Immunol. 154, 3333-3340, 1995
A:Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a m
A:Reference number: 156258; MUID:95204928; PMID:7897216
A:Accession: 156258
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-661 <RES>
A:Cross-references: UNIPROT:Q62192; GB:ID37797; NID:9761711; PTDN:BA07043.1; PTD:9761711

```

Alignment Scores:
Pred. No.:

Pred. No.:	1.7e-38	Length:	6
Score:	563.50	Matches:	1
Percent Similarity:	44.91%	Conservative:	1
Best local Similarity:	27.86%	Mismatches:	2
Query Match:	1.70%	Indels:	5
DB:	2	Gaps:	1

US-09-396-985B-47 x I56258 (1-661)

QY 12171 TTAATATTCATTTAGGTCCTA-----TTCAGCAGAATATT 12205

Db 58 LeuGluPhseSerPheAsnValLeuProThrIleGlnAsnThrThrPheSerArgLeuIle 77

12Z10 AHAHAI CAHIGLII IHIIC--IGAGIGI GHAHICAGAHCAHI IGAHGHIGG 12

[illegible][illegible]

QY	12327	TTAGCCCTGGGAGGCTTTTTCGACATTCAGAGTTTACAGAAAGTGGTGGCTGGAGACA	12386
Db	116	MetAlaGluThrAlaLeuSerGlyProGlyAlaLeuLysHisLeuPhePheIleGlnThr	135
QY	12387	AATCGACATCTCGAGGAAGCTTCCCATTTGGACATCTCAAAAGCTTTGAAAGACTTAT	12446
Db	136	GlyIleSerSerIleAspPheIleProLeuHisAsnGlnLysThrLeuGluSerLeuYr	155
QY	12447	GGGCGTCAACATCTTATTCACATCTTTCCAAATTACCTGAGATTTTTCATCTGACAAAT	12506
Db	156	LeuGlySerAsnHisIleIleSerSerIleLeuLeuProGlyGlyPheProThr---GluLys	174
QY	12507	CTAAGACACTTGGACCTTTCCAGCAGACAAAGATTCAAAAGTATTATTATTCACACACTTGGG	12566
Db	175	LeuLysValLeuAspPheGlnAsnAlaIleHisIleTyrLeuSerLysGluLysPheSer	194
QY	12567	GTTCTGACATCAAAATGGCCCATCTCAATCTCTCTTTAGACCTGGCCCTGAAACCTTGAGAC	12626
Db	195	SerLeuGlnGln-----AlaThrAsnLeuSerLeuAsnLeuAsnGlyAsnAspIleAla	212
QY	12627	TTTATTCACACAGGTGACATTTTAAAGAAATTAGGCTTCATPAGCTGACTTTAAGAAATAT	12686
Db	213	GlyIleGluProGlyAlaPheAspSerAlaValPheGlnSerLeu-----Asn	228
QY	12687	TTTGATAGCTTAAATGTAAATGAAAAGCTTGATTCAGAGCTGGCTGTTTACAGTCCAT	12746
Db	229	PheGlyGlyThrGlnAsnLeuLeuValIlePheLeuGlyLeuLysAsnSerThrIleGln	248
QY	12747	CGTTTGCTTGGGAGAAATTAGAAATGAAGAAAGAACTGGAAAGTTTGACAAATCTGCT	12806
Db	249	SerLeuThrPheGlyThrPheGluAspMetAspAsp---GluAspIleSerProAlaVal	267
QY	12807	CTAAGAGGCTCTGGCAATTTGGACCATTTGGAAGAAATTCGATACATATCTAGACTATAC	12866
Db	268	PheGluGlyLeuCySerGluMetSerValGluSerIleAsnLeu---GlnLysHisTyrPhe	286
QY	12867	CTCGATGATATTATGACTTATTATTAATGTTTGAAGAAAGTTTCTTCATTTTCCCTGGTG	12926
Db	287	PheAsnIleSerSerAsnThrPheHisCysPheSer-----	298
QY	12927	AGTGGACTATTGAAAGGTTAAAGAACTTTCTTATTAATTCGGATGGGACATTTAGAA	12986
Db	299	-----GlyLeuGlnGluLeuAsp	304
QY	12987	TTAGTTAATCTGAATTTTGGACAGTTTCCACA-----TTGAAATCTCAATCTGCAAA	13040
Db	305	LeuThrAlaThrHisLeuSerGlnLeuPheProSerGlyLeuValGlyLeuSerThrLeuLys	324
QY	13041	AGGCTTACTTCACTTCCACAAAGAGTGGGAAT-----GCTTTTTCAGAAAGTTATCTTA	13094
Db	325	LysLeuValLeuSerAlaLeuLysPheGluAsnLeuCySerGlnIleSerAlaSerAsnPhe	344
QY	13095	CCAAGCCTTGAGTTT-----	13109
Db	345	ProSerLeuThrHisLeuSerIleLysGlyAsnThrLysArgLeuGlnLeuGlyThrGly	364
QY	13110	-----CTAGATCTCGATGAAGATGGCTTGAGTTTC	13139
Db	365	CysLeuGluAsnLeuGluAsnLeuArgGlnLeuAspLeuSerHisAspPheIleGluThr	384
QY	13140	AAAGGTGCTGTCTTCAAAAGTATTTTGGGCAACACAGCTTAAAGTATTATTAATCTGAC	13199
Db	385	SerAspCysCyAsnAsnLeuGlnLeuArgAsnLeuSerHisLeuGlnSerLeuAsnLeuSer	404
QY	13200	TTTCATAGGTGTATTATTCATAGATTTCAAC---TTCTGGGGCTTTAAGAACATTAAGAACT	13256
Db	405	TyrAsnGluProLeuSerLeuLysThrGluAlaPheLysGluCysArgGlnLeuGlnLeu	424
QY	13257	CTGATTTTCCAGCACTTCAAAATTGAAACAATAGTGAGTTTTCAGATTTCCGATCAATC	13316
Db	425	LeuAspLeuAlaPheThrArgLeuValValLysAspAlaGlnSerProPheGlnAsnLeu	444
QY	13317	AGAAACCTCATTTTACTTGACATTTTCCATATCTCACACGAGTGGCTTTTCAATGGCAATC	13376

Db	445	HleleuenuyValleuenuSerHisSerLeuApsriLlSerSerCluInleu	464
Qy	13377	TTGATGGCTTGTTCAGCTTCGAAAGCTTGGAAATGGCTGGCAATCTTTCCAGGAAAC	13436
Db	465	PheaprolyleuProAlaleuGlnHleAanleuGlnGlyAanHlePheProlysgly	484
Qy	13437	TTTCCTT-----CCAGATATCTTCACAGAGCTGGAGAACTTGACCTCTCTGACCTCTCT	13490
Db	485	AsnHleGlnlyPheThrAanSerLeuGlnThrGlyAargLeuGluHleleuValleuSer	504
Qy	13491	CAGTGTCACTGGAGAGAGTGTGTCCAAAGAGATTTAACTCACTGTCCAGTGTTCAGGTA	13550
Db	505	PheCyaspLeuSerSerSerIleAargGlnHleAlaPheThrSerLeuLySweHleAanHis	524
Qy	13551	CTAAATATGAGCCACAAACACTCTTTTCAATGGATGACCTTTCTTATTAAGTGTGAAAC	13610
Db	525	ValAspLeuSerHisAanArg-----LeuThrSerSerSerIleGluAlaLeuSer	541
Qy	13611	TCCTCTCAG-----GTTCTTGATTAACGCTTCATCACAATAAGACTTCCAAAAACAG	13664
Db	542	HisleuysGlyIleTyLeuAanleuAlaSerAanHisHleSerIlele-----	558
Qy	13665	GAATCAAGACTTTTCCAGTAAGTCTAGCTTCTTA-----AATCTT	13706
Db	559	-----LeuProSerLeuLeuProIleLeuSerGlnGlnArgThrIleAanLeu	574
Qy	13707	ACTCAGATGACTTTCCTGTTACTGTATCTTGACAACACAGAGTTCCTGCAATGATCAAGAC	13766
Db	575	ArgGlnAanProleuAanPcySerThrCySerAanHleTyPheLeuGlnUtrPyrIlysgly	594
Qy	13767	CAGAGCAGCTCTTGTGTGAAGTTGAACAAATGAATGTGCACACCTTCAGATAGCAG	13826
Db	595	AsnMetGlnlyPheGlnAapThrGlnAapThrLeuCyGluAanProProleuAanArg	614
Qy	13827	GGCATGCTGTGCTGAGATTGAATATCACCCTGTCCAGATGAATTAAGACATCTTGGTGTG	13886
Db	615	GlyValArgLeuSerAapValThrLeuSerCySerMetAlaAlaValGlyIlePhePhe	634
Qy	13887	TCGGTCTCTCAGCTGTTGATGATCTGTGTGAGACAGTCTGTGATTAAGTTCTAT	13943
Db	635	LeuIleValPheleuLeuValPheAlaIleleuLeuIlePheAlaVallyIyrrhe	653

RESULT 2

T08664

roll protein-like receptor DKFZp54710610.1 - human

C.Species: Homo sapiens (man)

C.Date: 11-Jun-1999 #sequence, revision 11-Jun-1999 #ext_change 09-Jul-2004

C.Accession: T08664

R.Poulikra, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A.Reference number: Z16466

A.Accession: T08664

A.Molecule type: mRNA

A.Residues: 1-786 <POU>

A.Cross-references: UNIPROT:Q15399; EMBL:AL050262

A.Experimental source: fetal brain; clone DKFZp54710610

C.Genetics:

A>Note: DKFZp54710610.1

Alignment Scores:			
Pred. No.:	6,02e-31	Length:	786
Score:	474.00	Matches:	204
Percent Similarity:	41.80%	Conservative:	130
Best Local Similarity:	25.53%	Mismatches:	303
Query Match:	1.43%	Indels:	162
DB:	2	Gaps:	32

US-09-396-985B-47 (1-18989) x T08664 (1-786)

Qy 12345 TCTGGACTATCAAGTTTACGAAGCGTGGCGCTGTGGAGCAAACTAGCATCTTGAG 12404

Db 34 AAmHlyleuHleHisValProlyAapLeuSerGlnlyIyrrheThrIleleuAanHisSer 53

QY 12405 AACTTCCCATGACATCTCAAACT-----TTGAAAGAA 12440
DB 54 GlnAsnTrpIleSerGluLeuTrpThrSerAspIleLeuSerLeuSerIleuArgIle 73
QY 12441 CTTAAATGGCTCAATCTTATTCGAATCTTCAAAATTAACCTGATATTTTCTAATCTG 12500
DB 74 LeuIleIleSerHisAsnArgIleGlnTrpLeuAspIleSerValPheIysPheAsn--- 92
QY 12501 ACCAATAGAGCACTTGACCTTTCAGAGCAAGAAATTAACAATATTATTTATGACAGAC 12560
DB 93 GlnGluLeuGlnTrpLeuAspLeuSerHisAsnIleuValIlySileSerCys----- 110
QY 12561 TTGGGGGTTCATCAAAATGCCCTTACTCAATCTCTCT---TTAGACCTGCTCCCTGAAC 12617
DB 111 -----HisProThrValAsnLeuIyShiSleuAspLeuSerPheAsn 124
QY 12618 CCTATGAATCTTATC-----CAACCAAGTCGCAATTTAAAGAAATTAAGGCTTCAT 12665
DB 125 AlaPheAspAlaLeuProIleCysLeuGluPheGluIyAsnMetSerGlnLeuIyPheLeu 144
QY 12666 AAGCTGACTTAAAGAAATATTTGATAGTTAAATGTAATGAAGAACTGTGATTCAGAGT 12725
DB 145 GlyLeuSer-----ThrThrHisLeuGluIySerSerValLeuPro 158
QY 12726 CTGGCTGGTTTGAAGATGCATCGTTGGTCTG-----GGAGAAATT 12767
DB 159 IleAlaHisIleuAsnIleSerIySValIleuValLeuGluIyGlnTrpIyGlyGlnIyS 178
QY 12768 AGAAATGAGGAAACTTGAAGAAAGTTTGACAAATCTGCTTGAGAGCGCTGTGCATTTG 12827
DB 179 GluAspProGlyGlyLeuGlnAspPheAsnThrGluSerLeuHisIleValPheProThr 198
QY 12828 ACCATGAAGAATTCGATTAAGCATTACTAGACTACTACCTCGATGATATTATTAAGCTTA 12887
DB 199 AsnIySglu----- 201
QY 12888 TTTAATGTTTGAAGAAATGTTTCTTCAATTTCCCTGGTGAAGTGAATATTAAGAGGTA 12947
DB 202 PheHisIleHisIleuAspValSerValIyethrValAlaAsnLeuGluLeuSerHisIle 221
QY 12948 AAAGACTTTTCTTAATATTTGCGATGCAACATTGAATTAAGTTAACTGTAAATTTGA 13007
DB 222 LysCysValIleuGluAspSerIySerserIyPheLeuSerIleuAlaIySleuGln 241
QY 13008 CAGTTTCCCACTTGAAGAACTCAATCTCTCAAAAAGCTTACTTCACTTCCACAAA--- 13064
DB 242 ThrAsnProIySleuSerSerIleuThrLeuAsnAsnIleGluThrTrpAsnSerPhe 261
QY 13065 -----GGTGGGAATGCTTTTTCAGAGTT 13088
DB 262 IleArgIleLeuGlnIleuValTrpHisIleThrValTrpIySerSerIleSerAsnVal 281
QY 13089 GATCTACAA---AGCCTTGAAGTTTGAATCTGACAGTAAGAAATGGCTTGAAGTTCAAGGT 13145
DB 282 LysLeuGlnGlnIyGlnIleuAspPheArgAspPheAspIySergIyThrSerIleuIyAla 301
QY 13146 TCGCTTTCTCA-----AGTGAT----- 13163
DB 302 LeuSerIleHisGlnValIleSerAspValPheGluPheProGlnIserIyIleIyGln 321
QY 13164 -----TTTGGGACAAACCGACCTTAAG----- 13184
DB 322 IlePheSerAsnMetAsnIleIySAsnPheThrValIserGluThrArgMetValHisMet 341
QY 13185 -----TATTAGATCTGAGCTTCAATGGCTGTATT----- 13214
DB 342 LeuSerProSerIySileSerProPheLeuHisIleuAspPheSerHisAsnLeuLeuThr 361
QY 13215 ---ACCATGATCAAACTTCTGGCTTGAAGAACTTAAGAACTGAGATTTCCAGCAT 13271
DB 362 AspIleValPheGluIySgluIyHisIleuThrGluLeuGlnThrIleuIleuGlnMet 381

QY 13272 TCCAAATTTGAAGAAATGAGTGAAGTTTCA---GTAATCTCATCACTAGAAACCTCAT 13328
DB 382 AsnGlnLeuIySgluLeuSerIySileAlaGluMetThrGlnMetIySerLeuGln 401
QY 13329 TACCTGACATTTTCTCATTACTACACACCAGAGTTGTTCAAT-----GGCATCTTC 13379
DB 402 GlnLeuAspIleSer-----GlnAsnSerValSerIySAspGluIySgluIyAspCys 419
QY 13380 AATGGCTTTCGCAAGTCGCAAGTTCGAAAGAAATGGCTGGCAATCTTTCGAGAAACCTTC 13439
DB 420 SerTrpThrIySerSerLeuSerLeuAsnMetSerSerHisIleuThrAspThrIle 439
QY 13440 -----CTTCAGATATCTTACAGAGCTGAGAAACTTGAACCTTCTGACCTCTCT 13490
DB 440 PheArgCysLeuProPro-----ArgIleIySValIleuAspLeuHis 453
QY 13491 CAGTGTCACTGAGACAGTTGTCTCCAAAGCAATTAATCACTCTCCAGTCTTCAAGTA 13550
DB 454 SerAsnIySileSerIle---ProIySgluValIySleuGlnIleuGlnGln 472
QY 13551 CTTAAATGAGCCCAACAAACCTCTTTCATTTGATACCTTCT-----TAT 13598
DB 473 LeuAsnValAlaPheAsn-----SerLeuThrAspLeuProGlyCysGlySerPhe 489
QY 13599 AAGTGTCAAGTCCCTCCAGGTTCTTGATTAAGCTCAATCAATTAAGACTTCCAA 13658
DB 490 SerSerLeuSerValIleuIleIleAspHisAsnSerValSerHisProSerAlaAspPhe 509
QY 13659 AAACAGAACTACAGCAATTTTCCAGAGTCTTGAATCTTAAATCTTACTCAGAAATGAC 13718
DB 510 PheGlnSerCysGlnIySmetArgSer-----IleIySAlaGluAspAsnPro 525
QY 13719 TTTGCTTGTATCTTGAACCAAGATTTCTCCATGATCAAGACCAAGAGCGCTC 13778
DB 526 PheGlnCysThrCysGlnIySgluIyGluPhe-----ValIySAsnIleAspGlnVal 542
QY 13779 TTGGTGAAGTT-----GAACGAATGAATGTGCAACACCTTCAGATTAAG 13823
DB 543 SerSerGluValIleuGlnGluIyTrpProAspSerIyIySersAspIyTrpProGluSerIy 562
QY 13824 CAGGSC-----ATGCTGTGCTGAGTTTGAATATCACTTCAG 13862
DB 563 ArgGluThrLeuLeuIySAspPheHisIleMetSerGluLeuSerCysAsnIleThrLeu 582
QY 13863 ATGAATTAAGCACTCATGTGTGTGTGCTGCTCAAGTGTGTTAGATGTGTTTGAACA 13922
DB 583 IleValThrIleValAlaThrMetLeuValIleuValThrValThrSerIleuIySile 602
QY 13923 GTTCTGATCTAATGAAGTTTCAATTTTCACTGATGCTCTTCTGCTGCTGCAATTAAGTATGT 13982
DB 603 TyrLeuAspLeuProTrpIyIleuArg---MetValCysGlnTrpHisGlnThrArgArg 621
QY 13983 AGAGTGAAATCATC-----TATGATGCTTTTGT 14012
DB 622 ArgAlaArgAsnIleProIleuGlnIyGlnIyGlnIyGlnIyGlnIyGlnIyGlnIyGlnIyGln 641
QY 14013 ATTACTCAAGCAGGATGAGCACTGGTGAAGAAATGAGTGAATTAAGAAATTTGAAG--- 14069
DB 642 SerTyrSerGluIyHisAspSerPheTrpValIySAsnGlnIleuLeuProAsnLeuGluIyS 661
QY 14070 GAAGGGGTGCTCAATTTCAAGTCTGCTGCTTCACTAAGAGACTTTATCCCGGTGGGCC 14129
DB 662 GluIyIyMet-----GlnIleCysLeuHisIyGlnIyGlnIyGlnIyGlnIyGlnIyGlnIyGln 678
QY 14130 ATTGCTCCAACTCATTCATGAGAGTTTCCATTAAGAGTTCAGAAAGTGAATGTGTTGTG 14189
DB 679 IleValGlnAsnIleIle---ThrCysIleGluIySeryIySerserIlePheValIleu 697
QY 14190 TCCGACACTTCACTCAAGAGCGCTGTGATTTGATATGATGAATGTGCTCAGACCTGG 14249
DB 698 SerProAsnPheValGlnIserGlnIyTrpCysHisIyGluIyLeuIyTrpPheHisIleHisAsn 717
QY 14250 CAGTTTCTGAGCAGTGTGCTGATCATCTTCAATGTGCTGAGAAAGTG---GAGAGAG 14306

```

Db      718  LeupheHisgluGlySerAsnSerLeuIleLeuIleLeuLeuGluProIleProGlnTyr 737
      |||      :|||      |||      |||      |||      |||      |||      |||
Qy      14307 ACCCTGCTCAGGACGAGGCTGACCTTACCGCTTCTCAGACGAAACACTTACCTGAG 14366
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Db      738  SerLeProSerSerTyrHisGlyLeuGlySerLeuMetAlaGagGlyTrpTyrLeuGlu 757
      |||      |||      |||      |||      |||      |||      |||      |||
Qy      14367 TGGGAGGACAGATGCTCCGGGCGGACATCTTCTGAGACGACTCAGAAAAAGCCCTG 14423
      |||      |||      |||      |||      |||      |||      |||      |||
Db      758  TrpProGlySerGlySerTyrHisGlyLeuPheTrpAlaAsnLeuAlaIle 776

RESULT 3
A29943
Toll protein precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A29943
R:Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A:Title: The Toll gene of Drosophila, required for dorsal-ventral embryonic polarity, at
A:Reference number: A29943; MUID:88135760; PMID:2449285
A:Accession: A29943
A:Molecule type: DNA
A:Residues: 1-1097 <HAS>
A:Cross-references: UNIPROT:P08953; GB:M19969; GB:J02682; NID:g158640; PIDN:AAA28941.1;
C:Genetics:
A:Gene: FlyBase:TI
A:Cross-references: FlyBase:FBgn0003717
C:Keywords: transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-1097/Product: Toll protein #status predicted <MAT>

```

```

Alignment Scores:
Pred. No.:      3.91e-28      Length:      1097
Score:          441.00      Matches:      219
Percent Similarity: 38.96%      Conservative: 141
Best Local Similarity: 23.70%      Mismatches: 298
Query Match:      1.33%      Indels:      266
DB:              2      Gaps:      43

```

```

US-09-396-985B-47 (1-18989) x A29943 (1-1097)

Qy      12216 TCAATGCTTTTATTTCTCTGAGGTGTAATCCAGAACTTGAAGATGGGGCATATCAG 12275
      |||      |||      |||      |||      |||      |||      |||      |||
Db      175  AsnLeuSerHisLeuGluLeuAlaAsnIleGluMetProSerHisLeuPheAsp 194
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12276 AGCCTAAGCCACTCTCTTACTTAATATTGACAGAAACCCCATCCAGATTGACCCCTG 12335
      |||      |||      |||      |||      |||      |||      |||      |||
Db      195  AspLeuGluAsnLeuGluSerIleGluPheGlySerAsnIleuAlaArgGlnMetProArg 214
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12336 GGAACCTTTTCTGACATATCAAGTTTACAGAAAGCTGGTGGTGGAGACAAATCTAGCA 12395
      |||      |||      |||      |||      |||      |||      |||      |||
Db      215  GlnIlePheGlyLysMetProLysLeuGlySerIleuAsnLeuTrpSerAsnGlnLeuHis 234
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12396 TCTCTAGGAAGACTTCCCATTCGACATCTCAAACTTGAAGAAGACTTAATGAGCTCAC 12455
      |||      |||      |||      |||      |||      |||      |||      |||
Db      235  AsnLeuThrLysHisAspPheGluGlyAlaThrSerValLeuGlyIleAspIleHisAsp 254
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12456 AATCTTATCAATCTTTCAAAATTAAGT--GAGTATTTTCTTAATCTGACCAATCTAGAG 12512
      |||      |||      |||      |||      |||      |||      |||      |||
Db      255  AsnGlyIleGlu-----GlnLeuProHisAspValPheAlaHisLeuThrAsnValThr 272
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12513 CACTTGACCTTTCCAGCAAGAAGATTCAAGATAT-- 12548
      |||      |||      |||      |||      |||      |||      |||      |||
Db      273  AspIleAsnLeuSerAlaAsnLeuPheArgSerLeuProGlnGlyLeuPheAspHisAsn 292
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12549 ---TATTCACAGACTTGGGGTTCTA---CATCAATGCCCTTACATCTCTCTTTA 12602
      |||      |||      |||      |||      |||      |||      |||      |||
Db      293  LysHisLeuAsnGlnValArgLeuMetAsnAsnArgValProLeuAlaThrLeuProSer 312
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12603 GACCTGTCCCTGAACCTTATGAACTTTATCCACAGGCTGACATTTAAAGAAATTAAGCTT 12662
      |||      |||      |||      |||      |||      |||      |||      |||
Db      313  ArgLeuPheAlaAsn-----GlnPro-----GlnLeu 321

```

```

Qy      12663 CATAGCTGACTTTAAGAAATATTTGATAGTTA----- 12698
      |||      |||      |||      |||      |||      |||      |||      |||
Db      322  GlnIleLeuArgLeuArgAlaGluLeuGlnSerLeuProGlnLysLeuPheGluHisSer 341
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12699 -----ATGTAATGAAAATTGTATTTCAAGCTCTG 12728
      |||      |||      |||      |||      |||      |||      |||      |||
Db      342  ThrGlnIleThrAsnIleSerLeuGlyAspAsnLeuLeuLysThrLeuProAlaThr 361
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12729 GCTGGTTTGAAGTCCATCGTTTGTGTGGGAGAAATTTAGAAATGAAAGAACTTGAA 12788
      |||      |||      |||      |||      |||      |||      |||      |||
Db      362  LeuGlnHisGlnValAsnLeuLeuSerLeuAspLeuSerAsnAsn-----ArgLeuThr 379
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12789 AAGTTTGAACAAATCTCTCTAGAGGCTGTGCAATTTGACACTTGAAGATTTCCGATTA 12848
      |||      |||      |||      |||      |||      |||      |||      |||
Db      380  HisLeuProAspSerLeuPheAlaHisThrThrAsnLeuThr----- 393
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12849 GCATACTTACACTTACTACCTCGATGATATTAATTAATTTGTTGACAAATGTT 12908
      |||      |||      |||      |||      |||      |||      |||      |||
Db      394  -----AspLeuArgLeuGluAsp-----AsnLeuLeuThrGlyIle 405
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12909 TCTTCA-----TTTTC-----CTGGTAGTGTGACTATTGAAAG----- 12944
      |||      |||      |||      |||      |||      |||      |||      |||
Db      406  SerGlyAspIlePheSerAsnLeuGlyAsnLeuValThrLeuValMetSerArgAsnArg 425
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12945 -----GTAAAGACTTTTCTTATAATTTGCGATGCGCAACTTTAGAAATTA 12989
      |||      |||      |||      |||      |||      |||      |||      |||
Db      426  LeuArgThrIleAspSerArgAlaPheValSerThrAsnGlyLeuArgHisLeuHisLeu 445
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12990 -----GTT 12992
      |||      |||      |||      |||      |||      |||      |||      |||
Db      446  AspHisAsnAspIleAspLeuGlnGlnProLeuLeuAspIleMetLeuGlnThrGlnIle 465
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      12993 AACTGTAAATTTGGAGACAGTTTCC-----ACATTTGAATCTCAAAATCTCAAAAG 13043
      |||      |||      |||      |||      |||      |||      |||      |||
Db      466  AsnSerProPheGlyLysMetHisGlyLeuLeuThrLeuAsnLeuArgAsn---AsnSer 484
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      13044 CTACTTCTCACTTCCAAAGAGTGGGAATGCTTTTTCAGAAAGTTGATTCACCAAGCTT 13103
      |||      |||      |||      |||      |||      |||      |||      |||
Db      485  IleIlePheValLysThrAsnAspTrpLysAsnThrMetLeuGln-----Leu 499
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      13104 GAGTTTCTAGATCTCAGTGAAGAAATGGCTTGAGTTTCAAAAGTTGCTGTCTCAAGATGAT 13163
      |||      |||      |||      |||      |||      |||      |||      |||
Db      500  ArgGluLeuAspLeuSerTyrAsnAsnIleSer----- 510
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      13164 TTTGGACAAACGACCTTAAGATTTTAGATCTGACCTCAATGTTATTACCAATGAT 13223
      |||      |||      |||      |||      |||      |||      |||      |||
Db      511  -----SerLeuGlyLysGluAspLeuAlaPhe-----LeuSer 521
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      13224 TCAAACTTCTGGGCTTTAGAAACAACTAGACATCTGATTTCCAGCATTTCCAAATTTGAA 13283
      |||      |||      |||      |||      |||      |||      |||      |||
Db      522  GlnAsnArgLeu-----HisValAsnMetThrHisAsnLysIleArg 535
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      13284 CAAATGAGT--GAGTTTCAATTCCTATTC--CTCAGAAACCTCATTTAC 13331
      |||      |||      |||      |||      |||      |||      |||      |||
Db      536  ArgIleAlaLeuProGluAspValHisLeuGlyGluGlyLysAsnAsnLeuValHis 555
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      13332 CTTGACATTTCTGACTATCAC-----ACGAGAGTGTCTTCATGAGATC 13376
      |||      |||      |||      |||      |||      |||      |||      |||
Db      556  ValAspLeuAsnAspAsnProLeuValCysAspCysThrIleLeuTrpPheIleGlnLeu 575
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      13377 TTCAATGGCTTG----- 13388
      |||      |||      |||      |||      |||      |||      |||      |||
Db      576  ValArgGlyValHisLysProGlnTyrSerArgGlnPheLysLeuArgThrAspArgLeu 595
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      13388 ----- 13388
      |||      |||      |||      |||      |||      |||      |||      |||
Db      596  ValCysSerGlnProAsnValLeuGluGlyThrProValArgGlnIleGluProGlnThr 615
      :|||      :|||      :|||      :|||      :|||      :|||      :|||      :|||
Qy      13388 ----- 13388
      |||      |||      |||      |||      |||      |||      |||      |||
Db      616  LeuIleCysAspProLeuAspPheSerAspAspProArgGluArgLysCysProArgGlyCys 635

```

QY 13389 -----TCCAGTCTGCAAGTCTTGAAAATGGCTGCACATTTCT 13424
 Db 636 AasnCyshisValArgThrTyAspIlysalLeuValIleasnCyshisSerGlyAsnIleu 655
 QY 13425 TTCACGAGAAATCTCTCCGATATCTTCACAGAGCTGAGAAATCTGACCTTCTGAC 13484
 Db 656 ThrHisValProArgLeuProAsnIleHis-----LysAsnMetGlnLeuMetGln 672
 QY 13485 CTC-----TCTCAGTGTCACTGGAGCTGTTGCTCCCAACAGATTTAAAC 13529
 Db 673 LeuHisLeuGluAsnLeuHisLeuLeuArgLeuProSerIleAsnThrProGlyTyGlu 692
 QY 13530 TCACTCTCCAGCTTTCAGGTAATAATGAGCAACAATCTTTTTCATTGATAGC 13589
 Db 693 SerValThrSer-----LeuHisLeuValGlyAsnLeuLeuThrSerIleAsnVal 709
 QY 13590 -----TTCTCTTAAGTGTCTGAACCTCTCCAGGTTCTTGATTACAGTCTCAATCAC 13643
 Db 710 AspGlnLeuPro-----ThrAsnLeuThrHisLeuAspIleSerThrAsnHis 725
 QY 13644 ATAAATGACTTCCAAAAACAGAACTACAGATTTTCCAGTACTGTTCTTAAT 13703
 Db 726 Leu-----GlnMetLeuAsn-----AlaThrValLeuGlyPheLeuAsn 738
 QY 13704 -----CTTACTGAGAAATGACTTGTGCTTGTACTTGTGAA 13736
 Db 739 ArgThrMetLysThrArgSerValIlyLeuSerGlyAsnProThrMetCysAspCysThr 758
 QY 13737 CACCAAGATTCTTCGATGATGATCAAGACCAAGGAGCTTGTGTGGAAGTTGAACA 13796
 Db 759 AlaLysPheLeuLeuPheThrGlnAspAsnPheGlnArgIleGlyAspArgAsnGlu 778
 QY 13797 ATGGAATGTGCAACACCTTGATAGAGGAGGAGCTGTGCTGAGTTGATATACACC 13856
 Db 779 MetMetCysValAsnAlaGluMetCProThrArgMetValGluLeuSerThrAspAspIle 798
 QY 13857 TGTGAGATGATAAGACCATC--ATTGCTGTGTGCTGCT-----CTCAGTGTGCTT 13904
 Db 799 CysProAlaGluGlyValPheIleAlaLeuValValIleAlaLeuThrGlyLeu 818
 QY 13905 GTAGTATCTGTGTAGAGCTTGTGCTATTAAGTTC----- 13940
 Db 819 LeuAlaGlyPheThrAlaAlaLeuTyTyLysPheGlnThrGlnIleLysIleTryLeu 838
 QY 13941 TATTTACCTGAGCTTCTTGTGCTGCTGATTAAGTGTAGAGGTGAAGATC-- 13997
 Db 839 TyAlaHisAsnLeuLeu-----TrpPheValThrGluGluAspLeuAsp 854
 QY 13998 -----TATGATGCTTGTGTATCTCAAGCAAGATGAGATGAGTGAAG 14045
 Db 855 LysAspLysLysPheAspAlaPheIleSerTySerHisLysAspGlnSerPheIleGlu 874
 QY 14046 AATGAGCTAGTAAGAATTTGAAGAAAGGGTGCCTCAATTCAGCTGTGCTCACTAC 14105
 Db 875 AspTyLeuValProGlnLeuGlnHisGlyProGlnLysPheGlnLeuCysValHisGlu 894
 QY 14106 AGAGACTTATCCCGGTGTGGCCATGTGCTGCCAATCATCATGAAGTTCCATAAA 14165
 Db 895 ArgAspTrpLeuValGlyGlyHisIleProGluAsnIleMet--ArgSerValAlaAsp 913
 QY 14166 AGCCGAAAGGTGATTTGTGTGTGTCCACAGACTTTCACAGACCCGTGTATCTTT 14225
 Db 914 SerArgThrThrIleIleValLeuSerGlnAsnPheIleLysSerGluTrpAlaArgLeu 933
 QY 14226 GAATATGATTTGCTGAGACCTGCACTTTCAGCAGCTGTGCTGTATCATTTCAAT 14285
 Db 934 GluPheArgAlaAlaHisArgSerAlaLeuAsnGluLysArgSerArgIleIleValIle 953
 QY 14286 GTC-----CTGCAAGAAAGTGAAGAGACCTGTGTCAGGCAAGGAGGTGAGCTGAC 14336
 Db 954 IleTySerAspIleGlyAspValGluLys-----LeuAspGlnGluLeuLysAlaTy 971
 QY 14337 CGCCTTCTGACAGAAACATTAACCTGAGTGGAGAGACAGTGTCTGTGGGCGGACATC 14396

Db 972 -----LeuLysMetAsnThrTyLeuLysTrpGlyAspPro-----Trp 984
 QY 14397 TTCCTGAGAGACTCCGAAAAAGCCCTGCTGAGTGAATCATCATGATCCAGAGAGACA 14456
 Db 985 PheThrAspLysLeuAlaGlyPheAlaLeuProHisArgArg-----ProValGlyAsn 1001
 QY 14457 GTGGGTACAGGA 14468
 Db 1002 IleGlyAsnGly 1005
 RESULT 4
 T13852
 gene wheeler protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 20-Sep-1999 #sequence: revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T13852
 R:Elton, E.; Kooyer, S.; D'aveylyn, D.; Duman, M.; Lawinger, P.; Botas, J.; Beilen, H.
 Development 120, 885-899, 1994
 A:Title: The Drosophila 18 wheeler is required for morphogenesis and has striking siml.
 A:Reference number: 217796; MUID:95324375; PMID:7600965
 A:Accession: T13852
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1389 <ELD>
 A:Cross-references: UNIPROT:Q24591; EMBL:L21171; NID:9415682; PID:G1019104; PID:AAA792;
 C:Genetics:
 A:Gene: wheeler
 A:Cross-references: FlyBase:FBgn0004364
 Alignment Scores:
 Pred. No.: 9,85e-24 Length: 1389
 Score: 389.00 Matches: 222
 Percent Similarity: 38.28% Conservative: 139
 Best Local Similarity: 23.54% Mismatches: 363
 Query Match: 1.18% Indels: 219
 DB: 2 Gaps: 38
 US-09-396-985b-47 (1-18989) x T13852 (1-1389)
 QY 12065 GGGCTTCTTATTTGCTTATTCATCATCATCTGTCTCTGTAAGTCTTGGCTATGAC 12124
 Db 301 GlyLeuLeu-----HisArgLeuGluGlnLeuLeuValIleuAspLeuSer 315
 QY 12125 ---AATCATATGACCCATCATCATCTGTATGTAAGAAGCTGATGACTAGATTAATA----- 12176
 Db 316 GlyAsnGlnLeuThrSerHisHisValAspAsnSerThrPheAla-GlyLeuIleArgLe 335
 QY 12176 ----- 12176
 Db 335 uIleValLeuAsnLeuSerHisAsnAlaLeuThrArgIleGlySerLysThrPheLysGlu 355
 QY 12177 ---TCTATTTAGGTTCTTATTCAGCAGAAATATTAGATTAATCATATGCTTTTATTC 12232
 Db 355 uLeuTyPheLeuGlnIleLeuAspMetArgAsn----- 366
 QY 12233 CTGTAGTGTGAATTCACAGATTTGAAGATGGGGCATATCAGAGCTTAAGCCACTCTC 12292
 Db 367 -----AsnSerIleGlyHisIleIleGluGlnGlyAlaPheLeuProLeuTyAsnLeuHis 384
 QY 12293 TACCTTAATATTGACAGAAACCCATCCAGAGTATTAGCCCTGAGAGCTTTTCTGAGCT 12352
 Db 384 sThrLeuAsnLeuAlaGluAsnArgLeuHisThrLeuAspAsnArgIlePheAsnGlyLe 404
 QY 12353 ATCAAGTTTACAGAGCTGTGCTGTGAGAGACAAATTTAGCATCTCTA---GAGAACTT 12409
 Db 404 uTyValLeuThrLysLeu---ThrLeuAsnAsnLeuValSerIleValGluSerGlu 423
 QY 12410 CCCCATTTGACATCTCAAAACTTTGAAGAAGATTAATGTGGCTCACAATCTTATCCAAATC 12469
 Db 423 nAlaPheArgAsnCysSerAspLysGluLeuAspLeuSerSerAsn-----GlnIle 441
 QY 12470 TTTCAAATTATTCAGATATTTTCTAATCTGACCAATCTAGACACTTGAACCTTCCAG 12529

[illegible][illegible]

QY	13283	ACAAATAGAGTACGTTTTCAGATTTCCATATCCATACACGAAAACCTCATTTACCTTGACATTTCC	133342
Db	790	epcrglnasprvalserasprleuuyrileuabergilyaasnaimecProgluleuglivalgl	810
QY	13343	TCATATCTCACACGAGAGTGGCTTTCAATGGATCGCATTTCAATGGCTTTCCAGCTCGGAAGT	13402
Db	810	yhi1sleuthrcl1ytrgrarganleuathrgalaleuylrleuabnahlserasleueth	830
QY	13403	CTTGAAAATGGCTGGCAATTCCTTCCAGAAAACCTTCCTCCAGATATCTTCAACAAGCT	13462
Db	830	rleuglnanogl1yser-----leualaglme	839
QY	13463	GAGAAACTTGACCTTCTGGAACCTCTCAGCTGCAACTGGAGCACTTGTCTCCAAAGC	13522
Db	839	uvalasmeulhrgval1leuhi1sleugluabnaml1leuthralaleuglul1ytrcl	859
QY	13523	ATTTAATCACTCTCCAGCTCTTGAGATACATTAATATAGSCAACAACTCTTTTCATT	13582
Db	859	upheargserleucl1yleuabnargluleuylrleuhi1sasnaimleuthrhi1srl	879
QY	13583	GGATACGTTTCTTATAGTGTGAACTCCCTCCAGGTTCTTGATTAACATCTCAATCA	13642
Db	879	eserabnahlathrphenglProleuValserleugluval1leuargleuabrsbnhr	899
QY	13643	CATATAGCTTCCAAAAACAGAACTACAGACATTTTCCAAAGTCTAGCTTTCTTAA	13702
Db	899	gleuserxserleuBrohi1sleuglul1ytragh1s-----Serleuglnl1leuuh	916
QY	13703	TCTTACTCAGAAATGACTCTTGCTTGTACTCTAGTGAAC-----CAGAGTTTCTCGAAATGAT	13759
Db	916	rleucl1ytrgrasnalatrpsercyabgcybglnglnleuargluleuadl1leuahlpheva	936
QY	13760	CAGAGACCAAGGAGCGACTCTTGATGGAAGTTGAACGAATGGAATGTGCAACCTTGACA	13819
Db	936	1serasprbnahlmetvalValargasprahl1h1saprll1etyCy1leuabrsprlaagl1yl	956
QY	13820	TAAAGAGGGCATGCGCTGTGCTG-----	13841
Db	956	elysargl1leuugluu1legl1yaasleuual1aasngl1ProabpCyserasprleuue	976
QY	13842	-----AGTTTGAATATCACCTCGACATGAAT-----AA	138707
Db	976	uasprlaser11aserasbn11eserSererglnasprleuad1gl1y1ytrargleuDr	996
QY	13871	GACCACTATGGGTGTGTGCGATCCACAGTGTGCTGTGTGTCTGTGTAGCACTTGTGT	13930
Db	996	oleuenuah1a1a1leuValleu1leu1leu1leu1leu1leu1leu1le1val1pheva	1016
QY	13931	CTATAAGTTCTATATTTCACTGAGTGCCTTCTTGCTGCTGCAATAAATAGTGT-----	13982
Db	1016	1pheargleu1serValargmet1rleu1pheala-----Hi1ytrcl1yValargva	1033
QY	13983	-----AGAGGTGAANAAC-----ATGTATGATGCTTTGTATCTACACGAG	14023
Db	1033	1CysgluProahrghegl1uabrsprlaagl1y1sleu1y1asprla1le1leuuh1s1ercl	1053
QY	14024	CCAGATGAGGACTGGGTAGAGAAATGACTAGTAAAGATTTGAAGAAAGGGGTGCTCC	14083
Db	1053	uhsaspr1yrglupheval1cybsargan1le1a1a1gl1leugln1h1srl1yargrProPr	1073
QY	14084	ATTTCAGCTCGCTTCACTACACAGACTTATATCCCGGTGTGGCCATTCTCCCAACAT	14143
Db	1073	opheargleu1srl1egln1n1argasp-----leuProgl1n11serhi1sleu1nle	1092
QY	14144	CATCCATGAAGGTTTCCATAAAGCGGAAGGTATTTGTTGTGTGTCACAGACTTCAT	14209
Db	1092	uval1---glugl1y1aarg1a1aspr1y1srl1e1leuval1leu1h1r1arg1s1leu1e	1111
QY	14204	CCAGAGCCGGTGTATCTTTGTAATATGAATGATTTCTCAGACCTCGAGATTTCTGACAG	14263
Db	1111	uhalathrgcl1u1rpsnaargl1legl1uphearg1asna1a-----Phehi1sleu1e	1127
QY	14264	TGTCCTGTATCATCTTCAATGTCCTGCGACAG-----GTGAGAAAGACCTTGCT	14314

Db 1127 rleuargllyleu-----AlaGlnlybyleuValIleIleGlnGluThrSerVa 1143

Qy 14315 CAGGACAGACGTGTGAGCTGTACCGCTTCTTGTACAGAGAACTTACTCTGGAGTGGAGGA 14374

Db 1143 lserlagnlualaglnaerValAlaGlnleuser-----ProTyrleuys----- 1158

Qy 14375 CAGTGTCTGGGGCGCGACATC-----TTCTGGAGACGACTGAGAA 14416

Db 1159 -SerValProSerAenAryleuThrCysAspArgTyrPheTyrGlnlybyleuArgTyr 1178

Qy 14417 AGCCCTG 14423

Db 1178 rAlaIle 1180

RESULT 6

B34087

hypoetical protein (L1H 3' region) - human

C.Species: Homo sapiens (man)

C.Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 03-Jul-2004

C.Accession: B34087

R.Scott, A.P.; Schmeckpeper, B.J.; Abdelrazik, M.; Comey, C.T.; O'Hara, B.; Rossiter, J.

Genomics 1, 113-125, 1987

A.Title: Origin of the human LI elements: proposed progenitor genes deduced from a comparison of human LI elements with mouse L1 elements

A.Reference number: A34087; MUID:88085185; PMID:3692483

A.Accession: B34087

A.Status: preliminary; not compared with conceptual translation

A.Molecule type: DNA

A.Residues: 1-1280 <SC0>

A.Cross-references: UNIPROT:O9Y5K0

C.Superfamily: pol polypeptide

Alignment Scores:

Pred. No.:	2,666-21	Length:	1280
Score:	360.00	Matches:	70
Percent Similarity:	64.67%	Conservative:	27
Best Local Similarity:	46.67%	Mismatches:	53
Query Match:	1.09%	Indels:	1
DB:	2	Gaps:	0

US-09-396-985B-47 (1-18989) x B34087 (1-1280)

Qy 2697 AGACCAAGAAAGTAAATTAATTAAGCTTGTGCAAGATGTGAAAATAAGAACTCTGTACAC 2756

Db 1128 lylslySerglYAspAsnArgCysrTrpArglyCySgylGlnlIeIlyThrleuLeuHis 1147

Qy 2757 CATTGTGGAGATGTAAATATGTATGACAGATGCTGTGGAGAAATATATGCTGGCTCAAA 2816

Db 1148 CysTrpTrpAspCyslybyleuValGlnProleuTrpIlyThrValTrpArgPheleuLys 1167

Qy 2817 AAATTAATAATGATTTACGACATGATCCAGCAATCTCACTTCTGAGTACGTATCCAAA 2876

Db 1168 AspleuGlnleuGlnIleProPheAspProAlaIleProleuLeuIlyleTyrProlys 1187

Qy 2877 GAATGAAAACAGAGACTTTAAGAGATATTTGTACACACATGTTATGCGACATTAATC 2936

Db 1188 AspTyrLysSerCysCysTyrLysAspThrCysThrArgMetPheIleAlaAlaLeuPne 1207

Qy 2937 ACAATAGCTTAACGTGTGGCAACATGACATGCTCCATGAACAGACAAATGAGATTAACAA 2996

Db 1208 ThrIleAlaIlyThrTrpAsnGlnProlysCysProSerMetIleAspTrpIleLys 1227

Qy 2997 ATGTGGTGTATACATACAAATGGAATATTTGTCAGCTTTAAAGAAGAGAGCTTGATC 3056

Db 1228 MetTrpHisIleTyrThrMetGlnTyrTyrAlaAlaIleIleYAsnAspGlnPheMetSer 1247

Qy 3057 TATTAACAC-ACGAAAAGAACTTGAAGACATTTATGCAAGTCAATTAAGCCAGTACAA 3115

Db 1248 PheValGlyThrTrpMetLysleuGlnThrIleIleLeuSerLysleuSerglnIylGln 1267

Qy 3116 AAAGATACACTACTGTATGATTCACACTTCA 3145

Db 1268 LysThrLysHisArgMetPheSerLeuIle 1277

RESULT 7

S23650
 retrovirus-related hypothetical protein II - human retrotransposon LINE-1
 C/Species: Homo sapiens (man)
 C/Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
 C/Accession: S23650
 R/Hohjoh, H.; Minakami, R.; Sakaki, Y.
 Nucleic Acids Res. 18, 4099-4104, 1990
 A/Title: Selective cloning and sequence analysis of the human L1 (LINE-1) sequences which
 A/Reference number: S23649; MUID:90333398; PMID:2165587
 A/Accession: S23650
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-712 <HOH>
 A/Cross-references: UNIPROT:Q15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:000363; UNIPROT:Q14754; UNIPROT:Q915K0; UNIPROT:000366; UNIPROT:081E30; UNIPROT:000375; EMBL:X52235
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
 C/Genetics:
 A/Mobile element: LINE-1
 A/Start codon: GTG
 C/Superfamily: pol polyprotein

Alignment Scores:
 Pred. No.: 6,07e-21 Length: 712
 Score: 355.00 Matches: 69
 Percent Similarity: 64.67% Conservative: 28
 Best Local Similarity: 46.00% Mismatches: 53
 Query Match: 1.07% Indels: 1
 DB: 2 Gaps: 0

US-09-396-985b-47 (1-18989) x S23650 (1-712)

QY 2697 AGACGAGAAAGTATATAGTGTGTAAGATGTGAAAGAAATGAGAACTCTGTAC 2756
 Db 560 LysylserglyshenanaargcysetrparyglycsglyglutlleglythrleuLeuHis 579
 QY 2757 CATTGGGAGATGTAATAATGTACAGATGCTGTGAGAAATCATATCATGTGGTGTGCA 2816
 Db 580 CysTrpTrparyCyslyshleuValGlnProleuTrpysSerValITrpaGpHeuAarg 599
 QY 2817 AAAATTAATAATAGATTATACCATGATCCAGCAATCTCACTTGTAGTACGTATCCAAA 2876
 Db 600 AspLeuGluProGluIleProPheAspProAlaIleProleuGluIleTyProlys 619
 QY 2877 GAATGAAAACAGAGACTTAAAGATTTGTTCACATGTTTATGACGACTTATTC 2936
 Db 620 AspSerlyserCysCysTyryLysAspThrCysThrargMetPheIleAlaIleuPhe 639
 QY 2937 ACAATAGCTACGCTGCAACATGCAAGTGTCCATGAAACAGACAAATGATAGCAA 2996
 Db 640 ThrIleAlaLysThrTrpAnGlnProLysCysProThrMetIleAspTrpIleLysLys 659
 QY 2997 ATGTGCTATATACATACATGATATATGTTACGCTTTAAAGAAAGAGGCTTGTATC 3056
 Db 660 MetTrpIleIleTyThrMetGluTyTyAlaIleLysAsnAspGluPheValSer 679
 QY 3057 TATATCTAC-ACAGAAAAGAACTTGAGAGACTTATGCAAAATGCAATAGCCAGTCA 3115
 Db 680 PheValGlyThrTrpMetLysLeuGluIleIleLeuSerLysLeuSerGlnGluGln 699
 QY 3116 AAGATACATACATGATGATTCCTCTCA 3145
 Db 700 LysThrLysHisCysIlePheSerLeuIle 709

RESULT 8

T15864
 hypothetical protein C56B6.6 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T15864
 R/Fulton, L.
 submitted to the EMBL Data Library, November 1995

A/Description: The sequence of C. elegans cosmid C56B6.

A/Reference number: S69019

A/Accession: T15864

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1066 <FUL>

A/Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:G1055114; PID:G1055120; PIDN:AAA81

C/Genetics:

A/Gene: C56B6.6

A/Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 679/2; 769/2; 833/3; 892/3;

Alignment Scores:

Pred. No.: 2.6e-20 Length: 1066
 Score: 348.00 Matches: 140
 Percent Similarity: 43.64% Conservative: 90
 Best Local Similarity: 26.57% Mismatches: 205
 Query Match: 1.05% Indels: 92
 DB: 2 Gaps: 22

US-09-396-985b-47 (1-18989) x T15864 (1-1066)

QY 12243 GAATCCAGCAATGTAAGTGGGCATATCAAGCCTAAGCCACTCTACTTATA 12302
 Db 179 GlnIleGlnThrValGlnPheSerSerPheGluThrValGlyHisMetGlnSerLeuAsp 198
 QY 12303 TTGACAGAAACCCCATCCAGAGTTTAGCCCTGGAGCCTTTCTGACTATCAAGTTTA 12362
 Db 199 LeuSerTyrrshnarglleAlaTyLeuProArgly----- 210
 QY 12363 CAGAGCTGTGCTGTGAGACAAATCTAGACTCTTACAGAACTTCCCATTTGACAT 12422
 Db 211 -----MetLeuAsnPhe----- 215
 QY 12423 CTGAAACCTTGAAAGCAATTAATGTGCTCAACATTTTCCATTTCAATTTACT 12482
 Db 216 AlaLysThrLeuLysThrLeuLysLeuAlaGluAsnMetIleHisAla-----ThrPro 233
 QY 12483 GAGTATTTTCTATATGACCAATCTAGACACTTGGACCTTTCCAGCAACAAGATTCAA 12542
 Db 234 GluAlaLeuArgAspLeuArgAsnLeuThrHisLeuAsnLeuGlnGlyAsnLysLeuAsn 253
 QY 12543 AGTATT-----TATTCACAGACTTGGGGTCTTACATCAATGCC 12584
 Db 254 ArgIleAspLysPheValLeuLysGlyCysThrAspThrLeuVal----- 268
 QY 12585 CTACTCAATCTCTTTAGACCTGTCCCTGACACCTTATGACTTTTCCACAGGTGCA 12644
 Db 269 -----GluLeuPheIleAlaAsnAsnTyLeuGlnHisIleProHisGlyVal 284
 QY 12645 TTTAAAGAAATTAGGCTTCAATAGCTGACTTAAAGAAATATTGATATTAAATGTA 12704
 Db 285 LeuSerGlyMetLys-----GlnLeuGlnHisLeuAspIle 296
 QY 12705 ATGAAACCTTGATTCAGGCTGTGCTGTTTAGAATCCATGCTTGTGTTGGAGAA 12764
 Db 297 SerLysAsnLysIleMetSerLeu----- 304
 QY 12765 TTTGAAATGAGAAAGAACTTGAGAAAGTTGACAAATCTGCTTACAGGCTGTGCAAT 12824
 Db 305 ---LysLeuProThrSerLeuSerLeuSerIleThrLysGlnGluThrSerThrValArgArg 323
 QY 12825 TTGACATTCAGAAATTCGATTTAGCATCTTACACTTACACTGATGATATTTATGAC 12884
 Db 324 LeuAsnLeuAlaGlyAsnArgIleAsnAsnMetSerAspTyLeu-----IlePheGln 341
 QY 12885 TTATTTAATTTTGACAAATGTTCT--TCATTTCCCTGGTGAAGTGAATTTGAA 12941
 Db 342 HisMetProLeuLeuThrTyrrValAspValSerPheAsnArgIleArgPheIleSerPro 361
 QY 12942 AGGGTAAAGACTTTTCTTATTAATTTTCGATGAGCAACTTGAATTTAGTTAACTGAAA 13001
 Db 362 ArgValPheGluLysLeuLysAsnLeu-----GluSerLeuPheLeuGlnAsnGln 379

[illegible]

Alignment Scores:		length:
Pred. No.:	3 3s-20	1275
Score:	347.00	Matches: 68
Percent Similarity:	64.00%	Conservative: 28
Best Local Similarity:	45.33%	Mismatches: 54
Query Match:	1.05%	Indels: 1
DB:	2	Gaps: 0

US-09-396-985B-47 (1-18989) x S65824 (1-1275)

2697 AGACCAGAACTAATAAAGTGTGTGAAGATGTGAAAAATGAGAACTCCTGTACAC 2756

Db 1123 LysLysSerGlyAsnAsnArgCysTrpArgGlyCysGlyGluIleGlyThrLeuLeuHis 1142

Qy 2757 CATTGTGGGAATGTAACAGATGCTGTGAGAATCATATGCTGGTCTCAA 2816

Db 1143 CysTrpTrpAspCysLysLeuValGlnProLeuTrpLysSerValTrpArgPheLeuArg 1162

2817 AAATTAAATAGATTTACCACATGATCCAGCAATCTCACTTCTGAGTACGTATCCAAA 2876

Db 1163 AspleuGluleuGlIlePropheAspProAlaIleProleuLeuGlyIleTyrProAsn 1182

2877 GAATTGAAACAGAGACTTTAAGAGATTTGTACCAACCATGTTTATGGCAGCATTATTC 2936

Db 1183 GluTyrLysSerCysCysTyrLysAspThrCysThrArgMetPheIleAlaIaLeuPhe 1202

2937 ACAATAGCTAACGTGTGGCAACAATGCAAGTGTCCATGAACAGACAAATGGATAAGCAA 2996

Db 1203 ThrIeaIaIySThrTpASngIInProIySCySProThrmEtIleASpTrIleIySlys 1222

2997 ATGTGCTATACATACATGAATATGTTCAAGCTTTAAAGAAGAGAGCTTTGATC 3056

Db 1223 MetTyrHisIleTyrThrMetGluTyrTyrAlaAlaIleLysAsnAspGluPheIleSer 1242

3057 TATACTAC-ACAGAAAGAACCTTGAGGACATTATGCCAAAGTGAATAGCCAGTGACAA 3115

Db 1243 phevAlGlyThrTrpMetLysLeuGluThrIleIleLeuSerLysLeuSerGlnGln 1262

QY 3116 AAAGATACATACTGTATGATTCACCTTCTA 3145

Db 1263 LysThrLysHisArgIlePheSerLeuIle 1272

RESULT 10

probable pol polyprotein-related protein 4 - rat

C:\Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

R;Schmitz, E.; Mohr, E.

A/Reference number: S21345

A;Molecule type: DNA

A; Cross-references: UNIPROT:Q63306; EMBL:X53581; NID:g56586; PIDN:CAA37647.1; P

C;Keywords: polypeptide

Alignment Scores:

Score:	346.50	Matches:	68
--------	--------	----------	----

Best Local Similarity:	46.58%	Mismatches:	46
------------------------	--------	-------------	----

DB:	2	Gaps:	1
-----	---	-------	---

US-09-396-985B-47 (1-18989) x S21348 (1-275)

2709 AATAAAGTGTGGTGAAGATGTGAAAAAATGAGAACTCCTGTACACCATTTGTGGAA 2768

Db 128 AspaAsnArgSTrArgGlyCysGlyIuArgGlyThrLeuLeuHisCysSTrTrpAsp 147

2769 TGTAAATGTTACAGATGCTGTGGAGATCATATGTTGGGTCTCAAAAATTAAAAATA 2828

```
Db 148 CysLeuValIglProPheTrpLysSerValTrpArgPheLeuArgLysLeuAsp167
Qy 2829 GATTACACATGATGCAGCATCATCTGAGTACAGTATCCAAAAGATTGAAAACA 2888
Db 168 GluLeuProGluAspProAlaIleProLeuGluGlyIleTyProLysAspAlaProThr 187
Qy 2889 GAGACTTAAAGATATTGTGACCAACATGTTATGACGATTTATTCACATAGCTAAC 2948
Db 188 TyrLys--LysAspThrCysSerThrMetPheIleAlaIleuPheIleIleAlaArg 206
Qy 2949 GTGGGCAACATGACAGTGTCCATGAAACAGCAATGATPAGCAAAATGTGCTATA 3008
Db 207 SerTrpLysGluProArgCysAspSerThrGluGluTrpIleGluLysMetTrpTyrIle 226
Qy 3009 CATCAATGAAATATTGTTGCTTAAAGAAAGAGGCTTGATCTATCAACACAG 3068
Db 227 TyrThrMetGluTyrTrpSerAlaIleLysAsnAsnGluPheMetLysPheValGlyLys 246
Qy 3069 AA-AAGAACCTTGAGAGCATTTATGCAAAATGAAATACCCAGTGCACAAAAGATACATAC 3127
Db 247 TrpLeuGluLeuGluAsnIleIleLeuSerLysLeuThrGlnSerGlnLysAspIleHis 266
Qy 3128 TGATGATTCACCTTCTA 3145
Db 267 GlyMetHisSerLeuIle 272
```

RESULT 11

```
138588 reverse transcriptase homolog - human retrotransposon L1
N/Alternate names: ORF2 protein
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 138588
R/Holmes, S.E.; Dombroski, B.A.; Krebs, C.M.; Boehm, C.D.; Kazazian, H.H.
Nature Genet. 7, 143-148, 1994
A/Title: A new retrotransposable human L1 element from the LBR2 locus on chromosome 1q
A/Reference number: 138587; MUID:95004577; PMID:7920631
A/Accession: 138588
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1275 <RES>
A/Cross-references: UNIPROT:Q12881; EMBL:U09116; NID:9483914; PIDN:AAB60345.1; PID:94839
C/Superfamily: pol polypeptide
```

Alignment Scores:

```
Pred. NO.: 4.87e-20 Length: 1275
Score: 345.00 Matches: 67
Percent Similarity: 64.67% Conservative: 30
Best Local Similarity: 44.67% Mismatches: 53
Query Match: 1.04% Indels: 1
DB: Gaps: 0
```

US-09-396-985b-47 (1-18989) x 138588 (1-1275)

```
Qy 2697 AGACCAAGAAATGTAATTAAGTGTGGAAGATGTGAAAAATGAGAACTCTGTACAC 2756
Db 1123 LysLysSerGlyAsnAsnArgCysTrpArgGlyCysGlyGluIleGlyThrLeuLeuHis 1142
Qy 2757 CATTGTGGGAATGTAATTAAGTACAGATGCTGTGAGAAATCATGTTGGTGGCTCAAA 2816
Db 1143 CysTrpTrpAspCysLysLeuValGlnProLeuTrpLysSerValTrpArgPheLeuArg 1162
Qy 2817 AAATTAATAATGATTTTACCAATGATCCAGATCTCACTTGCAGTACATCAACAA 2876
Db 1163 AspLeuGluLeuGluIleProPheAspProAlaIleProLeuLeuGlyIleTyProGlu 1182
Qy 2877 GAATTAAGAAACAGAGACTTAAAGATATTGTGACCAACATGTTATGAGAGATTTATTC 2936
Db 1183 AspTyrLysSerCysCysTyrLysAspThrCysThrArgMetPheIleAlaIleuPhe 1202
Qy 2937 ACAATAGCTAACGTTGGCAACATGCAAGTGTCCATGAAACAGCAAAATGATAGCAAA 2996
Db 1263 LysThrLysHisArgIlePheSerLeuIle 1272
```

```
Db 1203 ThrIleAlaLysThrTrpAsnGlnProLysCysBProThrMetIleAspTrpIleLysLys 1222
Qy 2997 ATGTGCTATATACATACAAATGAAATATTGTTACGCTTTAAAAAGAGAGCTTTGATC 3056
Db 1223 MetTrpHisIleTyrThrMetGluTyrTrpAlaIleLysAsnAspGluPheIleSer 1242
Qy 3057 TATACTAC-ACAGAAAAGAACTTGAGACATTTATGCAAAATGAAATAGCCAGTGCACA 3115
Db 1243 PheValGlyThrTrpMetLysLeuGluThrIleIleLeuSerLysLeuSerGlnGluGln 1262
Qy 3116 AAAGATACATACCTGATGATTCACCTTCTA 3145
Db 1263 LysThrLysHisArgIlePheSerLeuIle 1272
```

RESULT 12

```
B28096 line-1 protein ORF2 - human
C/Species: Homo sapiens (man)
C/Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 09-Jul-2004
C/Accession: B28096
R/Skowronski, J.; Fanning, T.G.; Singer, M.F.
Mol. Cell. Biol. 8, 1385-1397, 1988
A/Title: Unit-length line-1 transcripts in human teratocarcinoma cells.
A/Reference number: A28096; MUID:88246405; PMID:2454389
A/Accession: B28096
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1275 <SKO>
A/Cross-references: UNIPROT:Q15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:000363; UNIPROT:Q9Y5K0; UNIPROT:000366; UNIPROT:08TE30; UNIPROT:000375
C/Superfamily: pol polypeptide
```

Alignment Scores:

```
Pred. NO.: 5.91e-20 Length: 1275
Score: 344.00 Matches: 67
Percent Similarity: 64.00% Conservative: 29
Best Local Similarity: 44.67% Mismatches: 54
Query Match: 1.04% Indels: 1
DB: Gaps: 0
```

US-09-396-985b-47 (1-18989) x B28096 (1-1275)

```
Qy 2697 AGACCAAGAAATGTAATTAAGTGTGGAAGATGTGAAAAATGAGAACTCTGTACAC 2756
Db 1123 LysLysSerGlyAsnAsnArgCysTrpArgGlyCysGlyGluIleGlyThrLeuLeuHis 1142
Qy 2757 CATTGTGGGAATGTAATTAAGTACAGATGCTGTGAGAAATCATGTTGGTGGCTCAAA 2816
Db 1143 CysTrpTrpAspCysLysLeuValGlnProLeuTrpLysSerValTrpArgPheLeuArg 1162
Qy 2817 AAATTAATAATGATTTTACCAATGATCCAGATCTCACTTGCAGTACATCAACAA 2876
Db 1163 AspLeuGluLeuGluIleProPheAspProAlaIleProLeuLeuGlyIleTyProAsn 1182
Qy 2877 GAATTAAGAAACAGAGACTTAAAGATATTGTGACCAACATGTTATGAGAGATTTATTC 2936
Db 1183 AspTyrLysSerCysCysTyrLysAspThrCysThrArgMetPheIleAlaIleuPhe 1202
Qy 2937 ACAATAGCTAACGTTGGCAACATGCAAGTGTCCATGAAACAGCAAAATGATAGCAAA 2996
Db 1203 ThrIleAlaLysThrTrpAsnGlnProLysCysBProThrMetIleAspTrpIleLysLys 1222
Qy 2997 ATGTGCTATATACATACAAATGAAATATTGTGACCAACATGTTATGAGAGATTTATTC 3056
Db 1223 MetTrpHisIleTyrThrMetGluTyrTrpAlaIleLysAsnAspGluPheSer 1242
Qy 3057 TATACTAC-ACAGAAAAGAACTTGAGACATTTATGCAAAATGAAATAGCCAGTGCACA 3115
Db 1243 PheValGlyThrTrpMetLysLeuGluThrIleIleLeuSerLysLeuSerGlnGluGln 1262
Qy 3116 AAAGATACATACCTGATGATTCACCTTCTA 3145
Db 1263 LysThrLysHisArgIlePheSerLeuIle 1272
```


A:Reference number: A93381; MUID:86230917; PMID:2423883

A:Accession: B25313

A:Status: conceptual translation of pseudogene

A:Molecule type: DNA

A:Residues: 1-1260 <HAT>

A:Cross-references: UNIPROT:P08548

A>Note: This sequence was constructed from an alignment of six sequences, determined by

C:Keywords: reverse transcriptase; pseudogene

Alignment Scores:

Pred. No.:	3,13e-18	Length:	1260
Score:	323.50	Matches:	62
Percent Similarity:	66.67%	Conservative:	28
Best Local Similarity:	45.93%	Mismatches:	44
Query Match:	0.98%	Indels:	2
DB:	4	Gaps:	1

US-09-396-985b-47 (1-18989) x GNLRL1 (1-1260)

```

QY 2709 AATATAAGTGTGTGTAAGATGTGAAAAAATGAGAACTCTGTACACCATTTGTGGGA 2768
    ||| :||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1126 AsnGlnArgCysTrpArgGlyCysGlyGlyLysGlyThrLeuLeuHisCysTrpTrpGlu 1145
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2769 TGTAAATGTACAGAGCTGTGAGAAATCATATGTGGTCTCAAAAAATTAAATA 2828
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1146 CysProLeuIleArgSerPheTrpLysAspValTrpArgIleLeuArgAspLeuIle 1165
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2829 GATTACACATGATCCAGCATCTCATCTTGAGTACGTATCCAAAAAATGAAACA 2888
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1166 AspLeuProPheAspProIleIleProLeuGlyLeuTyProGluAspGlnLysSer 1185
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2889 GAGACTTTAAGAGATTTGTACAAACCATGTTATGCGAGCATATTTCACATAGCTAAC 2948
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1186 GlnTyrsenLysAspIleCysThrArgMetPheIleAlaGlnPheIleIleAlaLys 1205
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 2949 GTGGGCAACATGCAAGTGTCCATGAACAGACAATGATAGCAAAATGTGCTATA 3008
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1206 SerTrpLysLysProLysCysProSerThrIsgluTrpHisSerLysLeuTrpTyrMet 1225
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3009 CATACATGGAATTTGTTGACGCTT-AAAAGAAGAGAGGCTTGAATCTATAC--TAC 3064
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1226 TyrThrMetGluTyTyAlaAlaLeuLysLysAspGlyAspPheThrSerPheMetCphe 1245
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3065 ACAGAAAAAGAACTTGAGAGCATTTATGCAAGTGAATTAAGCCAG 3109
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1246 ThrTrpMetGluLeuGlnHisIleLeuLeuSerLysValSerGln 1260
    ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

Search completed: March 29, 2005, 19:47:42
Job time : 445 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:30:23 ; Search time 964.5 Seconds

(without alignments)
20163.549 Million cell updates/sec

Title: US-09-396-985B-47

Perfect score: 33065

Sequence: 1 tccctctctctctcacatc.....catgaabdcabdcabdc 18989

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
	Ygapop 10.0	Ygapext 0.5
	Fgapop 6.0	Fgapext 7.0
	Delop 6.0	Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p model -DEV=xlh
-Q=/cgn2_1/USFNO_spool/US09396985/runat_28032005.155743.21146/app.query.fasta.1.85098
-DB=UniProt_03 -QEXT=faetan -SUFFIX=rup -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09396985 @CGN 1.1 5213 @runat 28032005.155743.21146 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUEYER -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt 03:*

1: uniProt_sprot:.*
2: uniProt_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3905.5	11.8	839	1	TTR4_HUMAN
2	3891.5	11.8	839	1	TTR4_PANPA
3	3878.5	11.7	837	2	Q8SPB8
4	3750.5	11.3	828	1	TTR4_PONPY
5	3621.5	11.0	826	1	TTR4_PAPAN
6	2977.5	9.0	843	1	TTR4_HORSE
7	2971.5	9.0	841	1	TTR4_BOVIN
8	2968.5	9.0	841	2	Q8SQS5
9	2966.5	9.0	841	2	Q8WCD5
10	2957.5	8.9	841	2	Q6WCD4
11	2937	8.9	833	1	TTR4_PELCA
12	2867	8.7	841	1	TTR4_PIG
13	2753.5	8.3	839	2	Q8MIQ2
14	2738	8.3	838	1	TTR4_CRIGR
15	2599	7.9	835	2	Q8K2T5
16	2594	7.8	835	1	TTR4_MOUSE

17	2579.5	7.8	835	1	TTR4_RAT	O9GX05	rattus norv
18	2206	6.7	836	2	Q8SOH3	O86H33	canis famli
19	1696.5	5.1	843	2	Q7ZTG5	Q7ZTG5	gallus gall
20	1173.5	3.5	819	2	Q6TS41	Q6TS41	brachydanio
21	1162.5	3.5	817	2	Q6NV08	Q6NV08	brachydanio
22	834.5	2.5	258	2	Q70EK4	Q70EK4	sus scrofa
23	637.5	1.9	991	2	Q6RSN8	Q6RSN8	mus musculu
24	626.5	1.9	961	2	Q76CT9	Q76CT9	parallichth
25	620.5	1.9	940	2	Q8T753	Q8T753	branchiost
26	618.5	1.9	945	2	Q801F9	Q801F9	carassius a
27	618.5	1.9	961	2	Q76CT7	Q76CT7	parallichth
28	595.5	1.8	973	2	Q6KCT7	Q6KCT7	oncorhynch
29	575.5	1.7	785	2	Q76L24	Q76L24	sus scrofa
30	571.5	1.7	784	2	Q6YGM2	Q6YGM2	rattus norv
31	570.5	1.7	784	2	TTR2_MOUSE	Q9GQ77	mus musculu
32	569.5	1.7	784	2	Q8K3D9	Q8K3D9	mus musculu
33	566.5	1.7	784	2	Q811T5	Q811T5	mus musculu
34	564.5	1.7	785	2	Q6TN21	Q6TN21	sus scrofa
35	563.5	1.7	661	1	C180_MOUSE	Q62192	mus musculu
36	562	1.7	781	1	T122_CHICK	Q9GQ66	gallus gall
37	560.5	1.7	784	1	TTR2_HUMAN	O60603	homo sapien
38	560.5	1.7	793	1	T121_CHICK	Q9GQ78	gallus gall
39	553.5	1.7	784	1	TTR2_CRIGR	Q9G1F8	cricetulus
40	549	1.7	784	2	Q6T752	Q6T752	equus caball
41	548.5	1.7	784	1	TTR2_MACFA	Q95M53	macaca fasc
42	545.5	1.6	661	2	Q8C251	Q8C251	mus musculu
43	543.5	1.6	785	2	Q689D1	Q689D1	canis famli
44	543.5	1.6	1032	1	TTR8_MOUSE	P58682	mus musculu
45	536	1.6	1050	1	TTR7_MOUSE	P58681	mus musculu

ALIGNMENTS

RESULT 1

ID	TTR4_HUMAN	STANDARD;	PRT;	839 AA.
AC	O00206; Q9UK78; Q9UW57;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	25-JAN-2005 (Rel. 46, Last annotation update)			
DE	Toll1-like receptor 4 precursor (Toll1).			
GN	Name=TTR4;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RX	MEDLINE=97379437; PubMed=9237759; DOI=10.1038/41131;			
RA	Medzhitov R., Preston-Hurlbut P., Janeway C.A. Jr.;			
RT	"A human homologue of the Drosophila Toll protein signals activation			
RT	of adaptive immunity.";			
RL	Nature 388:394-397(1997).			
RN	[2]			
RP	SEQUENCE OF 41-839 FROM N.A.			
RC	TISSUE=Fetal liver, lung, and placenta;			
RX	MEDLINE=98118556; PubMed=9435236; DOI=10.1073/pnas.95.2.588;			
RA	Rock F.L., Hardman G., Timans J.C., Kastelein R.A., Bazan J.F.;			
RT	"A family of human receptors structurally related to Drosophila			
RT	Toll.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 95:588-593(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.			
RX	MEDLINE=20558910; PubMed=11104518;			
RA	Smirnova I., Poltorak A., Chan R.K.L., McBride C., Beutler B.;			
RT	"Phylogenetic variation and polymorphism at the Toll-like receptor 4			
RT	locus (TTR4).";			
RL	Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANTS GLY-299 AND ILE-399.			
RX	MEDLINE=20296622; PubMed=10835634; DOI=10.1038/76048;			
RA	Arbour N.C., Lorenz E., Schutte B.C., Zahner J., Kline J.N., Jones M.,			

RA Frees K, Matt J.L., Schwartz D.A.;
RA "TLR4 mutations are associated with endotoxin hyporesponsiveness in
RT humans.";
RL Nat. Genet. 25:187-191(2000).
RN [5]
RP SEQUENCE OF 24-38.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RL verified cleavage sites.";
RN Protein Sci. 13:2819-2824(2004).
RP MUTAGENESIS OF GLU-697; ARG-710; ASP-711 AND PRO-714.
RX MEDLINE=20531768; PubMed=11081518; DOI=10.1038/35040600;
RA Xu Y., Tao X., Shen B., Hornig T., Medzhitov R., Manley J.L., Tong L.;
RT "Structural basis for signal transduction by the Toll/interleukin-1
RL receptor domains";
RN Nature 408:111-115(2000).
RP CARBOHYDRATE-LINKAGE SITES, AND MUTAGENESIS OF ASN-526 AND ASN-575.
RX MEDLINE=21648731; PubMed=11706042; DOI=10.1074/jbc.M109910200;
RA da Silva Correia J., Ulevitch R.J.;
RT "MD-2 and TLR4 N-linked glycosylations are important for a functional
RL 11polysaccharide receptor.";
RN J Biol. Chem. 277:1845-1854(2002).
RP VARIANTS ARG-188; SER-246; GLY-299; SER-329; ILE-399; LEU-443;
RX LYS-474; HIS-510; ARG-694; HIS-766 AND HIS-834.
RA MEDLINE=21405531; PubMed=11514453;
RT Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RL "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
in humans.";
RN Genetics 158:1657-1664(2001).
RP FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
RX immune response to bacterial lipopolysaccharide (LPS). Acts via
RA MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
RT secretion and the inflammatory response.
RL
RN
RP SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
RX multi-protein complex containing at least CD14, LY96 and TLR4.
RA Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
RT their respective TIR domains.
RL
RN SUBCELLULAR LOCATION: Type I membrane protein.
RX
RP TISSUE SPECIFICITY: Highly expressed in placenta, spleen and
RA peripheral blood leukocytes. Detected in monocytes, macrophages,
RT dendritic cells and several types of T-cells.
RL
RN PTM: N-glycosylated. Glycosylation of Asn-526 and Asn-575 seems to
RX be necessary for the expression of TLR4 on the cell surface and
RA the LPS-response. Likewise, mutants lacking two or more of the
RT other N-glycosylation sites were deficient in interaction with
RL LPS.
RN
RP POLYMORPHISM: Allele TLR4*B (GLY-299, ILE-399) is associated with
RX a blunted response to inhaled LPS.
RA
RP SIMILARITY: Belongs to the Toll-like receptor family.
RX
RP SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
RA
RP SIMILARITY: Contains 1 TIR domain.
RX
RP THIS SWISS-PROT entry is copyright. It is produced through a collaboration
RA between the Swiss Institute of Bioinformatics and the EMBL outstation -
RT the European Bioinformatics Institute. There are no restrictions on its
RL use by non-profit institutions as long as its content is in no way
RN modified and this statement is not removed. Usage by and for commercial
RX entities requires a license agreement (see <http://www.isb-sib.ch/announcement/>
RA or send an email to license@isb-sib.ch).
RT
RL
RN EMBL; U93091; AAC60327.1; -
RX EMBL; U88880; AAC34135.1; -
RA EMBL; AF177765; AAF05316.1; -
RT EMBL; AF177766; AAF07823.1; -
RL EMBL; AF172171; AAF69753.1; -
RN EMBL; AF172169; AAF69753.1; JOINED.
RX EMBL; AF172170; AAF69753.1; JOINED.
RA HSSP; 060603; 1EYV.
RT
RL
RN Genew; HGNC:11850; TLR4.

DR	MIR; 60030;	-	C:integral to plasma membrane; TAS.
DR	GO; GO:0005887;		C:lipopolysaccharide receptor complex; NAS.
DR	GO; GO:0046886;		F:lipopolysaccharide binding; NAS.
DR	GO; GO:0001530;		F:transmembrane receptor activity; NAS.
DR	GO; GO:0004888;		P:activation of NF-kappaB-inducing kinase; ISS.
DR	GO; GO:0016046;		P:detection of fungi; NAS.
DR	GO; GO:0009598;		P:detection of pathogenic bacteria; NAS.
DR	GO; GO:0006935;		P:immune response; TAS.
DR	GO; GO:0042116;		P:macrophage activation; IMP.
DR	GO; GO:0045576;		P:negative regulation of osteoclast different. . ; NAS
DR	GO; GO:0045671;		P:negative regulation of interleukin-1 biosyn. . ; ISS
DR	GO; GO:0045084;		P:positive regulation of interleukin-12 biosyn. . ; NAS
DR	GO; GO:0004538;		P:positive regulation of interleukin-13 biosyn. . ; ISS
DR	GO; GO:0045410;		P:positive regulation of interleukin-6 biosyn. . ; ISS
DR	GO; GO:0007165;		P:signal transduction; TAS.
DR	GO; GO:0042088;		P:T-helper 1 type immune response; NAS.
DR	InterPro; IPR001611;	LRR	
DR	InterPro; IPR000483;	LRR_Cterm.	
DR	InterPro; IPR003591;	LRR_Typ.	
DR	InterPro; IPR001571;	TIR.	
DR	Pfam; PF00560;	LRR; 12.	
DR	Pfam; PF01463;	LRRCT; 1.	
DR	Pfam; PF01582;	TIR; 1.	
DR	PRINTS; PR00019;	LEURICHRPT.	
DR	SMART; SMO0369;	LRR_Typ; 2.	
DR	SMART; SMO0082;	LRRCT; 1.	
DR	SMART; SMO0255;	TIR; 1.	
KM	PROSITE; PS50104;	TIR; 1.	
KM	Direct protein sequencing; Glycoprotein; Immune response; Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;		
KW	Inflammatcry response; Leucine-rich repeat; Polymorphism; Receptor;		
KW	Repeat; Signal; Transmembrane.		
FT	SIGNAL	1	23
FT	CHAIN	24	839
FT	DOMAIN	24	631
FT	TRANSNEM	632	652
FT	DOMAIN	653	839
FT	REPEAT	52	76
FT	REPEAT	77	100
FT	REPEAT	101	124
FT	REPEAT	128	149
FT	REPEAT	150	173
FT	REPEAT	174	197
FT	REPEAT	203	225
FT	REPEAT	228	252
FT	REPEAT	277	303
FT	REPEAT	307	330
FT	REPEAT	332	350
FT	REPEAT	351	372
FT	REPEAT	373	398
FT	REPEAT	400	421
FT	REPEAT	422	445
FT	REPEAT	447	469
FT	REPEAT	470	494
FT	REPEAT	495	518
FT	REPEAT	520	541
FT	REPEAT	543	566
FT	REPEAT	568	592
FT	DOMAIN	672	818
FT	CARBOHYD	35	35
FT	CARBOHYD	173	173
FT	CARBOHYD	205	205
FT	CARBOHYD	282	282
FT	CARBOHYD	309	309
FT	CARBOHYD	497	497
FT	CARBOHYD	526	526
FT	CARBOHYD	575	575
FT	CARBOHYD	624	624
FT	CARBOHYD	630	630
FT	VARIANT	188	188
FT	VARIANT	246	246
FT	Toll-like receptor 4. Extracellular (Potential). Potential. Cytoplasmic (Potential). LRR 1. LRR 2. LRR 3. LRR 4. LRR 5. LRR 6. LRR 7. LRR 8. LRR 9. LRR 10. LRR 11. LRR 12. LRR 13. LRR 14. LRR 15. LRR 16. LRR 17. LRR 18. LRR 19. LRR 20. LRR 21. TIR. N-linked (GLcNAc. . .) N-linked (GLcNAc. . .) N-linked (GLcNAc. . .) N-linked (GLcNAc. . .) N-linked (GLcNAc. . .) N-linked (GLcNAc. . .) N-linked (GLcNAc. . .) N-linked (GLcNAc. . .) N-linked (GLcNAc. . .) N-linked (GLcNAc. . .) O -> R. /FTID=VAR_018729. C -> S.		

D	220	roglYalAphEylsGluIlIeArgLeuHlVlyslsLeuthrLeuArGdaAenPheApsSeL	240
Q	12697	TAAATGTAATGAAAACTTGTAATCAAGGCTCGGCTGGTTAGAAAGTCAATCGTTGGTTC	12756
D	240	euaenValmeLysrThrCyAlIeGInGlyLeuAlIagIleuGluValHlEArGLeuValL	260
Q	12757	TGGGAGAAATTTAGAAATGAAAGAAACTTGGAAGAAATTGCAAAATCTGCTCTAGAGGCC	12813
D	260	eugIyGluPheArGsaenGluGlyAsnLeuGluYlsPheApsLysSerAlaLeuGluGlyL	280
Q	12817	TGTGCAATTTGACCAATGGAAGAAATTCGAAATTCACATTAATTAAGCTCTACCTCGATGATA	12876
D	280	eucYsaenLeuThrIlIeGluGluPheArgLeuAlArYLeuApsLyrTYrLeuApsApsI	300
Q	12877	TTATTAATTAATTAATTTGTTTGACAAATGTTTCTTCAATTTCCCTGGAGAGTGACTA	12936
D	300	lelleApsLeuPheAenCyLeuThrAsnValSerSerPheSerLeuValSerValThrI	320
Q	12937	TTGAAAGGGTAAAGACTTTTCTTAATTAATTCGATGCGAACACTTTAGAATTAGTTAACT	12996
D	320	legIuArGValYlsApsPheSerTYAsnPhedYIyrpGlnHlsleuGluLeuValAsnC	340
Q	12997	GTAATTTTGACAGTTTCCCAACTTGAAACTCAAACTCTCAAAAGCTTACTTCACTT	13056
D	340	YslYsPheGlyGlnPheProThrLeuYlsLeuYlsSerLeuYsArGLeuThrPheThrs	360
Q	13057	CCAACAAAGGTGGGAATGCTTTTTCAGAAAGTTGATATACCAAGCTTGAAGTTCTGATC	13116
D	360	erAenYsGlyGlyAsnAlaPheSerGluValApsLeuProSerLeuGluPheLeuApsI	380
Q	13117	TCAGTAGAAAYGGCTTGAGTTTCAAGAGTGTCTGTTCTCAAGATGATTTTGGACAAACA	13176
D	380	eusErArGaenGlyLeuSerPheYsGlyCyecYserGlnSerApsPheGlyThrThrs	400
Q	13177	GCTTAAGATTTTAAGATCTGAGCTTCAAGGCTTATTAACATGAGTTCAAACTTCTTG	13236
D	400	erleuYsTYrLeuApsLeuSerPheAsnGlyAlIeThrMetSerSerAenPheLeuG	420
Q	13237	GCTTAGAACATCAGAACATCTGGAATTCAGAGATTCCAATTTGAAACAAATGAGAGAT	13296
D	420	lyeugIuGlnLeuGluHlsleuApsPheGlnHlsSerAenLeuYsGlnMetSerGlnP	440
Q	13297	TTTCAGTATTCCTATCACTCAGAAACCTCATTTACCTTGACATTTCTCACTCAACCA	13356
D	440	heserValPheLeuSerLeuArGAsnLeuIlIeYrLeuApsIlIeSerHlsThrHlsThAr	460
Q	13357	GAGTTGCTTTCAATGCAATCTTCATAGGCTTGTCAGGTCGAAAGTCTTGAAATGCGCTG	13416
D	460	rgYAlaAPheAenGlyIlIePheAsnGlyLeuSerSerLeuGluValLeuYsMetAlaG	480
Q	13417	GCAATTCCTTCCAGGAAAACTTCCTCCAGATATCTTCAACAGCGTGAAGAACTTGACCT	13476
D	480	lyAsnErPheGlnGluAenPheLeuPheApsIlIePheHrGluAeArGAsnLeuThrP	500
Q	13477	TTCCTGACCTCTCAGTGTCAACTGGAAGAGTGTGCCAACAGACTTAACTCACTCT	13536
D	500	heleuApsLeuSerGlnCyGlnLeuGluGlnLeuSerProThrAlaPheAenSerLeuS	520
Q	13537	CGAGTCTTCAAGTACTTAATATGAGCCACAAACAATCTTTTCATTGATAGTTCCTT	13596
D	520	erSerLeuGlnValIlIeAenMetSerHlsAsnApsPheSerLeuApsThrPheProT	540
Q	13597	ATTAAGTCTCGAATCCCTCCAGGTTCTTGATTAACGTTCAATACAAAGACTTCCA	13656
D	540	YrlyrCyAsLeuAenSerLeuGlnValLeuApsLYrSerLeuApsHlsIlIeMetThrSerL	560
Q	13657	AAAAACAGAACTACAGCAATTTTCCAAAGTAGTCACTTCTTAATCTTACTCAGAATG	13716
D	560	YslYsGlnGluLeuGlnHlsPheProSerSerLeuAlaPheLeuAenLeuThrGlnApsA	580
Q	13717	ACTTTGCTTGTACTGTGAACACCAAGTTTCTCGAATGATCAAGACCAAGAGCAGC	13776
D	580	sPheHlsCyThrCyAsGluHlsGlnSerPheLeuGlnTrpIlIeYsArGlnApsGlnL	600

QY	13177	TCCTGGTGAAGTTGAACGAATGGAATGTGCAACACCTTCAGATTAAGCGGGAGTCCTG	13836
Db	600	euleuValaGluValaGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProV	620
QY	13837	TGCTGAGTTTGAATATCACTCGTCAGATGAATGAAGCAATCATTTGGTGTGTGGATCTCA	138966
Db	620	alleuSerLeuAsnIleThrCysGlnMetAsnLysIleIleGlyValSerValLeuS	640
QY	13897	GTCGTCTTGTAGTATCTGTTGTAGACGTTCTGGCTATTAAGTTCTATTTTCACTGTATGC	139566
Db	640	erValleuValaValSerValaValaValleuValaGlyLysPheThyPheHisLeuMetL	660
QY	13957	TTCTTGCTGGCTGCAATAAAGTAGTATGAGGTGAAAAACATCTATGATGCTTTGTATCT	140166
Db	660	euleuValaGlyCysIleLeuValGlyArgGlnGlnAsnIleThyArgAlaAlaPheValIleT	680
QY	14017	ACTCAAGCCAGGAATGAGAGCATGGGGTAGAAGAAAGCATAGCATTAAGAAATTTAGAGAAAGGGG	140767
Db	680	yrSerSerGlnAspGlnAspTrpValaArgAsnGlnLeuValaLysAsnLeuGlnGlnGlyV	700
QY	14077	TGCCTCCATTTACAGCTCTGCGCTTCACATACAGAGACTTATTTCCCGGTGTGGCCATTGCTG	141366
Db	700	alPProPheGlnIleuCysLeuHisIleThyArgAspPheIleProGlyValaIleAlaIaA	720
QY	14137	CCAAATCATTCATGAAGAGTTTTCATATAAGCCGAAAGGATGTTGTGTGGTGTCCACAC	141966
Db	720	IaenIleIleHisGlnGlnGlyPheHisLysSerArgLysValaIleValaValaSerGlnH	740
QY	14197	ACCTCATCCAGAGCGCGGTGGTGTATCTTTGAATATGAGATGTGCTCAGACCTGGCACTTTC	142566
Db	740	IsPheIleIleGlnSerArgTrpCysIleLeuPheIleuThyGlnIleAlaGlnIleThrPglInPheL	760
QY	14257	TGAGCAGTCGTGCTGTATCATCTTCACTTGTCTCTGCAAGAGGTGAGAAAGACCTCTGCTCA	143166
Db	760	eusSerSerArgAlaGlyIleIlePheIleValleuGlnLysValaGlnLysThyLeuLeuA	780
QY	14317	GGCAGCAGGTGGAGCTGTACCGGCTTTCAGACGAAACAATTACCTGGAGTGGAGAGACA	143767
Db	780	rGlnGlnIleValaGlnLeuThyArgLeuLeuSerArgAsnIleThyGlnGlnIleThrPglInAspS	800
QY	14377	GTCGTCTGGGCGGACATCTTCTGTGAGAGCACTCAGAAAAGCCCTGCTGATGTATTAAT	144366
Db	800	erValleuGlnIleArgHisIleIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysS	820
QY	14437	CATGGAAATCCAGAAAGAAACAGTGGGTACAGATGCAATTTGGCGAAGAAACAATCTATTC	14495
Db	820	erTrpAsnProGlnGlnIleThyValaGlnThyGlnCysAsnIlePglInGlnIleAlaThrSerIle	839
RESULT 2			
TLR4_PANPA	STANDARD;	PRT;	839 AA.
AC	Q9TTN0;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Toll-like receptor 4 precursor.		
GN	Name=TLR4;		
OS	Pan paniscus (Pygmy chimpanzee) (Bonobo).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.		
OX	NCBI_TaxId=9597;		
FN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20558910; PubMed=11104518;		
RA	Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;		
RT	"Polygenetic variation and polymorphism at the Toll-like receptor 4		
RT	locus (TLR4).";		
RL	Genome Biol. 1:RESEARCH002.1-RESEARCH002.10 (2000).		
CC	-I- FUNCTION: Cooperates with Lys6 and CD14 to mediate the innate		
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via		
CC	MyD88, TRAF6 and IRAK4, leading to NF-kappa-B activation, cytokine		
CC	secretion and the inflammatory response (by similarity).		

CC	-1	SUBUNIT:	Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via their respective TIR domains (By similarity).	
CC	-1	SUBCELLULAR LOCATION:	Type I membrane protein (By similarity).	
CC	-1	SIMILARITY:	Belongs to the Toll-like receptor family.	
CC	-1	SIMILARITY:	Contains 21 leucine-rich (LRR) repeats.	
CC	-1	SIMILARITY:	Contains 1 TIR domain.	
CC			-----	
CC			This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch).	
CC			-----	
DR	EMBL	AF179220	AAFO5330.1; -	
DR	EMBL	AF179218	AAFO5330.1; JOINED.	
DR	EMBL	AF179219	AAFO5330.1; JOINED.	
DR	HSSP	Q15399	1FVY.	
DR	GO	GO:0046696	C:lipopolysaccharide receptor complex; ISS.	
DR	GO	GO:0001530	F:lipopolysaccharide binding; ISS.	
DR	GO	GO:0004888	P:transmembrane receptor activity; ISS.	
DR	GO	GO:0007250	P:activation of NF-kappaB-inducing kinase; ISS.	
DR	GO	GO:0016046	P:detection of fungi; ISS.	
DR	GO	GO:0009598	P:detection of pathogenic bacteria; ISS.	
DR	GO	GO:0042116	P:macrophage activation; ISS.	
DR	GO	GO:0045576	P:mast cell activation; ISS.	
DR	GO	GO:0045671	P:negative regulation of osteoclast different. . . ; ISS.	
DR	GO	GO:0045362	P:positive regulation of interleukin-1 biosyn. . . ; ISS.	
DR	GO	GO:0045084	P:positive regulation of interleukin-12 biosyn. . . ; ISS.	
DR	GO	GO:0045366	P:positive regulation of interleukin-13 biosyn. . . ; ISS.	
DR	GO	GO:0054510	P:positive regulation of interleukin-6 biosyn. . . ; ISS.	
DR	GO	GO:0042088	P:T-helper 1 type immune response; ISS.	
DR	InterPro	IPR001611	LRR	
DR	InterPro	IPR000483	LRR_Cterm	
DR	InterPro	IPR003591	LRR_Typ.	
DR	InterPro	IPR001571	TIR	
DR	Pfam	PF00560	LRR; 12.	
DR	Pfam	PF01463	LRRCT; 1.	
DR	Pfam	PF01582	TIR; 1.	
DR	PRINTS	PR00019	LEURICRPT.	
DR	SMART	SM00369	LRR_Typ; 2.	
DR	SMART	SM00082	LRRCT; 1.	
DR	SMART	SM00255	TIR; 1.	
DR	PROSITE	PS50104	TIR; 1.	
KW	Glycoprotein		Immune response; Inflammatory response; Leucine-rich repeat; Receptor; Signal; Transmembrane.	
FT	SIGNAL	1	23	Potential.
FT	CHAIN	24	839	Toll-like receptor 4.
FT	DOMAIN	24	631	Extracellular (Potential).
FT	TRANSMEM	632	652	Potential.
FT	DOMAIN	653	839	Cytoplasmic (Potential).
FT	REPEAT	52	76	LRR 1.
FT	REPEAT	77	100	LRR 2.
FT	REPEAT	101	124	LRR 3.
FT	REPEAT	128	149	LRR 4.
FT	REPEAT	150	173	LRR 5.
FT	REPEAT	174	197	LRR 6.
FT	REPEAT	203	225	LRR 7.
FT	REPEAT	228	252	LRR 8.
FT	REPEAT	277	303	LRR 9.
FT	REPEAT	307	330	LRR 10.
FT	REPEAT	332	350	LRR 11.
FT	REPEAT	351	372	LRR 12.
FT	REPEAT	373	398	LRR 13.
FT	REPEAT	400	421	LRR 14.
FT	REPEAT	422	445	LRR 15.
FT	REPEAT	447	469	LRR 16.
FT	REPEAT	470	494	LRR 17.
FT	REPEAT	495	518	LRR 18.
FT	REPEAT	520	541	LRR 19.

FT REPEAT 543 566 LRR 20.
 FT REPEAT 568 592 LRR 21.
 FT DOMAIN 612 818
 FT CAROXYD 173 35 N-linked (GlcNAc . . .) (potential)
 FT CAROXYD 173 35 N-linked (GlcNAc . . .) (potential)
 FT CAROXYD 205 205 N-linked (GlcNAc . . .) (potential)
 FT CAROXYD 205 205 N-linked (GlcNAc . . .) (potential)
 FT CAROXYD 282 282 N-linked (GlcNAc . . .) (potential)
 FT CAROXYD 309 309 N-linked (GlcNAc . . .) (potential)
 FT CAROXYD 497 497 N-linked (GlcNAc . . .) (potential)
 FT CAROXYD 497 497 N-linked (GlcNAc . . .) (potential)
 FT CAROXYD 526 526 N-linked (GlcNAc . . .) (potential)
 FT CAROXYD 575 575 N-linked (GlcNAc . . .) (potential)
 FT CAROXYD 624 624 N-linked (GlcNAc . . .) (potential)
 FT CAROXYD 630 630 N-linked (GlcNAc . . .) (potential)
 SQ SEQUENCE 839 AA; 95637 MW; 3B328C5682127D37 CRC64;

Alignment Scores:

Pred. No.: 5,38e-305 Length: 839
 Score: 3891.50 Matches: 770
 Percent Similarity: 93.34% Conservative: 15
 Best Local Similarity: 91.56% Mismatches: 21
 Query Match: 11.77% Indels: 35
 DB: 1 Gaps: 6

US-09-396-985B-47 (1-18989) x TLR4_PANPA (1-839)

QY 11992 TGCCTATCATGATGCTTACATGACAAAGAGCTATCATGACAGCATATGATTA 12051
 DB 29 CysValaIGluValaProAsnIleThrItyrGlnCysMetGluLeuAsn----- 44
 QY 12052 TACTCATGTCGTGGGCTTCTTATTTGCTT-----ATTCATCATCATCTGCTG 12102
 DB 45 -----PheTyrIlePheProAsnLeuProPheSerThrIlyAsn 58
 QY 12103 CTTCATGCTTTCCTATGACACATCATATGACCA---TCACATCTGATGAAAGAGCTG 12159
 DB 59 LeuAspLeu-----SerPheAsnProLeuArgHis----- 68
 QY 12160 GATGACTAGATTAATTTCTATTTAGGTTCTTATTTCA--GCAGAAATATTAGATAT 12216
 DB 69 -----LeuGlySerTyrSerPhePheSerPheProGluLeu 80
 QY 12217 CAATGCTTTTATTCCTGTAGTGTGAATTCAGACAAATTGAGATGGGCTATTCAGA 12276
 DB 81 GluValaLeuAspLeu--SerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlns 100
 QY 12277 GCCTAAGCACCCTCTTACCTTAATATTTGACAGAAACCCCATCCAGAGTTTACGCCCTG 12336
 DB 100 erLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuG 120
 QY 12337 GAGCCTTTTCTGACATCAAGTTTACAGAGCTGTGGCTGTGAGACAAATCTAGCAT 12396
 DB 120 IlyAlaPheSerGlyLeuSerSerLeuGlnIlybLeuValaIAlaValaIuthrAsnLeuAlaS 140
 QY 12397 CTTCAGACACTTCCCATTTGACATCTCAAAACTTTGAAAGACTTATATGTGCTCA 12456
 DB 140 erLeuGluAsnPheProIleGlyHisLeuIlybThrLeuIlybGluLeuAsnValaIAlaHis 160
 QY 12457 ATCTTATTCATCTTTCAAAATTAAGTATTTTCTTAATTTGACCAATCTAGAGCACT 12516
 DB 160 snLeuIleGlnSerHisLeuSerProGluIlyrPheSerAsnLeuThrAsnLeuGluHis 180
 QY 12517 TGGACCTTTCCAGACAAAGATTCAAGATTTATTTGACAGACTTGGGGGTTCTACATC 12576
 DB 180 euAspLeuSerSerAsnIlybIleGlnSerIleTyrCysThrAspLeuArgValaLeuHisG 200
 QY 12577 AAATGCCCTTACTCATCTCTTTTAACTGTCCCTGAACCCCTATGAATTTATTCAC 12636
 DB 200 IlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnP 220
 QY 12637 CAGGTCATTTTAAAGAAATTTAGGCTTCAATAGCTGATTTTAAAGAAATATTTGATAGT 12696
 DB 220 roGlyAlaPheIlybGluIleArgLeuHisIlybLeuThrLeuArgAsnAsnPheAspSerL 240

QY 12697 TAAATGATGAAAACTTGATTCAGAGCTGCGTGGTTTGAAGACTCGTTGGTTTC 12756
 DB 240 euAsnValMetIlybThrCysIleGlnGluLeuAlaGlyLeuGluValaHisIlybGluVal 260
 QY 12757 TGGGAGAAATTTGAAGATGAAGAACTTGAAAAAGTTTGAACAATCTGCTTACAGGGCC 12816
 DB 260 euGlyGluPheArgAsnGluGlyAsnLeuGluIlybPheAspIlybSerAlaLeuGluGlyL 280
 QY 12817 TGTGCAATTTGACCACTTGAAGAAATTCGATTAAGCATTTGACACTACCTCGATGATA 12876
 DB 280 euCysAsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAsp 300
 QY 12877 TTAATGACTTATTAATGTTTGAACAATGTTTCTTCAATTTCCCTGCTGATGATGATA 12936
 DB 300 IeIleAspLeuPheAsnGlyLeuThrAsnValSerSerPheSerLeuValSerValThrI 320
 QY 12937 TTGAAGGGTAAAGACTTTTCTTATTAATTTGCAATGGCAACATTTAGAAATTAAGTAACT 12996
 DB 320 IeIlybSerValIlybAspPheSerTyrAsnPheGlyTyrGlnHisIleuGluLeuValaAsn 340
 QY 12997 GTAAATTTGACAGTTTCCCATTTGAACCTCAATCTCAAAAGCTTACCTTCACTT 13056
 DB 340 IlybAspPheGlyGlnPheProThrLeuIlybLeuIlybSerLeuIlybArgLeuThrPheHis 360
 QY 13057 CCAACAAAGTGGGAATGCTTTTTCAGAACTTGATCTTACCAAGCTTGAGTTTCTAGATC 13116
 DB 360 erAsnIlybGlyGlyAsnAlaPheSerGlyValaAspLeuProSerLeuGluIlybLeuAspL 380
 QY 13117 TCAGTAGAAATGCTTGAGTTTCAAGGTTGCTGTTCTCAAGTGATTTGGACACCA 13176
 DB 380 euSerArgAsnGlyLeuSerPheIlybGlyCysCysSerGlnSerAspPheGlyThrThrS 400
 QY 13177 GCCTAAGTATTTGATGATGCTTCAATGCTGTTCAATGCTTATTCAGATGATCAACTCTTGG 13236
 DB 400 erLeuIlybTyrLeuAspLeuSerPheAsnGlyValaIleThrMetSerSerAsnPheLeuG 420
 QY 13237 GCTTAGAACCACTGAACATCTGATTTCCAGCAATTTCCAAATTTGAACAAATGAGTAGT 13296
 DB 420 IlybLeuGluGlnLeuGluHisIleuAspPheGlnHisSerAsnLeuIlybGlnMetSerGluP 440
 QY 13297 TTTGAGATTTCTTACTCATCGAAGAACTCATTTAATTGACATTTCTCATCTCACCA 13356
 DB 440 heserValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThr 460
 QY 13357 GAGTTCCTTGAAGGCACTCTTCAATGCTTGTCCAGCTCGAAGCTCTTGAAGATGGCTG 13416
 DB 460 rGlyAlaAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValaLeuIlybMetAlaG 480
 QY 13417 GCAATTCCTTTCAGAAAACTTCTCCAGATATCTTCAAGAGCTGAGAACTTGAACCT 13476
 DB 480 IlyAsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrP 500
 QY 13477 TCGTGACCTTCTCAAGTTCACATGAGCAGTTGTCTCAAGACATTTAACTCACTCT 13536
 DB 500 heLeuAspLeuSerGlyCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuS 520
 QY 13537 CCAATCTTCAAGTCTTAATTAAGCCACCAACACTTCTTTCATGGAATCGTTCTCTT 13596
 DB 520 erSerLeuGlnValaLeuAsnMetSerHisAsnAsnPheSerLeuAspThrPheProT 540
 QY 13597 ATTAAGTCTGAACTCCCTCAGAGTTCTTGATTAAGTCAAGTCAATCAATATGACTTCA 13656
 DB 540 IlybAspCysLeuAsnSerLeuGlnValaLeuAspTyrSerLeuAsnHisIleMetThrSerL 560
 QY 13657 AAAAAGAGAACTACAGCATTTTTCAGATGCTTACGCTTTCTTAAATCTTACAGAAATG 13716
 DB 560 IyIlybGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnA 580
 QY 13717 ACTTGTCTGATCTTGGAACACAGAGTTTCCCTGCAATGGAATGAAGACAGAGGACG 13776
 DB 580 sPheAlaCysThrCysGlnHisIleGlnSerPheLeuGlnIlybIlybAspIlybArgGlnL 600
 QY 13777 TCTTGATGAAGTTGAAGAAATGGAATGTGCAACACTTCAGATTAAGAGGAGCATGCTG 13836

```

Db      600 euLeuValGIuValGIuArGMeGIuCyAlaThrProSerAspGluGlyMetProV 620
Qy      13837 TGCTGATTTGAATATCAGCTGTGAGATGAATPAAGCCATTCGTGTGCTGCTCA 13896
Db      620 alLeuSerLeuSnnIleThrCySGInMeAsnIysThrIleGlyValSerValLeuS 640
Qy      13897 GATGCTTGAGATCTGTTGTGAGCTTGTGCTATATAGTTCATATTTTCACTGATGC 13956
Db      640 eValLeuValValSerValValAlaValLeuValIlyrIysPheIyrrPheHISLeuMeL 660
Qy      13957 TTCTTGCTGCTGCTGCATAAAGATAGTAGAGGTAAGAAACCTATAGATGCTTTGATATCT 14016
Db      660 euLeuValGIySerIleYrGlyArgGlyGluHnIleYrAaPalaPheValIleT 680
Qy      14017 ACTCAAGCCAGATGAGACTGGGTAAAGAAATGACTAGTAAGATTTTGAAGAGGGG 14076
Db      680 ySerSerGIuAspGIuAspTrpValAlaArgAsnGIuLeuValIySaenLeuGIuGluGIly 700
Qy      14077 TGCTTCATTTAGCTCTGCTTCCTCAGTACAGAGACTTTATTCGGGTGTGGCCATTCGTG 14136
Db      700 alProProPheGIuLeuCySLeuHISrYrArgAspPheIleProGIyValAlaIleAla 720
Qy      14137 CCAACATCATCCATGAAGGTTTCCATPAAGCCGAAGGTGATTTGTGTGCTCCAGC 14196
Db      720 lAsnIleIleHISGIuGlyPheHISySerArgIySerValIleValValSerGIuH 740
Qy      14197 ACTTCATCCAGAGCCCGCTGTGTATCTTTGAATAGATGCTGCTGAGACTGGCACTTC 14256
Db      740 lAspHeIleGIuSeraArgTrpCyIlePheGIuIyGIuIleAlaGIuInTrIyGIuInPheL 760
Qy      14257 TGAGCAGTCGTGTGTATCATCTTTCATTCCTTCGAGAGAGGTGAGAGAACCTGCTCA 14316
Db      760 euSerSerArgAlaGIyIleIlePheIleValLeuGIuIySValGIuIySThrLeuLeuH 780
Qy      14317 GGCAGCAGGTGAGAGCTGTACCCGCTTCTCAGCAGAGAACTTACCTGAGTGGAGAGACA 14376
Db      780 rArgGIuValGIuLeuIyYrArgLeuLeuSerArgSnnTrIyLeuGIuIyTrpGIuAspS 800
Qy      14377 GTGTCTCTGGGGGGCCGACATCTTTGTGAGAGAGACTCAGAAAAGCCGTGCTGAGTGAAT 14436
Db      800 eValLeuGIyArgHISlIlePheTrpArgLeuArgIySAlaLeuAspGIyLys 820
Qy      14437 CATGATTCAGAGAGAAAGCTGGGTACAGAGATGACATTCGAGAGAGAACTATC 14495
Db      820 eTrIyAsnProGIuGIyThrValGIyThrGIyCySnnTrpGIuInAlaThrSerIle 839

RESULT 3
Q8SP8 PRELIMINARY; PRT; 837 AA.
ID      08SP8 AC
DT      01-JUN-2002 (T-EMBLrel. 21, Created)
DT      01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT      01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE      Toll-like receptor 4.
GN      Name=TLR4;
OS      Gorilla gorilla (gorilla).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
OX      NCBITaxID=9593;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21405531; PubMed=11514453;
RA      Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
RT      "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
RL      in humans."
RL      Genetics 158:1657-1664 (2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Beutler B., Smirnova I., Hamblin M.T., McBride C., Di Rienzo A.;
RL      Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF497563; AAM18617.1; JOINED.

```

```

DR      EMBL; AF497564; AAM18617.1; JOINED.
DR      HSP; 060603; 1077.
DR      GO; 0046696; C:lipopolysaccharide receptor complex; ISS.
DR      GO; 0001530; F:lipopolysaccharide binding; ISS.
DR      GO; 0004888; F:transmembrane receptor activity; ISS.
DR      GO; 0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR      GO; 0016046; P:detection of fungi; ISS.
DR      GO; 0009598; P:detection of pathogenic bacteria; ISS.
DR      GO; 0042116; P:macrophage activation; ISS.
DR      GO; 0045576; P:mac cell activation; ISS.
DR      GO; 0045671; P:negative regulation of osteoclast different. . .; ISS.
DR      GO; 0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR      GO; 0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR      GO; 0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR      GO; 0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR      GO; 0042088; P:T-helper 1 type immune response; ISS.
DR      InterPro; IPR001611; LRR.
DR      InterPro; IPR00483; LRR Cterm.
DR      InterPro; IPR003591; LRR typ.
DR      InterPro; IPR00157; TIR.
DR      Pfam; PF01463; LRRCT; 1.
DR      Pfam; PF00560; LRR_1; 10.
DR      Pfam; PF01582; TIR; 1.
DR      PRINTS; PR00019; LEURICRPT.
DR      SMART; SM00082; LRRCT; 1.
DR      SMART; SM00369; LRR typ; 2.
DR      SMART; SM00255; TIR; 1.
DR      PROSITE; PS50104; TIR; 1.
KW      Receptor.
SQ      SEQUENCE 837 AA; 95497 MW; 5A17BAB41396DD CRC64;

Alignment Scores:
Pred. No.: 6, 04e-304 Length: 837
Score: 3878.50 Matches: 752
Percent Similarity: 98.31% Conservative: 4
Best Local Similarity: 97.79% Mismatches: 9
Query Match: 11.73% Indels: 9
DB: 2 Gaps: 1

US-09-396-985B-47 (1-18989) x Q8SP8 (1-837)
Qy      12216 TCAATGCTCTTTTATTC-----GTAGGTGGAATC 12248
Db      69 SerTySerPhePheSerPheProGIuLeuGIuValLeuAspLeuSerArgCyGIuIle 88
Qy      12249 CAGCAATTTGAAGATGGGCGCATATCAGAGCCCTTAAGCCCTTATATTTGACA 12308
Db      89 GIuThrIleGIuAspGIyAlaTyGIuSerLeuSerHISLeuSerThrLeuIleuThr 108
Qy      12309 GGAACCCCATCCAGAGTTTACCCCTGGAGGCTTTTCTGACTATCAAGTTTACGAAG 12368
Db      109 GIyAsnProIleGIuSerLeuAlaLeuGIyAlaPheSerGIyLeuSerSerLeuGIuIyS 128
Qy      12369 CTGGTGGCTGTGAGACAAATGTACATCTTGAAGAACTTCCCATTTGAGACTGAAA 12428
Db      129 LeuValAlaValAlGIuThrAsnLeuAlaSerLeuGIuAsnPheProIleGIyHISLeuIyS 148
Qy      12429 ACTTTGAAGAACTTAATGTGCTCACAATCTTTATCCAACTTTTCAAATTTACCTGAT 12488
Db      149 ThrLeuIySGluLeuAsnValAlaHISAsnLeuIleGIuSerPheIySerProGIuIyYr 168
Qy      12489 TTTTTCATCTGACCAATCTAGAGCTTGAACCTTTCCAGAGCAAGATCAAGATAT 12548
Db      169 PheSerAsnLeuThrAsnLeuGIyTrpAlaAspLeuSerSerAsnIySISleGIuSerIle 188
Qy      12549 TATTCAGAGACTTGGGGTTTACATCAATCAATGCCCTTACTCAATCTCTTTAGACTG 12608
Db      189 TyrCyThrAspLeuArgValLeuHISGIuMetProLeuLeuAsnLeuSerLeuAspLeu 208
Qy      12609 TCCCTGAACCTTATGAACTTTATCCACAGAGGTGCAATTTAAAGAAATTTAGGCTCTAAG 12668
Db      209 SerLeuAsnProMetThrPheIleGIuProGIyAlaPheIyGIuIleArgLeuHISIyS 228

```

QY 12669 CTGACTTGAAGAAATATTTGATGATTTAAATGTAAGAACTTGATTTCAAGGCTG 12728
 Db LeuThrLeuArgAsnPhaAspSerLeuAsnValMetLysThrCysIleGlnGlyLeu 248
 QY 12729 GCTGGTTTGAAGAGTCATCGTTTGTTGCTGGAGAAATTTAGAAATGAAGAACTTGGA 12788
 Db AlaGlyLeuGluValArgArgLeuValLeuGlyGluPheArgAsnGluGlyAsnLeuGlu 268
 QY 12789 AAGTTTGAAGAAATCGCTCTGAGAGGGCTGTGCAATTTGACATTTGAAGAAATTCGATTA 12848
 Db LysPheAspLysSerAlaLeuGluGlyLeuCysAsnLeuThrIleGluGluPheArgLeu 288
 QY 12849 GCATCTTGAAGCTATCTGATCTGATGATATTAATGATCTTATTTAAATTTGTTGACAAATGT 12908
 Db AlaTyrLeuAspTyrTyrLeuAspAspIleIleLeuPhePheAsnCysLeuThrAsnVal 308
 QY 12909 TCTTCATTTTCCCTGGTGAAGTGTGACTATTTGAAGAGGTAAGAACTTTCTTATTAATTTG 12968
 Db SerSerPheSerLeuValSerValThrIleGluArgValLysAspPheSerTyrAsnPhe 328
 QY 12969 GGATGGCAACATTTAGAAATTTGTTAACTGTTAAATTTGACAGTTTCCACATTTGAAACTC 13028
 Db GlyTyrGlnHisLeuGluValAsnCysLysPheGlyGlnPheProThrLeuLysLeu 348
 QY 13029 AATATCTCAAAAGGCTTACTTCTTCACTTCAACAAGGAGGGAATGCTTTTTCAGAGTT 13088
 Db LysSerLeuLysArgLeuThrPheThrSerAsnLysGlyAlaAsnAlaPheSerGluVal 368
 QY 13089 GATCTACCAAGCCTTGAGTTCTGATGATCTGATGAAATGGCTTGAGTTCAANAGTTGC 13148
 Db AspLeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCys 388
 QY 13149 TGTCTCAAGTGAATTTGGGCAACAGCCTAAAGTATTTAGATCTGAGCTTCAAGTGC 13208
 Db CysSerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGly 408
 QY 13209 GTTATTAACATGAGTTCAAACTTCTTGAGCTTAGAACAACATGAGATCTGATTTTCAG 13268
 Db ValIleThrMetSerSerAsnPheLeuGlyLeuGluGlnLeuGluHisLeuAspPheGln 428
 QY 13269 CATTCAATTTGAAACAATGAGTGAAGTTTTCAGTATCTGATCTCAAGAACTTCATT 13328
 Db HisSerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuArgAsnLeuIle 448
 QY 13329 TACCTGACATTTCTCACTACTACACAGAGTGGCTTCAATGAGATCTTCAAGGCTTG 13388
 Db TyrLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 468
 QY 13389 TCCAGTCTCGAAGCTTGAAATGAGTGGCAATCTTCTCAAGAAACTTCTTCCAGAT 13448
 Db SerSerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGluAsnPheLeuProAsp 488
 QY 13449 ATCTTCACAGAGCTGAGAACTTGACCTTCTGAGACCTTCTCAAGTGTCAACTGAGAGAG 13508
 Db IlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGln 508
 QY 13509 TTGCTCCACAGACATTTAACTCACTCTCCAGCTTTCAGGACTTAATTAAGACACAC 13568
 Db LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 528
 QY 13569 AACTCTTTTCAATGAGTATCGTTCTTAAAGTGTGCAAGCTCCCTCAGAGTCTTCTGAT 13628
 Db AsnPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuArgValLeuAsp 548
 QY 13629 TACAGTCTCAATCAATATGATCTTCAAAAAACAGAACTTACAGATTTTCAAGTAGT 13688
 Db TyrSerLeuAsnHisIleMetThrSerLysGlnGluLeuGlnHisPheProSerSer 568
 QY 13689 CTACCTTTCTTAATCTTACTCAGAAAGACTTTCGTTGATTTGTAACACCAAGTTTC 13748
 Db LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlyHisIleGlnSerPhe 588
 QY 13749 CTGCAATGATCAAGACACAGAGCAGCTTGTGTGAAGTTGAACGAATGATGTGCA 13808

Db 589 LeuGlnThrIleLysAspGlnArgGlnLeuLeuValGluValGluArgMetGluCysAla 608
 QY 13809 AACCTTCAGATTAAGCAAGGGCAGACCGCTGCTGAGTTTGAATATCACTGTCAAGATAT 13868
 Db ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 628
 QY 13869 AAGACATCATTTGGTGTGTGCGGTCTCAGTGTGCTTGAATATCTGTTGAGAGTTCTG 13928
 Db LysThrIleIleGlyValSerValLeuSerValLeuValValSerValValAlaValLeu 648
 QY 13929 GTCTAATGTTCTATTTTCACTGATGCTTCTGCTGCTGCTGATTAAGTATGTAAGGT 13988
 Db ValTyrLysPheTyrPheHisLeuMetLeuAlaGlyCysIleLysTyrGlyArgGly 668
 QY 13989 GAAACATCATGATGCTTGTGTTATCTACTCAAGCCAGATGAGGACTGGGTAAAGAAAT 14048
 Db GluAsnValTyrAspAlaPheValIleTyrSerSerGlnAspGluAspTyrValArgAsn 688
 QY 14049 GAGCTAGTAAGAAATTTAGAAAGAGGGGTGCTTCATTTGAGTCTGCTTCACTACAGA 14108
 Db GluLeuValLysAsnLeuGluGluGlyValProProPheGlnLeuCysLeuHisTyrArg 708
 QY 14109 GACTTATTTCCCGGTGTGGCCATTGCTGCCAACATCATTCATGAAGGTTTTCATTAAGC 14168
 Db AspPheIleProGlyValAlaIleAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSer 728
 QY 14169 CGAAGGTGATTTGTGTGTGTGTGCCAGACTTCATCCAGAGCCGTGTGATTTTGAA 14228
 Db ArgLysValIleValValAlaValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlu 748
 QY 14229 TATGAGATTTGCTGAGACTGTCGAGTTTCTGAGCAGTGTGTGCTGATCATCTTCAATGTC 14288
 Db TyrGluIleAlaGlnThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 768
 QY 14289 CTGCAAGGTGAGAAAGACCTGCTCAGCAGAGGTGAGCTGTACCGCTTCTCAGC 14348
 Db LeuGlnLysValGluLysThrLeuLeuArgGlnGlnValGluLeuTyrArgLeuLeuSer 788
 QY 14349 AGGAACCTTACTCGAGGTGAGAGACAGTGTCTGTGGGCGGCACATCTTCTGAGACGA 14408
 Db ArgAsnThrTyrLeuGluTyrGluAspSerValLeuGlyArgHisIlePheThrArgArg 808
 QY 14409 CTGAGAAAGCCCTGCTGATGTGAATCATGGAATCCAGAGGAACAGTGGGTACAGGA 14468
 Db LeuArgLysAlaLeuLeuAspGlyLysSerTyrAsnProGluGlyThrValGlyThrGly 828
 QY 14469 TGCATTTGCGAGAGCAACATCTATC 14495
 Db 829 CysAsnTyrGlnGluAlaThrSerIle 837

RESULT 4
 TLR4_PONFY ID_TLR4_PONFY STANDARD; PRT; 828 AA.
 AC OSSEP9;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Pongo pygmaeus (Ozangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 OC NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2140553; Pubmed=11514453;
 RA Smirnova I., Hamblin M.T., McBrier C., Beutler B., Di Rienzo A.;
 RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
 RL in humans."
 CC Genetics 158:1657-1664(2001).
 CC -I- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via

CC MYD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TIR4.
 CC Binds LY96 via the extracellular domain. Binds MYD88 and TIRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
 CC or send an email to license@1sb-sib.ch).
 CC -----
 DR EMBL: AF497562; AAM18616.1; -
 DR EMBL: AF497560; AAM18616.1; JOINED.
 DR EMBL: AF497561; AAM18616.1; JOINED.
 DR HSSP: O60603; 1FVW.
 DR GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO: GO:0007280; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO: GO:0016046; P:detection of fungi; ISS.
 DR GO: GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO: GO:0042116; P:macrophage activation; ISS.
 DR GO: GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO: GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO: GO:0045368; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO: GO:0045410; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO: GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cleam.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR001571; TIR.
 DR Pfam: PF00560; LRR_12.
 DR Pfam: PF01463; LRRCT_1.
 DR Pfam: PF01582; TIR_1.
 DR PRINTS: PR00019; LEURICHRPT.
 DR SMART: SM00369; LRR_Typ_1.
 DR SMART: SM00082; LRRCT_1.
 DR SMART: SM00255; TIR_1.
 DR PROSITE: PS50104; TIR_1.
 DR GlycoProtein: Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 828 Toll-like receptor 4.
 FT DOMAIN 24 629 Extracellular (Potential).
 FT TRANSMEM 630 650 Potential.
 FT DOMAIN 651 828 Cytoplasmic (Potential).
 FT REPEAT 50 74 LRR 1.
 FT REPEAT 75 98 LRR 2.
 FT REPEAT 99 122 LRR 3.
 FT REPEAT 126 147 LRR 4.
 FT REPEAT 148 171 LRR 5.
 FT REPEAT 172 195 LRR 6.
 FT REPEAT 201 223 LRR 7.
 FT REPEAT 226 250 LRR 8.
 FT REPEAT 275 301 LRR 9.
 FT REPEAT 325 348 LRR 10.
 FT REPEAT 349 370 LRR 11.
 FT REPEAT 371 396 LRR 12.
 FT REPEAT 398 419 LRR 13.
 FT REPEAT 420 443 LRR 14.
 FT REPEAT 445 467 LRR 15.
 FT REPEAT 468 492 LRR 16.
 FT REPEAT 493 516 LRR 17.

FT REPEAT 518 539 LRR 18.
 FT REPEAT 541 564 LRR 19.
 FT REPEAT 566 590 LRR 20.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 33 33 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 171 171 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 203 203 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 280 280 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 307 307 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 524 524 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 573 573 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 622 622 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 628 628 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 828 AA; 94340 MW; 51AC0984E5970DF CRC64;
 Alignment Scores:
 Pred. No.: 1,33e-293 Length: 828
 Score: 3750.50 Matches: 728
 Percent Similarity: 96.97% Conservative: 9
 Best Local Similarity: 95.79% Mismatches: 14
 Query Match: 11.34% Indels: 9
 DB: 1 Gaps: 1
 US-09-396-985b-47 (1-18989) x TIR4_PONPY (1-828)
 QY 12216 TCAGTGGTGTATATCC-----TGAGTGTGAATC 12248
 DB 69 SerTyrSerPheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIle 88
 QY 12249 CAGACATTTGAAGATGGGCGCATTCAGAGCCTTAAGCCACTCTTCAATTATTTGACA 12308
 DB 89 GlnThrIleGlnAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrIleLeuThr 108
 QY 12309 GGAACCCCATCCAGAGTTTGAAGCCCTTGGAGCCTTTTCTGACTATTCAGATTCAGAG 12368
 DB 109 GlyAsnProIleGlnIleAsnLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLys 128
 QY 12369 CTGGTGGCTGTGAGACAAATCTAGCATCTCTAGAGACTCCCAATTTGACATCTGAAA 12428
 DB 129 LeuValAlaValGlnThrAsnLeuAlaSerLeuGlnAsnProIleGlyHisLeuLys 148
 QY 12429 ACTTTGAAGAACTTAATGTGGCTCACAATCTTATCCAACTTTTCAAAATTAAGCTGATAT 12488
 DB 149 ThrLeuLysIleLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyr 168
 QY 12489 TTTTCTAATCTGACCAATCTTAGAGCACTTGACCTTTCCGACAAACAGATTCAGATATT 12548
 DB 169 PheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIle 188
 QY 12549 TATTTGCACAACTTGGGGGTTTTCATCATCAATGCCCTACTCAATCTCTTTAGACCTTG 12608
 DB 189 TyrCysLysAspLeuGlnValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 208
 QY 12609 TCCCTGAACCTTATGAACCTTATCCAAACAGGTGATTTAAAGAAATTAAGCTTCATTAAG 12668
 DB 209 SerLeuAsnAlaMetAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLys 228
 QY 12669 CTGACTTAAAGAAATAATTTTGATAGTTTAATGTAATGAATACTGTATTCAGAGCTGTG 12728
 DB 229 LeuThrLeuArgAsnSerPheAspSerLeuAsnValMetCysThrCysIleGlnGlyLeu 248
 QY 12729 GCTGGTTTAAGATCCATCTGTTGGTTCGGGAAATTTGAATGAAGAACTTGAA 12788
 DB 249 AlaGlyLeuGlnValHisHisLeuValLeuGlyGlnPheArgAsnGlnLysAsnLeuGln 268
 QY 12789 AAGTTTGACAAATCTGCTTAGAGGGGCTTGCAATTTGACCAATTGAAGATTCAGATTA 12848
 DB 269 LysPheAspThrSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGlnPheArgLeu 288
 QY 12849 GCATTACTTAAGCTAAGCTCGATGATATTTATTTATTTATTTATTTATTTATTTATTTAT 12908
 DB 289 AlaTyrLeuAspTyrTyrTyrLeuAspAspIleIleAspLeuPheAsnCysLeuAlaAsnVal 308

OY	12909	TCCTCATTTTCCCGGAGAGGAGCATATGAAAGCGTAAAGAATTTTCTTATATTTCC	12966
Db	309	SerSerPheSerLeuValSerValThrIleuyservalIlysaaspPheSerIYraenPhe	328
OY	12969	GGATGGCAACATTTAGAAATTAGTTAACTGTAAATTTGACAGATTCCTCCACATTTGAACATC	13028
Db	329	GlyTrpGlnHisLeuGluLeuValAsnCylysaPheGlyGlnPheProThrLeuGluLeu	348
OY	13029	AAATCTCTCAAAAGGCTTACTTTCACTTCCAAACAAAGTGGGAATGCTTTTCAGAAATT	13088
Db	349	LysSerLeuLysArgLeuThrPheThrAlaAsnIleGlyGlyLeuAlaPheSerGluVal	368
OY	13089	GATCTACCAAGCCTTTGAGGTTCTTAGATCTCAGTNGAAATGGCTTGAGTTTCAAGGTTGC	13148
Db	369	AspLeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCys	388
OY	13149	TGTTCTCAAGATGATTTTGGGACCAACAGCCTAAAGATTTTAAATCGAGCTTCATGGAT	13208
Db	389	CysSerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnAsp	408
OY	13209	GTTATTCACATGAGTTCAAACTTTCTTGGGCTTTGAAACAATAGACATCGATTTTCCAG	13268
Db	409	ValIleThrMetGlySerSerAsnPheLeuGlyLeuGlnGluLeuHisIleuAspPheGln	428
OY	13269	CATTCCATTTGAAACAATAGAGTGGATTTTCAGATTTCTTACTACTCGAAACCTCATTT	13328
Db	429	HisSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIle	448
OY	13329	TACCTTGACANTTCTCTACTCACACACAGAGTTGCTTTCAAATGGCAATCTTCAATGGCTTG	13388
Db	449	TyrLeuAspIleSerHisIleThrIleSerThrArgValAlaPheAsnGlyIlePheAsnGlyLeu	468
OY	13389	TCCAGTCTCCGAGGCTTTGAAAAATGGCTGGCAATTTCTTCCAGGAAAACTTCTCCAGAT	13448
Db	469	SerSerLeuLysValLeuLysMetAlaGlyAsnSerPheGlnGluAsnPheLeuProAsp	488
OY	13449	ATCTTTCACAGAGCTGAGAAACTTGACCTTGCGACTCTCTCAGTGTCACTGAGCGAG	13508
Db	489	IlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnGln	508
OY	13509	TTTGCTCCACAGATTTTAACTCACTCTCCAGTCTTCAGGTACTTAATATGAGCCACAAC	13568
Db	509	LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn	528
OY	13569	AACCTCTTTTCATTTGGAATPAGTTCCTTAAATGATGTCGAACCTCCTCCAGAGTCTTGAT	13628
Db	529	AsnPhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAsp	548
OY	13629	TACAGTCTCAATCAATATGACTTCCAAAAACAGAACTACAGACATTTTCCAGTACT	13688
Db	549	TyrSerLeuAsnHisIleMetThrSerLysLysGlnGluLeuGlnHisIlePheProSerSer	568
OY	13689	CTAGCTTTCTTAAATCTTACTCAGAAATGACTTTTGTTGTTGTTGTAACACAGAGTTTC	13748
Db	569	LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe	588
OY	13749	CTGCAATGGATCAAGAGCACAGAGGAGCTTGTTGGGAAGTTGAAGAAATGGAAATGTGA	13808
Db	589	LeuGlnTrpIleLysAspGlnArgGlnLeuLeuValGluValGlnArgMetGlnCysAla	608
OY	13809	ACACCTTCAGATTAAGCAGGAGCATGCCCTGCTGCTAGTTTGAATATCACTGTCAGATGAAT	13868
Db	609	ThrProSerAspLysGlnGlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn	628
OY	13869	AAGACCATCATGGTGTGTGGTCTTCAAGTGTGCTTGATGATCTGTGTAGACAGTTCTG	13928
Db	629	LysThrValIleGlyValSerValPheSerValLeuValValSerValAlaValLeu	648
OY	13929	GTCATATAGTTCTAATTTTCAACCTGAGACCTCTTGCTGGCTGCACTAAAGATGCTAGAGT	13988
Db	649	ValTyrLysPheTyrPheHisIleMetLeuLeuAlaGlyCysAlaLeysTrpGlyArgGly	668

QY	13399	GAAGACATCATATGATGCTTTGTATATCTCATCTCAGACGAGAAAGGAGCTGGTAAGGAT	14048
Dd	669	Glusnshnrlyrpsaplaahveallletryrserseghlaspdlusprtpvalhrpsan	688
QY	14049	GAGCTAGTAAGAATTATTAAGAAGAGGGGGGCCCTCCATTCCAGCTCGCTTCACTACAGA	14108
Dd	689	GlueuvallysahenleuglulgylvalProthrPhglnleucysleuhtslyrarg	708
QY	14109	GACTTATATCCCGGTGTGGCCATGTGTCGCCAATCATCATGAAGTTTCCATAAAGC	14168
Dd	709	AsphehelleProciGylalalaiaalelaaleaenllelehlsglulgylphehtslysser	728
QY	14169	CGAAGGTGATGTGTGTGGTGTCTCCGACGACCTTATCCAAAGCCCGTGTGTATCTTTGAA	14228
Dd	729	Arglysvallllevalvalvalserghlnhsphelleglinsersrargtrpysllepeglu	748
QY	14229	TATAGATGTCCTCAGACCTCGGACGTTTCTGAGCAGTCGTCGAGTATCATCTTCATATGTC	14288
Dd	749	Tyrglullelaaglnhrtrpghlnpeleuserserarglslellyellellelleval	768
QY	14289	CTGCAGAGGTGGAGAGAGACCTCTGCTCAGACGACAGGTGAGACCTGTACCGCCTTCCACG	14348
Dd	769	LeudlnlyerValglulysrthrleuLeuArglnglnlnvalGluleuLyrrargleuLeuser	788
QY	14349	AGGAACCTTACTCGAGAGTGGAGGACAGTGTCTCTGGGGCGGACACTCTTCTGGAGACGA	14408
Dd	789	ArgshnhrlyrkleuGlultrpghluspservalleuGllyARghlsllephetrpArgarg	808
QY	14409	CTCGAAGAACCCGTCGTCGATGGTGAATCATGGAATCCGAAGGAACATGGGTTCACAGA	14468
Dd	809	LeuarglysalaleuLeuuspghlylyssertrpamhrpoglulgylthrvalgyltnrgly	828
RESULT 5			
TLR4_PAPAN			
ID	TLR4_PAPAN	STANDARD;	prt; 826 AA.
AC	Q9TSP2:		
DT	28-FEB-2003	(Rel. 41, Created)	
DT	28-FEB-2003	(Rel. 41, Last sequence update)	
DT	05-JUL-2004	(Rel. 44, Last annotation update)	
DE	Toll-like receptor 4 precursor.		
CN	Name=TLR4;		
OS	Papio anubis (Olive baboon).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;		
OC	Cercopitheciinae; Papio.		
OX	NCBI_TaxID=9555;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20558910; PubMed=11104518;		
RA	Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;		
RT	"Phylogenetic variation and polymorphism in the Toll-like receptor 4 locus (TLR4).";		
RL	Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).		
CC	-1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate		
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via		
CC	MyD88, TIRAP and TRAM6, leading to NF-kappa-B activation, cytokine		
CC	secretion and the inflammatory response (By similarity).		
CC	-1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a		
CC	multi-protein complex containing at least CD14, LY96 and TLR4.		
CC	Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via		
CC	their respective TIR domains (By similarity).		
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).		
CC	-1- SIMILARITY: Belongs to the Toll-like receptor family.		
CC	-1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.		
CC	-1- SIMILARITY: Contains 1 TIR domain.		
CC	-----		
CC	This SWISS-PROT entry is copyrighted. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		

FT	SEQUENCE	826 AA;	94678 MW;	4422777318E5F1769 CRC64;
DR	EMBL; AF180964; AAF07059.1; JOINED.			
DR	EMBL; AF180963; AAF07059.1; JOINED.			
DR	HSSP; Q15399.1.FV.			
DR	GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.			
DR	GO; GO:0001530; F:lipopolysaccharide binding; ISS.			
DR	GO; GO:0004888; F:transmembrane receptor activity; ISS.			
DR	GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.			
DR	GO; GO:0016046; P:detection of fungi; ISS.			
DR	GO; GO:0009598; P:detection of pathogenic bacteria; ISS.			
DR	GO; GO:0042116; P:macrophage activation; ISS.			
DR	GO; GO:0045576; P:mast cell activation; ISS.			
DR	GO; GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.			
DR	GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.			
DR	GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.			
DR	GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.			
DR	GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.			
DR	GO; GO:0042088; P:T-helper 1 type immune response; ISS.			
DR	InterPro; IPR001611; LRR.			
DR	InterPro; IPR000483; LRR_Cterm.			
DR	InterPro; IPR003591; LRR_Typ.			
DR	InterPro; IPR000157; TIR.			
DR	Pfam; PF005560; LRR; 13.			
DR	Pfam; PF01463; LRRCT; 1.			
DR	Pfam; PF01582; TIR; 1.			
DR	PRINTS; PRO0019; LEURICRPT.			
DR	SMART; SM00369; LRR_Typ; 2.			
DR	SMART; SM00082; LRRCT; 1.			
DR	SMART; SM00255; TIR; 1.			
DR	PROSITE; PS0104; TIR; 1.			
KW	Glycoprotein; Immune response; Inflammatory response; Lendicite-rich repeat; Receptor; Signal; Transmembrane.			
FT	SIGNAL	1	23	Potential.
FT	CHAIN	24	826	Toll-like receptor 4.
FT	DOMAIN	24	631	Extracellular (Potential).
FT	TRANSMEM	632	652	Potential.
FT	DOMAIN	533	826	Cytoplasmic (Potential).
FT	REPEAT	53	76	LRR 1.
FT	REPEAT	77	100	LRR 2.
FT	REPEAT	101	124	LRR 3.
FT	REPEAT	128	149	LRR 4.
FT	REPEAT	150	173	LRR 5.
FT	REPEAT	174	197	LRR 6.
FT	REPEAT	203	225	LRR 7.
FT	REPEAT	228	252	LRR 8.
FT	REPEAT	277	303	LRR 9.
FT	REPEAT	327	350	LRR 10.
FT	REPEAT	351	372	LRR 11.
FT	REPEAT	373	398	LRR 12.
FT	REPEAT	400	421	LRR 13.
FT	REPEAT	422	445	LRR 14.
FT	REPEAT	447	469	LRR 15.
FT	REPEAT	470	494	LRR 16.
FT	REPEAT	495	518	LRR 17.
FT	REPEAT	520	541	LRR 18.
FT	REPEAT	543	569	LRR 19.
FT	REPEAT	571	592	LRR 20.
FT	DOMAIN	672	818	TIR.
FT	CARBOHYD	35	35	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	173	173	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	205	205	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	282	282	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	309	309	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	497	497	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	526	526	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	575	575	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	624	624	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	630	630	N-linked (GlcNAc. . .) (Potential).
SEQ	SEQUENCE	826 AA;	94678 MW;	4422777318E5F1769 CRC64;

Score:	3621.50	Matches:	716
Percent Similarity:	90.80%	Conservative:	34
Best Local Similarity:	86.68%	Mismatches:	41
Query Match:	10.95%	Indels:	35
DB:	1	Gaps:	6
US-09-396-985B-47 (1-18989) × TLR4_PAPAN (1-826)			
QY 11992	TGCTTATGATGATAGCTTAATGACATGACAAAAAGCCATATCGATTCAGCCAGATGATTA	120511	
DB 29	CysValAlaGluValAlaProLeuIleThrTyrGlnCysMetGluLeuAsn-----	44	
QY 12052	TACTCACTCTGTGGGGCTTTATTTGCTT-----ATTCCATCATCATCTGTCCG	121012	
DB 45	-----PheTyrLysIleProAspAsnIleProPheSerThrLysAsn	58	
QY 12103	CTTGATGCTTTGGCCATGACACATATATGACCCA---TCACATCTGATGAGAGCTG	121559	
DB 59	LeuAspLeu-----SerPheAsnProLeuArgHis-----	68	
QY 12160	GATGACTAGGATTAATATCTATTTAGGTTCTTATTC---GCAGAAATATAGATAT	12216	
DB 69	-----LeuGlySerTyrSerPheLeuArgPheProGluLeu	80	
QY 12217	CAATGCTCTTTTATCTCTGAGTGTGAAATCCAGCAATTTGAAAGATGGGCATATCAGA	12276	
DB 81	GlnValLeuAspLeu---SerArgCysGluIleGlnThrIleGlnAspGlyAlaTyrGlns	100	
QY 12277	GCCTAAGCCACCTCTACCTTAATATTTAGACAGAAACCCCATCCAGATTTAGCCCTGG	12336	
DB 100	erLeuSerThrLeuSerThrLeuIleuThrGlyAsnProIleGlnSerLeuAlaLeuG	120	
QY 12337	GAGCCTTTTCTGCACTATCAAGTTTACAGAAAGCTGTGCTGTGAGACAAATCTAGCAT	12396	
DB 120	LysAlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlas	140	
QY 12397	CTCTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAGAATTAATGTGGCTCACA	12456	
DB 140	erLeuGluAsnPheProIleGlyHisIleuThrLeuGlySerGluLeuAsnValAlaHisArg	160	
QY 12457	ATCTTATCCAACTCTTCAAATTAACCGAGATTTTCTATGTCGACATCTAGAGCACT	12516	
DB 160	snLeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGluHis	180	
QY 12517	TGCACTTTCCAGACAAACAAATTCAAAGTATTTATTTAGTSCACAGACTTCCGGTTCTACATC	12576	
DB 180	euaBrLeuSerSerAsnLysIleGlnAsnIleTyrCysLysAspLeuGlnValLeuHisG	200	
QY 12577	AAATGCCCTATCTCAATCTCTCTTTAGACCTGTCCCTGAACCCCTATGAACCTTATCCAA	12636	
DB 200	lnMetProLeuProAsnLeuSerLeuAspLeuSerLeuAsnProIleAsnPheIleGlnP	220	
QY 12637	CAGGTGCAATTTAAAGAAATTAAGCTTCATAGCTGACTTTAAGAAATTAATTTTGAATGTT	12696	
DB 220	roGlyAlaPheLysGluIleArgLeuHisIleLysLeuThrLeuAspSerAsnPheAspArg	240	
QY 12697	TAAATGTATGAAGAACTTGATTCAGAGCTGTGGCTGGTTTGAAGAGCCATCGTTGGTTC	12756	
DB 240	euaAsnValMetLysThrCysIleGlnIleuValAspLeuGluValHisArgLeuVal	260	
QY 12757	TGGGGAATTTAGAAATGAAGAACTTGAGAAAGTTTGAACAATCTGCTTAGAGGCCC	12816	
DB 260	eugIyGluPheArgAsnGluArgAsnLeuGluIlePheAspLysSerAlaLeuGluGly	280	
QY 12817	TGTGCAATTTGACATTTGAAGAAATTCGATTTAGCATTTAGACTTACTCTCGATGATA	12876	
DB 280	eucYAsnLeuThrIleGluGluPheArgLeuThrTyrLeuAspTyrTyrLeuAspAsnI	300	
QY 12877	TTATTTGACTTATTAATTTGTTTGAACAAGTCTTCTCATTTTCCCGGAGAGTGACAT	12936	
DB 300	IleIleAspLeuPheAsnCysLeuAlaAsnAlaSerSerPheSerLeuValSerValAsnI	320	
QY 12937	TTGAAGGGTAAAGATTTTCTTATTAATTTCCGATGGGCAACATTTAGAAATTAGTTAACT	12996	


```

Db      320  l e l y s a r v a l g l u a s p h e s e r t y r a a n p h e a r g t r p g l n h i s e u g l u e u v a l a a n c 340
Qy      12997  G T A A T T T G A C A G T T T C C A C A T T G A A A C T C A A A G G T T C T T C A C T T 13056
Db      340  y l y s p h e g l u g l i n h e p r o t h r l e u g l u e g l u s e r l e u y a r g l e u t h r p h e i n r a 360
Qy      13057  C C A A C A A G G T G G A A T C T T T T C A G A A G T T G A T C C A A G C C T T A G T T T C A G A T C 13116
Db      360  l a a n l y g l y g l y a s n l a p h e s e r g l u v a l a s p l e u p r o s e r l e u d l u h e l e u a p l 380
Qy      13117  T C A G T A G A A A T G C T T G A G T T C A A A G T T G C T T C C A A A G T A T T T T G G A C A C C A 13176
Db      380  e u s e r a r s a n g l y l e u s e r p h e u s g l y c y s e r g i n s e r a p h e g l y t h r t h s 400
Qy      13177  G C C T A A G T A T T T G A T C T G A G C T T C A A T G G T T A T T A C C A T G A G T C C A A C T T C T T G 13236
Db      400  e r l e u y t r l e u a s p l e u s e r p h e a s n a s p v a l l e t h m e c l y s e r a s n p h e l e u g 420
Qy      13237  G C T T A G A C A C T A G A A C A T C T G A T T T C C A G A T T C C A A T T T G A A C A A T G A T G A G T 13296
Db      420  l y l e u g l u g l i n h e u g l u h i s t e u a s p h e g l i n h i s e r a s n l e u l y s e g l i n h e t s e r g l n p 440
Qy      13297  T T T C A G T A T T C C T C A C T C A G A A C C T C A T T T A C T T G A C A T T T C T A C T C A C A C C A 13356
Db      440  h e s e r v a l p h e l e u s e r l e u a r g a n l e u i l e t y r l e u a s p l e s e r h i s t h r i s t h r t 460
Qy      13357  G A G T T G C T T C A A T G G A C A C T T C A A T G G C T T G C A G C T C G A A G C T T G A A A T G G C T G 13416
Db      460  h r v a l a l a p h a s n g l y l e p h e a s p l y l e u l e u s e r l e u l y a l l e u l y s m e t a l a g 480
Qy      13417  G C A A T T C T T T C C A G A A A A C T T C C T C C A G A T A T C T T C A G A G G T G A A A C T T G A C C T 13476
Db      480  l y a n s e r p h e g l i n g l u a s n p h e l e u p r o a p l l e p h e t h a s p l e u l y a s n l e u t h r p 500
Qy      13477  T C T G G A C C T T C T C A G T G T C A C T G A G C A G T T G T C C A A C A G A C A T T T A C T C A C T T 13536
Db      500  h e l e u a s p l e u s e r g l n c y s g l i n e u g l u g l i n l e u s e r p r o t h r a l a p h a s p h r l e u a 520
Qy      13537  C C A G C T T C A G G T A T A A T A T G A G C C A C A C A C T T T T C A T T G A T A C G T T C T T 13596
Db      520  s n l y s l e u g l i n a l l e u a s n m e t s e r h i s a a n a n p h e s e r l e u a s p a l a p h e p r o t 540
Qy      13597  A T A A G T G T C T G A C T C C C T C C A G T T C T T G A T T A C A G T C A T C A T C A T A T G A C T T C C A 13656
Db      540  y l y s c y s l e u p r o s e r l e u d i n a l l e u a s p t y r s e l e u a s n h i s l e t h i s e r l 560
Qy      13657  A A A A A C A G A A C T A C A G A T T T T C C A A G T A G T A G C T T T T A A T C T T A C T C A G A T G 13716
Db      560  y s a n g l i n g l u p r o g l i n h i s p h e p r o s e r l e u a l a p h e l e u a s n l e u t h r g l n a s n a 580
Qy      13717  A C T T T G C T T G A C T T T G A A C C A G A G T T T C C T G C A A T G A T C A A G A C C A G A G G C A C 13776
Db      580  s p r p h e a l a c y s t h r c y s g l i n h i s g l i n s e r p h e l e u g l i n t r i l l y s a s p g l i n a r g l n l 600
Qy      13777  T C T T G T G A A G T G A A C G A A T G A T G C A C A C C T T C A G A T A G A G G G C A T G G C T G 13836
Db      600  e u l e u v a l g l u a l g l u h t g m e c l u c y s a l a t t r p r o s e r a s p l y s e g l i n l y e c p r o v 620
Qy      13837  T G C T G A T T T G A A T A T A C C T G T C A G A T G A A T A A G A C C A T T G T G T G C G T C T C A 13896
Db      620  a l l e u s e r v a l a s n l l e t h r c y s g l i n m e c a e n l y s t h r l l e g l y a l s e r v a l p h e s 640
Qy      13897  G T G G C T T T G A T T C T G T T A C A C A T T C G T G C T A T A A G T T C T A T T T T C A C T G A T G C 13956
Db      640  e r v a l l e u v a l s e r v a l a l a v a l l e u v a l t y r l y s p h e t y r p h e h i s l e u e t l 660
Qy      13957  T T C T T G C T G C T G A T A A G A T G T A G A G G T A A A C A T T A T G A T G A C C T T T G T A T C T 14016
Db      660  e u l e u a l a g l y c y l l e y s t r l y a r g l y g l u a n l l e t y r a s p l a p h e v a l l e t 680
Qy      14017  A C T C A A G C C A G A T A G A C T G G G T A A G A A T G A T G A T A A A A T T T A G A A G A G G G 14076

```

```

Db      680  y r s e r g e l n a s p l u a s p t r y v a l a r g a n g l u e u v a l l y a s n l e u g l u g l y v 700
Qy      14077  T G C C T C A T T T C A C T G C C T T C A C A G A C T T A T T C C G G T G C C A T T G C T G 14136
Db      700  a l p r o p r o p h e g l n e u c y s l e u h i s t y r a r g a s p h e i l e p r o g l y a l a l e a l a a 720
Qy      14137  C C A A C A T A T C A T G A A G T T T C A T A A A G C C A A G G T A T T G T G T G T C C A G C 14196
Db      720  l a a n l l e l l e h i s g l u g l y p h e i s l y s e r a r g l y v a l l e v a l a v a l s e r g l n h 740
Qy      14197  A C T T C A T C C A G A C C C G T G T G T A T T T G A A T A T G A T T G C T C A G C C T G C A C T T T C 14256
Db      740  i s p h e i l e g l i n s e r a r g t r p c y s i l e p h e g l u r y g l u l e a l g l i n t h r p g l n p h e l 760
Qy      14257  T G A C A G C G T G G T G A T A C T T C A T T G C C G A A G G T G A A G A C C T G C T C A 14316
Db      760  e u s e r s e r a r g a l a g l y l e l l e p h e l l e v a l l e u g l u s v a l g l u s t h r l e u e u a 780
Qy      14317  G G C A G A G T G A C T G A C C G C C T T C A G A C A G A A C A T T A C T G A G T G G A G A C A 14376
Db      780  r g l i n g l i n a l g l u l e u t y r a r g l e u s e r a r g a n t h r t y r l e u g l u t r p g l u s p s 800
Qy      14377  G T G T C T G G G G C C A C A C T T T C T G A G A C A C T C A G A A A C C C T G T G A T G A A T 14436
Db      800  e r v a l l e u g l y g l n h i s l e p h e t r p a r g a r g l e u a r g l y a l a l e u a s p g l y a r g s 820
Qy      14437  C A T G A A T C C A G A A 14450
Db      820  e r t r p a n p r o g l u 824

RESULT 6
TLR4_HORSE
ID_TLR4_HORSE STANDARD; PRT: 843 AA.
AC OSMYR3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandeplass M.L., McNeill B.W., Barton M.H., Moore J.N.;
RT "Cloning and sequencing of equine Toll-like receptor 4 (TLR4).";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
CC their respective TIR domains (By similarity). (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AY05808; AAF91076.1; -.
CC HSP: Q15399; LFYV.
CC GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
CC GO: GO:0001530; F:lipopolysaccharide binding; ISS.

```



```

Qy 13117 TCAGTAAATGCTGAGTTTCAAGGTTGCTTCTCAAGTATTTGGACAAACA 13176
Db 381 euserArghsbnhyleuserPheuserSerCyseSerGlnAlaSpLeuSthrtThra 401
Qy 13177 GCTTAAGTATTTAGATGTGAGCTTCAATGGTGTATTATACATGAGTTCAAACTTCTGG 13336
Db 401 rgleuYhNHisleuNpserPheNaMaarValIleSerMetSerSerPheMetG 421
Qy 13237 GCTTAGAACATGATGATGCTGATTTCCAGCATTTCCAAATTTGAAACAAATGAGTAgT 13296
Db 421 lyleuGlnGlnleuGlnHisleuNpserPheGlnHisSerThrlleuYsglnAlaSerAap 441
Qy 13297 TTTCAAGTATTTCTCACTCACTCAAACTTATTTAGCTTCACTTCACTGACACA 13356
Db 441 heProValPheleuserleuYsaNleuAArgIYleuNpIleSerYThrlhNthra 461
Qy 13357 GAGTTGCTTTCAATGGCATTTCAATGGCTTTCAGTCTGCAAGCTTGAAGAGCTG 13416
Db 461 rGValIValPheNHisGlyIlePheAapGlyleuValSerleuGlnValleuYsMetAlaG 481
Qy 13417 GCATTTCTTTCCAGGAAACTTCTCCAGATATTTTCAAGAGCTGGAACCTTGACT 13476
Db 481 lyaNserPheIYsaPsaNpPheleuProaNillePheArgIleuMetThrlhNleuThrt 501
Qy 13477 TCCTGACCTCTCTCAAGTGTCAACTGAGAGTTGCTCCAAAGCATTTAACTCACTCT 13536
Db 501 hrleuNpserleuSerleuCyseNleuGlnValSerGlnIleuAlaPheCyseleuNp 521
Qy 13537 CCACTCTTCAAGTATTAATATGAGCCAAACAATTTCTTTCATGATGATAGTTCCTT 13596
Db 521 roArgleuArgValleuNmetSerHisSaNpNleuPheleuNpMetleuProT 541
Qy 13597 ATAAGTGTCTGAACCTCTCCAGGTTCTTGAATACAGTCTCAATACATTAATGACTTCA 13656
Db 541 YrlYsProlleuNHisSerleuGlnIleleuNpCysePsaNpArgIleValAlaPheL 561
Qy 13657 AAAAAGAGAACTCAGCATTTTCCAAAGTATGAGCTTCTTAAATTTTCTCAAGATG 13716
Db 561 YsTrpGlnleuGlnHisPheProSerSerleuAlaSerleuNmetNpThrlhNpna 581
Qy 13717 ACTTGTCTTGAATGTGAAACAGAGTTTCTGCAATGATGATGAGGAGGAGGAGC 13776
Db 581 sPheNlaCyseValCyseIurYrGlnSerPheleuGlnTrpValIYsaPsaNpIArgIle 601
Qy 13777 TCTTGTGGAAGTGAAGATGGAATGGAATGCAACCTTCAAGATGAGGAGGAGCTG 13836
Db 601 euleuValGlnValGlnHisleuValCyseAlaIleProlleuGlnMetArgIleMetProV 621
Qy 13837 TGCTGAGTTTG---AATATCACTGTGAGATTAAGCATGATGAGTGTGCGGTC 13893
Db 621 alIleuGlyPheNpnaNpAlaThrcySglnIleSerYsThrlleValIleYalYserValP 641
Qy 13894 TCAGTGTCTTGTATGATCTGTGTAGAGATTTGCTATTAAGTCTTATTTCACTGA 13953
Db 641 heSerIleleuMetValSerValIleAlaValleuValYlyPhePheYrheHisleuM 661
Qy 13954 TGCTTTCTTGTGCTGCTCAATAAGTATGATGGAAGGTAACATCTATGATCCTTTGTA 14013
Db 661 etleuNleuAlaGlyCyseYsYsTrgIYArgGlyGlnSerIleYrPsaNpAlaPheValI 681
Qy 14014 TCTATCAAGCCAGAGTGAAGTGGGTAAGATGAGCTGTATTAAGATTTAGAGAG 14073
Db 681 lerySerSerGlnpnaNpIAspTrpValAlaGsaNpGlnleuValIYsaNpNleuGlnG 701
Qy 14074 GGGTGCCTTCATTTCACTTGTGCTTCACTAAGAGCTTATTTCCCGGTGTGCAATG 14133
Db 701 lYValProPheGlnleuNpCyseNpHisYrArgAsPhePheIleProGlyValAlaIleA 721
Qy 14134 CTGCCAATATCATCAAGATTTCCATTAAGCCGAAGAGGTATTTGTGTGCTGCC 14193
Db 721 lAaIaAsnIleIleGlnIleuGlyPheNHisYsSerArgIYValIleValIValIleSerg 741

```

```

Qy 14194 AGCACTTCATTCAGAGCGCGTGTGTATCTTGAATATGAGATTTGCTCAGACTGGCAGT 14253
Db 741 lNHisPheIleGlnSerArgTrpCyseIlePheGlnIurYrGlnIleAlaGlnThrtPsaNp 761
Qy 14254 TTTGAGAGAGTGTGCTGCTGATTCATTTCAATTTGCTTGCAGAGAGTGAAGAGCCTGC 14313
Db 761 heleuSerSerArgAlaGlyIleIlePheIleValleuNHisYsYleuGlnIYsSerleuL 781
Qy 14314 TCAGAGAGAGGTGAGCTGACCGCTTCTGACAGAGAACACTTACTGAGTGGAGAG 14373
Db 781 euArgGlnGlnValGlnleuYrArgleuNpnaAgaNpThrtYrleuGlnIurPsaNp 801
Qy 14374 ACAGTGTCTGGGCGGACATCTTCTGAGAGCACTCAGAAAAGCCCTGCTGAGTGA 14433
Db 801 sPsaNpIleuGlnYArgHisIlePheThrtPsaNpArgleuAlaGlyValleuNpGlyL 821
Qy 14434 AATCATGAATCCAGAGAAACA 14456
Db 821 YsProTrpSerProAlaGlyThr 828

RESULT 7
TR4 BOVIN STANDARD; PRT; 841 AA.
ID TR4 BOVIN Q9GL65;
AC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Guionaud C.T., Dubey C., Jungi T.W.;
RT "Bovine Toll-like receptor 4 (TLR4).";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MYD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -I- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TRAP.
CC Binds LY96 via the extracellular domain. Binds MYD88 and TRAP via
CC their respective TIR domains (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -I- SIMILARITY: Belongs to the Toll-like receptor family.
CC -I- SIMILARITY: Contains 18 leucine-rich (LRR) repeats.
CC -I- SIMILARITY: Contains 1 TIR domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF310952; AAC32061.2; -.
DR HSPB; 060603; 1PXY.
DR GO; GO:0046986; C:lipopolysaccharide receptor complex; ISS.
DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO; GO:0016046; P:detection of fungi; ISS.
DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR GO; GO:0042116; P:macrophage activation; ISS.
DR GO; GO:0045576; P:macrophage activation; ISS.
DR GO; GO:0045671; P:negative regulation of osteoclast different. . . ISS.
DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ISS.

```

```
DR GO: GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
DR GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
DR GO: GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR003591; LRR_Typ.
DR InterPro: IPR00157; TIR.
DR Pfam: PF00560; LRR; 13.
DR Pfam: PF01463; LRRCT; 1.
DR Pfam: PF01582; TIR; 1.
DR PRINTS; PR00019; LEORICHRPT.
DR SMART; SM00369; LRR_Typ; 1.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KM Glycoprotein; Immune response; Inflammatory response;
KM Leucine-rich repeat; Receptor; Signal; Transmembrane.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 841 Toll-like receptor 4.
FT DOMAIN 24 632 Extracellular (Potential).
FT TRANSMEM 633 653 Potential.
FT DOMAIN 654 841 Cytoplasmic (Potential).
FT REPEAT 53 76 LRR 1.
FT REPEAT 77 100 LRR 2.
FT REPEAT 102 124 LRR 3.
FT REPEAT 149 173 LRR 4.
FT REPEAT 174 197 LRR 5.
FT REPEAT 203 225 LRR 6.
FT REPEAT 277 300 LRR 7.
FT REPEAT 310 334 LRR 8.
FT REPEAT 350 372 LRR 9.
FT REPEAT 373 398 LRR 10.
FT REPEAT 400 421 LRR 11.
FT REPEAT 422 445 LRR 12.
FT REPEAT 446 469 LRR 13.
FT REPEAT 471 494 LRR 14.
FT REPEAT 495 518 LRR 15.
FT REPEAT 520 542 LRR 16.
FT REPEAT 544 566 LRR 17.
FT REPEAT 568 592 LRR 18.
FT DOMAIN 673 819 TIR.
FT CARBOHYD 35 35 N-linked (G1cNAc. . .) (Potential).
FT CARBOHYD 73 73 N-linked (G1cNAc. . .) (Potential).
FT CARBOHYD 205 205 N-linked (G1cNAc. . .) (Potential).
FT CARBOHYD 238 238 N-linked (G1cNAc. . .) (Potential).
FT CARBOHYD 282 282 N-linked (G1cNAc. . .) (Potential).
FT CARBOHYD 309 309 N-linked (G1cNAc. . .) (Potential).
FT CARBOHYD 497 497 N-linked (G1cNAc. . .) (Potential).
FT CARBOHYD 526 526 N-linked (G1cNAc. . .) (Potential).
FT CARBOHYD 575 575 N-linked (G1cNAc. . .) (Potential).
FT CARBOHYD 625 625 N-linked (G1cNAc. . .) (Potential).
SQ SEQUENCE 841 AA; 96026 MW; CSEIYCB9C798CD16 CRC64;

Alignment Scores:
Pred. No.: 1,24e-230 Length: 841
Score: 2971.50 Matches: 583
Percent Similarity: 84.18% Conservative: 77
Best Local Similarity: 74.36% Mismatches: 113
Query Match: 8.99% Indels: 11
DB: 1 Gaps: 4

US-09-396-985b-47 (1-18989) x TLR4_BOVIN (1-841)
QY 12165 CTAGAGTAATATATTC---TATTTAGGTTCTTATTCAGCAGAAATATTAATCAATG 12221
DB 59 LeuAspSerPheAsnTyrLeuAlaArgHisLeuGlySerHisAsnPro-----Ser 75
QY 12222 TCTTTTATTTCC-----TGTAGGTGTAATCCAGCAATGAAGAT 12263
DB 76 SerPheProGluLeuGlnValLeuAspLeuSerArgCysGlnIleValIleIleGlnAsp 95
QY 12264 GGGGCAATCAGACCTTAAGCCACCTCTTAACCTTAATATTGACAGAAACCCATCCAG 12323
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
DB 96 AspThrPheGlnGlyLeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleGln 115
QY 12324 AGTTTGGCCCTGGGAGACCTTTTCTGACATTAAGTTTCAGAAAGCTGGGCTGGAG 12383
DB 116 SerLeuAlaTrpGlyAlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGlu 135
QY 12384 ACAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAAGAACTT 12443
DB 136 ThrAsnLeuValSerLeuAsnAspPheProIleGlyHisLeuGlyAsnLeuGlyGluLeu 155
QY 12444 AATGGCTCAACAATCTTAATCCATGTTTCAATTAACCTGAGATTTTCTTAATCTGACC 12503
DB 156 AsnValAlaHisAsnPheIleHisSerPheGlyLeuProGluIlyrPheSerAsnLeuPro 175
QY 12504 AATCTAGACACTGGACCTTCCACCAACAATTCAAAGTTTAATTGACACAGACTTG 12563
DB 176 AsnLeuGlnHisLeuAspLeuSerAsnAsnValValIleGlnAsnIleTyrGlyAsnVal 195
QY 12564 CGGGTTCTACATCAAAATGCCCTACTCAATCTCTTTAGACCTGTCCCTGAACCTATG 12623
DB 196 LysValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeu 215
QY 12624 AACTTATCCAAACGAGTGCAATTTAAAGAAATTAGGCTTCATAGCTGACTTTAAGAAAT 12683
DB 216 AspPheIleGluProGlyThrPheGlyGlyIleValAsnGlnIlyLeuThrLeuArgSer 235
QY 12684 AATTTGATAGTTTAATGTAATGAAGAACTTGATTCAGAGTGCTGGCTGTTAGAGTC 12743
DB 236 AsnPheAsnSerSerHisValMetLysTyrCysIleGlnIleValIleGlyLeuLysThr 255
QY 12744 CATCGTTTGCTGGGAGAGAAATTGAAATGAAGAACTTGAAAGTTTGAACAATCT 12803
DB 256 AsnArgLeuValLeuGlyGluPheLysAsnGluArgLysLeuGlnArgPheAspArgSer 275
QY 12804 GCTCTAGAGGCGCTGGCAATTTGACCAATTGAAGAAATCCGATTAGCATTTAGACTAC 12863
DB 276 PheLeuGlnGlyLeuGlyCysAsnLeuThrIleGlnGlnPheArgIleAlaTyrLeuAspLys 295
QY 12864 TACCTGAGATGATTAATTGACTTAATTAAATGTTTGACAAAGTTTCTTATTCCTCCCTG 12923
DB 296 PheSerGlyAsnAspThrAspLeuPheAsnCysLeuAlaAsnValIleSerLeu 315
QY 12924 GTGAGTGTGACTATGAAAGGTTAAAGACTTTTCTTATTAATTTCCGATGGCAACATTTA 12983
DB 316 LeuSerIleSerLeuGlySerLeuGlnAlaLeuLeuLysAspPheArgTrpGlnHisLeu 335
QY 12984 GAATTAAGTTACTGTAAATTTGACAGATTTCCACATTTGAATCTCAAAAGG 13043
DB 336 GluIleLeuAsnCysAspPheAspLysPheProAlaLeuLysLeuSerSerLeuGlyLys 355
QY 13044 CTTAAGTTTCACTCCAAACAAGGTGGGAATGCTTTTTCAGAGTTGATTCACCAAGCTT 13103
DB 356 PheValAlaPheThrAspAsnLysAspLleSerThrPheThrGluPheGlnLysProSerLeu 375
QY 13104 GAGTTTCTAGATCTCAGTAAAGATGCTGAGTTTCAAAAGTTGCTGTTCTCAAGATGAT 13163
DB 376 GlnTyrLeuAspLeuLysValArgAsnHisLeuSerPheLysGlyCysSerHisIleThrAsp 395
QY 13164 TTTGGGCAACAACGCTTAAGATTTTGAATCTGAGCTTCAATGAGTGTATTAATCCAGAGT 13223
DB 396 PheGlyThrThrAsnLeuLysHisIleAspLeuSerPheAsnAspValIleThrLeuGly 415
QY 13224 TCAAACTTCTGGGCTTAAGAAACAATGACATCTGATTTCCAGACTTCCAAATTTGAA 13283
DB 416 SerAsnPheMetGlyLeuGlnValLeuGlnHisLeuAspPheGlnHisSerThrLeuLys 435
QY 13284 CAATAGAGTGAAGTTTCAAGATTTCTATCACTGAGAAACCTCAATTTTCAATTTCT 13343
DB 436 GlnIleAsnHisPheSerHisAlaPheLeuSerLeuArgAsnLeuArgTyrLeuAspLleSer 455
QY 13344 CATACTCAACAACAGTGTCTTCAATGAGCATTTCAATGAGCTTGTGTCAGTCTGCAAGTC 13403
DB 456 TyrThrAsnIleArgIleValPheHisGlyIlePheThrGlyLeuValSerLeuGlnThr 475
```

```

QY 13404 TTGAATGCTGGCAATTCCTTCCAGAGAAAATTCCTTCAGATATCTTCAGAGCTG 13463
DB 476 LeuysMetAlaGlyAsnSerPheGlnAsnMetLeuProAspIlePheThrIleu 495
QY 13464 AGAAATGACCTTCTGAGACTCTCTGAGTGTCACTGAGACCTGCTCCAGACCA 13523
DB 496 ThrAsnLeuThrValLeuAspLeuSerIleCysGlnLeuGlnValAlaGlnThrAla 515
QY 13524 TTTAACTGACTCCAGCTTCAGTCTTAATATGAGCCCAACAACCTCTTTTCATG 13563
DB 516 PheHisSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnIleLeuSerIleu 535
QY 13584 GATACGTTCCCTTAAGATGTGTGCACTCCCTCCAGTTCCTTATTAAGCTCAAC 13643
DB 536 AspThrPheLeuTyrluProLeuHisSerLeuAspGlyIleuAspCysSerPheAsnArg 555
QY 13644 ATTAATGACTTCCAAAAAAGAGAACTACAGCACTTTCCAGATGCTTAAAT 13703
DB 556 IleMetAlaSerIleGlnGlnIleuGlnAsnLeuProArgSerLeuThrIleuAsn 575
QY 13704 CTTACTGAGATGACTTGTGCTTGTACTGTGAACCAAGATTCCTTCATGATCAG 13763
DB 576 LeuThrGlnAsnAlaPheAlaCysValCysGlnHisSerPheLeuGlnThrValIle 595
QY 13764 GACCAGAGGAGAGCTCTTGTGGAAGTTGAGCAATGATGCAACACTTCAGATAG 13823
DB 596 AspGlnAspGlnLeuValAlaGlyAlaGlnIleMetCysAlaGlnProLeuAspMet 615
QY 13824 CAGGCAATGCTGTGCTGAGTTTG--AAATACCTGTGAGATGATTAAGCATCAT 13880
DB 616 GluAspMetProValLeuSerPheArgAsnAlaThrCysGlnLeuSerIleThrIle 635
QY 13881 GGTGTGCGGTCCAGTGTCTGTAGTATCTGTGAGAGATTCGTGCTTAAATGCTC 13940
DB 636 SerValSerValValThrValLeuValSerValAlaGlyValLeuValIlePhe 655
QY 13941 TATTTTCACTGAGCTCTTGTGCTGCTGCAATTAAGTGTGAGGAGGAAACATCAT 14000
DB 656 TyrPheHisLeuMetLeuLeuAlaGlyCysIleValIleValIleValIleValIle 675
QY 14001 GATGCTTTGTTATCTACTCAAGCCAGATGAGATGAGATGAGATGAGATGAG 14060
DB 676 AspAlaPheValIleIleTyrSerSerGlnAspGlnAspIleValIleValIle 695
QY 14061 AATTGAAGAAGAGGGGCTCCATTCATGAGCTTCCTTCATGAGAGATTTATTCCT 14120
DB 696 AsnLeuGlnGlnIleValProProPheGlnLeuIleuIleuIleuIleuIleuIle 715
QY 14121 GGTGTGCGCATTTGCTGCAACATCATCATGAGGTTCCATTAAGCCGAAAGGTGATT 14180
DB 716 GlyValAlaIleIleAlaIleAsnIleIleGlnIleuIlePheHisValIleValIle 735
QY 14181 GTTGTGTGTCCAGCACTTATCATGAGCCGCTGTGTATCTTTGATATGAGATTCCT 14240
DB 736 ValValValSerGlnHisPheIleGlnSerArgIlePheGlnIleValIleAla 755
QY 14241 CAGACCTGCGAGTTTCTGAGAGTGTGTGTATCATTTCTTCATGCTTCAGAGAGTGTG 14300
DB 756 GlnThrIlePheGlnPheLeuSerSerArgAlaGlyIleIlePheIleValIleGlnIleu 775
QY 14301 GAGAAGACCTGCTCAGGACAGAGTGTGAGCTGTACCGCTTCCTCAGAGAGAACATTAC 14360
DB 776 GluIleSerLeuLeuArgGlnIleValIleGlnIleuIleValIleSerHisAsnThrIle 795
QY 14361 CTGAGTGTGAGAGAGCAGTGTCTGTGGGCGGACATCTTCTGAGAGCACTCAGAAAAGCC 14420
DB 796 LeuGlnIlePheGlnAspSerValIleGlnIleValIlePheIlePheIleValIleGlnIleu 815
QY 14421 CTGCTGATGTGAATATCATGAAATCCAGAGAGAGAGGAGTACAGATGCAATTTGGCAG 14480
DB 816 LeuLeuAlaGlyIleProGlnIleuIleProGlnIleuIleAlaPheAlaGlnIleuIleAsnProGln 835

```

```

QY 14481 GAGCAACATCT 14492
DB 836 GluAlaThrThr 839
RESULT 8
ID 08S055 PRELIMINARY; PRT; 841 AA.
AC 08S055;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Toll-like receptor 4.
GN Name=TLR4;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Ito T., Morimatsu M.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056444; BAB86840.1; -.
DR HSSP; 060603; 1077.
DR GO; GO:0046696; P:lipopolysaccharide receptor complex; ISS.
DR GO; GO:0001530; P:lipopolysaccharide binding; ISS.
DR GO; GO:0004888; P:transmembrane receptor activity; ISS.
DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR GO; GO:0016046; P:detection of fungi; ISS.
DR GO; GO:0005988; P:detection of pathogenic bacteria; ISS.
DR GO; GO:0042116; P:macrophage activation; ISS.
DR GO; GO:0045576; P:mast cell activation; ISS.
DR GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . .; ISS.
DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Typ.
DR InterPro; IPR000157; TIR.
DR Pfam; PF01463; LRRCT; 1.
DR Pfam; PF00560; LRR_1; 11.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00369; LRR_Typ; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PSS0104; TIR; 1.
KW Receptor.
SQ SEQUENCE 841 AA; 96054 MW; E08DCA840EA12D6F CRC64;
Alignment Scores:
Pred. No.: 2,16e-230 Length: 841
Score: 2968.50 Matches: 582
Percent Similarity: 84.18% Conservative: 78
Best Local Similarity: 74.23% Mismatches: 113
Query Match: 8.98% Indels: 11
DB: Gaps: 4
US-09-396-985b-47 (1-18989) x 08S055 (1-841)
QY 12165 CTAGATTAATATTC--TATTTAGGTTCTTTCAGAGAAATATTAATGATATCAATG 12221
DB 59 LeuAspLeuSerPheAsnTyrluAlaArgHisLeuGlySerHisAsnPhe-----Ser 75
QY 12222 TCTTTTATTC-----TGTAGGTGTAATCCAGACAAATTTGAAGAT 12263
DB 76 SerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIleIleIleGlnAsp 95
QY 12264 GGGGCATATCAGAGCCTAAGCCACCTCTTACTTATATTAATGACAGAAACCCATCCAG 12323

```

Db 96 AsprThrheGlnGlyLeuAsnHisLeuSerThrIleuIleuThrGlyLeuProIleGln 115
:::|||||
Qy 12324 AGTTTACGCTGGAGGACCTTTTGTGACATTAACAATTACAGAAAGCTGGTGGTGGAG 12383
Db 116 SerLeuAlaTrpGlyAlaPheSerGlyLeuSerSerLeuGlnIleuValAlaValGln 135
Qy 12384 ACAATCTAGACATCTAGAGAACTCCCATTTGAGACATCTCAAACTTTGAAGAACTT 12443
|||||
Db 136 ThrAsnLeuValSerLeuAsnAspPheProIleGlyHisLeuIleuValAsnLeuArgIleu 155
Qy 12444 AATGTGCTCAAACTTTATCCAAATCTTCAAAATTAACCTGAGTATTTTCTAATCTGACC 12503
|||||
Db 156 AsnValAlaHisAsnPheIleHisSerPheLeuIleuProGlyIleuPheSerAsnLeuPro 175
Qy 12504 AATCTAGACATCTTGACATCTTCCAGCAACAAGTTCAAAGTATTTATTCACAGACTTG 12563
|||||
Db 176 AsnLeuGlnHisLeuAspPheLeuSerAsnAsnIleGlyIleuAsnIleuIleuIleuVal 195
Qy 12564 CGGGTTCTACATCAAAATGCGCTCTCAATCTCTTTAGACCTGTCCCTGACCTTAATG 12623
|||||
Db 196 LysValIleuHisGlnMetProLeuLeuAsnLeuSerLeuAspPheLeuAsnProLeu 215
Qy 12624 AACTTTATCCAAACGAGTGACATTTAAAGAAATTAAGCTTCAAGCTGACATTTAAGAAAT 12683
|||||
Db 216 AspPheIleGlnProGlyThrPheLeuGlnIleLeuLeuAsnGlyLeuThrLeuArgSer 235
Qy 12684 AATTTTGATAGTTTAAATGTATAAGAAACTTGATTCAGAGCTGGCTGTTTGAAGTC 12743
|||||
Db 236 AsnPheAsnSerSerHisValMetLeuThrCysIleGlnIleuValGlyLeuIleuIleuThr 255
Qy 12744 CATGGTTGGTTCTGGGAGATTTAGAAATGAAGAAACTTGAAGAAAGTTTGAACAATCT 12803
|||||
Db 256 AsnArgLeuValIleGlyGlnPheLeuAsnGlnArgIleuGlnArgPheAspArgSer 275
Qy 12804 GCTTGAAGGCGCTGTGCAATTTGACCAATGAAGAAATTCGATTAAGCACTTACACTAC 12863
276 PheLeuGlnIleuLeuCysAsnLeuThrIleGlnIleuPheArgIleuAlaIleuLeuAspArg 295
Qy 12864 TACCTCCATGATATTATTTGACTTATTATTTGTCACAAATGTTTCTTCAATTTCCCTG 12923
|||
Db 296 PheSerGlyAspAspThrAspLeuPheAsnIleuValAsnValIleuValIleuSerIleu 315
Qy 12924 GTGAGTGACATTAATGAAGGTAAGAACTTTCTTATTAATTCGATGGCAACTTAA 12983
|||||
Db 316 LeuSerIleSerLeuGlySerLeuGlnAlaLeuLeuIleuValAspPheArgIleuIleu 335
Qy 12984 GAATTAAGTAACTGTAAATTTGACAGTTTCCCAATGAAGTCAAACTCTCAAAAGG 13043
|||||
Db 336 GlnIleIleAsnIleuValAspPheAspArgPheProAlaLeuIleuLeuSerSerLeuIleuVal 355
Qy 13044 CTTTACTTTCACTTCCCAACAAAGGTGGCAATGCTTTTTCAGAAAGTTGATCTCAAGCTT 13103
|||||
Db 356 PheValPheThrAspAsnIleuAspIleSerThrPheThrGlnPheGlnIleuProSerIleu 375
Qy 13104 GAGTTTCTAGATCTCAGTAGAAATGCTTGAATTTCAAGGTGCTGTTTCAAAAGTAT 13163
|||||
Db 376 GlnIleuLeuAspLeuValArgAsnHisLeuSerPheIleuValCysCysSerHisThrAsp 395
Qy 13164 TTTGGGCAACAGCTTAAAGTATTTAGATCTGAGCTTCAATGCTGTTATTTACAGAGT 13223
|||||
Db 396 PheGlyThrThrAsnLeuIleHisIleuAspPheSerPheAsnAspValIleThrLeuIleu 415
Qy 13224 TCAAACTTTGGGCTTGAACCACTAGAACATCTGAGATTTCCAGACTTCCAAATTTGAAA 13283
|||||
Db 416 SerAsnPheMetGlyLeuGlnIleuGlnIleuIleuIleuPheGlnHisSerThrLeuIleu 435
Qy 13284 CAATAGAGTGAATTTTCAATCTTATCACTCAGAAACCTCAATTAATCTTGAACATTTCT 13343
|||||
Db 436 GlnIleAsnAlaPheSerAlaPheLeuSerLeuHisGlnLeuValArgIleuAspIleSer 455
Qy 13344 CATATCTCACACAGAGTTGCTTTCATGAGCATCTTCAATGAGCTTGTCCAGTCTGAAATC 13403
|||||

Db 456 TyrThrAsnIleArgIleValPheHisGlyIlePheThrGlyLeuValSerLeuGlnThr 475
Qy 13404 TTGAAATGCTGGCAATCTTTCCAGAAAACTTCTCCAGATATCTTCCAGAGCTG 13463
|||||
Db 476 LeuIleuMetAlaGlyAsnSerPheGlnAsnAsnLeuLeuProAspIlePheThrGlyLeu 495
Qy 13464 AGAACTTGACCTTCCGAGACTCTCTGACATGTCCTCACTGGAGAGCTTGTCTCCAGACA 13523
|||||
Db 496 ThrAsnLeuThrValLeuAspLeuSerIleuValGlnIleuGlnIleuAlaGlnThrAla 515
Qy 13524 TTTTACTACTCTCCAGCTTCCAGGTACTAATATATAGCCCAACAACTTCTTTCAATG 13583
|||||
Db 516 PheHisSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnIleuLeuSerLeu 535
Qy 13584 GATACCTTCTTATTAAGTCTGAATCCCTCCAGGTTCTTGAATTAACGCTCAATCAC 13643
|||||
Db 536 AspThrPheLeuIleuIleuProLeuHisSerLeuValGlyLeuAspCysSerPheAsnArg 555
Qy 13644 ATAAATGCTTCCAAAACAGAAACATACAGCATTTTCCAAAGTATGCTTATGATTAAT 13703
|||||
Db 556 IleMetAlaSerIleuValGlnIleuGlnIleuGlnAsnLeuProArgSerIleuThrIleuAsn 575
Qy 13704 CTTTACTCAGAAATGACTTGTCTTACTGTGAAACCAAGATTTCTGCAATGATCAAG 13763
576 LeuThrGlnAsnAlaPheAlaCysValCysGlnHisGlnSerPheLeuGlnThrValIleu 595
Qy 13764 GACCAGAGGAGCTTGTGGTGAAGTTCAGCAAGTGAAGTGCACACCTTCAGATTAAG 13823
|||||
Db 596 AspGlnArgGlnIleuLeuValGlyAlaGlnIleuMetCysAlaGlnProLeuAspMet 615
Qy 13824 CAGGACATGCTGTGTGAGTTTG---AATATCACTGTTCAGATGAATAAGACATCAT 13880
|||||
Db 616 GlnAspPheProValLeuSerPheArgAsnAlaThrCysGlnIleuSerIleuIleIle 635
Qy 13881 GGTGTGCTGCTCCTCAGTGTCTTGATGATCTGTGTGACAGTTTCTGCTATTAAGTTC 13940
|||||
Db 636 SerValSerValAlaThrValLeuLeuValSerValValGlyLeuValIleuValIleuPhe 655
Qy 13941 TATTTTCACTGATGCTTCTGTGCGTGCATTAAGTATGATGAGTGAAGCAATGAT 14000
|||||
Db 656 TyrPheHisLeuMetLeuLeuAlaGlyCysIleuValIleuValIleuValIleuValIleu 675
Qy 14001 GATGCTTTGTTATCTATCAACCCAGATAGAGACTGAGTGAAGTGAAGTGAAGTGAAG 14060
|||||
Db 676 AspAlaPheValIleuIleuSerSerGlnAspGlnAspArgIleuValIleuValIleu 695
Qy 14061 AATTTAGAAAGAGGCTCTCAATTCAGCTGTGCTTCACTACAGAGACTTATTCCTC 14120
|||||
Db 696 AsnLeuGlnIleuGlyAlaProPheGlnIleuCysIleuHisIleuIleuValIleuPheIleuPro 715
Qy 14121 GGTGTGCTGCTGTGCAATCATCATCAATGAAGTTCATTAAGCCGAAAGGTGAT 14180
|||||
Db 716 GlyValAlaIleuAlaAsnIleuIleGlnIleuGlyPheHisIleuValIleuValIleu 735
Qy 14181 GTTGTGCTGCCAGCACTTCAATCCAGAGCCGCTGTGATCTTTGAATATGAGATTCCT 14240
|||||
Db 736 ValValValSerGlnHisPheIleGlnSerArgIleuIleuIleuValIleuValIleuVal 755
Qy 14241 CAGACTGGCAGTTTCTGAGCAGTCTGTGCTGTATCATCTTCAATGTTCTGTGCAAGAGT 14300
|||||
Db 756 GlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValIleuGlnIleuVal 775
Qy 14301 GAGAAGACCTGCTCAGAGCAGAGGTGAGCTGTAACGCTTCCAGCAGAAACACTTAC 14360
|||||
Db 776 GlnIleuSerLeuLeuValGlnIleuValGlnIleuValIleuValIleuValIleuVal 795
Qy 14361 CTGAGTGGAGGACAGTGTCTGTGGGCGGCACTCTTCTGAGACGACTCAGAAAAAGCC 14420
|||||
Db 796 LeuGlnIleuTrpGlnAspSerValIleuGlyArgHisIleuAlaPheThrArgIleuValGlyAla 815
Qy 14421 CTGCTGATGATAATCATGAATCCAGAGAAACAGTGGGTACAGGATSCAATTTGGCAG 14480
|||||
Db 816 LeuLeuAlaGlyIleuValIleuValIleuValIleuValIleuValIleuValIleuVal 835

Qy 14481 GAAGCAATCT 14492
 |||||
 Db 836 GluAlaThrThr 839

RESULT 9
 Q6WCDS5 PRELIMINARY; PRT; 841 AA.

ID Q6WCDS5
 AC Q6WCDS5;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_Taxid=9913;
 RX MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.1333957100;
 RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.E.;
 RT "Haplotype variation in bovine Toll-like receptor 4 and computational
 prediction of a positively selected ligand-binding domain."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
 DR EMBL: AY297040; AAG62700.1;
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0004888; F:Citramembrane receptor activity; IEA.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003885; LRR_Cysm.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR001571; TIR.
 DR Pfam: PF01463; LRRCT; 1.
 DR Pfam: PF00560; LRR_1; 12.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PR00019; LEURICHREP.
 DR SMART: SM00082; LRRCT; 1.
 DR SMART: SM00365; LRR_SD22; 6.
 DR SMART: SM00369; LRR_Typ; 13.
 DR SMART: SM00255; TIR; 1.
 DR PROSITE: PS50104; TIR; 1.
 DR Receptor.
 SQ SEQUENCE 841 AA; 96014 MW; 603936A17B834735 CRC64;

Alignment Scores:
 Pred. No.: 3,14e-230 Length: 841
 Score: 2966.50 Matches: 582
 Percent Similarity: 84.06% Conservative: 77
 Best Local Similarity: 74.23% Mismatches: 114
 Query Match: 8.97% Indels: 11
 Gaps: 4

US-09-396-985b-47 (1-18989) x Q6WCDS (1-841)

Qy 12165 CTGAGTAAATATTC--TATTTAGGTTCTTATTCAGCAAAATATTAGATAATG 12221
 |||||
 Db 59 LeuAspLeuSerPheAsnTyrLeuArgHisLeuGlySerHisAsnPe-----Ser 75

Qy 12222 TCTTTTATTC-----TGTAGGGTGAATTCAGCAATTCAGAT 12263
 |||||
 Db 76 SerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIleIleIleGluAsp 95

Qy 12264 GGGGCATATCAGAGCTTAAGCCACTTCTTACCTTAATATTCAGAGAAACCCCATTCAG 12323
 ::::|
 Db 96 AspThrPheGlnGlyLeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleGln 115

Qy 12324 AGTTTGGCTCGGAGAGCTTTCTTGACATTCAGATTACAGAAAGCTGGCTGGAG 12383
 |||||
 Db 116 SerLeuAlaThrGlyAlaPheSerGlyLeuSerSerLeuGlnIleLeuValAlaGlu 135

Qy 12384 ACAATCTAGCATCTCTAGAGAACTTCCCATTCAGATCTCAAACTTTGAAGAAGCTT 12443

Db 136 ThrAsnLeuValSerLeuAsnAspPheProIleGlyHisLeuLysAsnLeuLysGluLeu 155
 |||||
 Qy 12444 AATGTGGCTCACAACTCTTATCCAACTTTCAATTTCCGAGTATTTTCTAATCGACC 12503
 |||||
 Db 156 AsnValAlaHisAsnPheIleHisSerPheLysLeuProGluLysPheSerAsnLeuPro 175

Qy 12504 AATCTAGAGCACTTGGACCTTTCAGCAACAAGATTCAAAGTATTAATTCAGACACTG 12563
 |||||
 Db 176 AsnLeuGluHisLeuAspLeuSerAsnAsnLysIleGlnAsnIleTyrTyrGluAspVal 195

Qy 12564 CGGGTTCTACATCAAAATGCCCTACTCAATCTCTTTAGACCTGTCCTGAACCTTATG 12623
 ::::|
 Db 196 LysValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeu 215

Qy 12624 AACTTTATCCAAACAGAGTGCATTTAAAGAAATTTAGCTTCATAGCTTCAAGAAAT 12683
 ::::|
 Db 216 AspPheIleGluProGlyThrPheLysGluIleLysLeuAsnGlyLeuThrLeuArgSer 235

Qy 12684 AATTTGATAGTTTAAATGTAATGAAGACTGTATTCAGAGTGGCTGGTTGAGATC 12743
 |||||
 Db 236 AsnPheAsnSerSerHisValMetLysThrCysIleGlnGlyLeuAlaGlyLeuLysThr 255

Qy 12744 CATGTTTGGCTTCGGAGAAATTTAGAAATGAAGAACTTGGAAAGTTGACAAATCT 12803
 ::::|
 Db 256 AsnArgLeuValLeuGlyGluPheLysAsnGluArgLysLeuGlnArgPheAspArgSer 275

Qy 12804 GCTCTAGAGGCGCTGTGCAGATTTGACCATTTGAAGAAATTCGATTCAGATTCAGACTAC 12863
 |||||
 Db 276 PheLeuGlnGlyLeuLysAsnLeuThrIleGlnGlnPheArgIleAlaTyrLeuAspLys 295

Qy 12864 TACCTGATAGATTAATTAATGATTAATTTGTTGACAAAGTTTCTCATTTGCCG 12923
 ::::|
 Db 296 PheSerGlyAspAspThrAspLeuPheAsnCysLeuAlaAsnValSerValIleSerLeu 315

Qy 12924 GTGAGTGTACTATTTGAAGGTAAGAAAGCTTTCTTAATATTCGATGCGACAATTTA 12983
 ::::|
 Db 316 LeuSerIleSerLeuGlySerLeuGlnAlaLeuLeuLysAspPheArgIleGlnHisLeu 335

Qy 12984 GAATTGATTAATCTGTAATTTTGGACAGTTTCCACATTTGAAGTCAAAATCTCAAAAG 13043
 |||||
 Db 336 GluIleIleAsnLysAspPheAspLysPheProAlaLeuLysLeuSerSerLeuLysLys 355

Qy 13044 CTTACTTCACTTCCAAAGAGTGGAGATGCTTTTCAAGAGTTGATTCACCAACCTT 13103
 |||||
 Db 356 PheValPheThrAspAsnLysAspIleSerThrPheThrGluPheGlnLeuProSerLeu 375

Qy 13104 GAGTTTCTAGATCTCAGTAAGATGGCTTGAAGTTTCAAGTTGCTGTTCTCAAGATGAT 13163
 ::::|
 Db 376 GlnTyrLeuAspLeuLysArgAsnHisLeuSerPheLysGlyCysCysSerHisThrAsp 395

Qy 13164 TTTGGACACCAAGCTTAAGATTTAGATCTGAGCTTCAATGGTGTATTTACATGAGT 13223
 |||||
 Db 396 PheGlyThrThrAsnLeuLysHisLeuAspLeuSerPheAsnAspValIleThrLeuGly 415

Qy 13224 TCAAACTTCTGGGCTTAAGAAACATGAAACATTCGATTTCCAGATTCGAATTTGAA 13283
 |||||
 Db 416 SerAsnPheMetGlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLys 435

Qy 13284 CAAATAGAGAGTTTCAATATTCATATCTCAGAAACCTGATTTACCTTGCATTTCT 13343
 |||||
 Db 436 GlnIleAsnAlaPheSerAlaPheLeuSerLeuAsnLysArgLysIleuAspIleSer 455

Qy 13344 CATATCTACACAGAGTGTCTTCAATGAGCATTTCAATGGCTTGTCCAGTCTCGAAGTC 13403
 ::::|
 Db 456 TyrThrAsnIleArgIleValPheHisGlyIlePheThrGlyLeuValSerLeuGlnThr 475

Qy 13404 TTGAAAATGGCTGGCAATCTTCTTCAAGAAACCTTCCAGATTCCTTCCAGAGCTG 13463
 |||||
 Db 476 LeuLysMetAlaGlyAsnSerPheGlnAsnAsnLeuLeuProAspIlePheThrGluLeu 495

Qy 13464 AGAAACTTGACCTTCCGAGCTTCTCAGTGTCAACTGAGACAGTGTCTCCAAAGCA 13523
 |||||


```

Db      496 ThrAsnLeuThrValLeuAspLeuSerLysCysGlnLeuGlnValAlaGlnThrAla 515
Qy      13524 TTTAACSTCACTCCAGTCTTTCAGGTACATATATATAGCAACAACATCTTTTCATTG 13583
Db      516 PheHisSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnLysLeuSerLeu 535
Qy      13584 GATACGTTTCCCTAATAAGTGTGCAATCCGCTCCAGTCTTTCATTAACAGTCCATCAC 13643
Db      536 AspThrPheLeuThrGlnProLeuHisSerLeuArgIleLeuAspCysSerPheAsnArg 555
Qy      13644 ATAAATGACTTCCAAAAACAGAACTACACATTTTCCAGTAGTCTAGCTTTCTTAAT 13703
Db      556 IleMetAlaSerLysGlnGlnGlnValLeuGlnAsnLeuProArgSerLeuThrTrpLeuAsn 575
Qy      13704 CTTAATCTAGAAATGACTTTGCTTTGTTACTTTGTAACACCAAGATTTCTCTGCAATGGATCAAG 13763
Db      576 LeuThrGlnAsnAlaPheAlaCysValCysGlnHisGlnSerPheLeuGlnTrpValLys 595
Qy      13764 GACCAGAGGAGAGCTTTGGTGGAAAGTTGAAGAAATGACCAACCTTCAGATTAAG 13823
Db      596 AspGlnArgGlnLeuLeuValGlyAlaGlnMetCysAlaGlnProLeuAspMet 615
Qy      13824 CAGGGACATGCTGTGCTGAGTTTG--AAATACCTGTTCAGATGAATAAGACCATCAT 13880
Db      616 GlnAspMetProValLeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrIleIle 635
Qy      13881 GGTTGTCCGTCCTCAAGTGTCTTGATGATCTGTTGTGTAGCAATTCGTGCTTAAGTTTC 13940
Db      636 SerValSerValAlaThrValLeuLeuValSerValAlaGlyValLeuValTyrLysPhe 655
Qy      13941 TATTTTCACTGATGCTTTCGCTGCGTCATAAAGTATGAGTGAAGAAACATCTAT 14000
Db      656 TyrPheHisLeuMetLeuLeuAlaGlyCysLysLysTyrGlyArgLysSerThrTyr 675
Qy      14001 GATGCTTTGTATCTACTACAGCCAGATGAGAGACTGGTGAAGAAATGACTGAAG 14060
Db      676 AspAlaPheValIleTyrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLys 695
Qy      14061 AATTTAGAAAGAGGGGCTCCATTTCACTGCTGCTTCATACATACAGAACTTATTTCC 14120
Db      696 AsnLeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrTrpArgAspPheIlePro 715
Qy      14121 GGTGTGGCCATTTGCTGCGCAACATCATCATGAGTTTCCATTAAGCCGAAAGGTGATT 14180
Db      716 GlyValAlaIleAlaAsnIleIleGlnGlnGlyPheHisLysSerArgLysValIle 735
Qy      14181 GTTGTGGTGTCCAGCACTTCATCCAGAGCCGCTGTGATCTTTGAATATGAGATTGCT 14240
Db      736 ValValAlaSerGlnHisPheIleGlnSerArgTrpCysIlePheGlnTyrGlnIleAla 755
Qy      14241 CAGACCTGGCAATTTCTGAGACAGTCGCTGATCATCTTTCATTTGCTTCGCAAGAGTG 14300
Db      756 GlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeu 775
Qy      14301 GAGAAGACCCGCTCAGAGCAGAGTGGAGTGAACCGCTTCAGACAGAAACACTTAC 14360
Db      776 GlnLysSerLeuLeuArgGlnGlnValGlnLeuTyrTrpGlnLeuSerTrpArgAsnThrTyr 795
Qy      14361 CTGAGAGTGGAGGACAGTGTCTGTGGGCGGCACTTCTTGAGACGACTCAGAAAAGCC 14420
Db      796 LeuGlnTrpGlnLysSerValLeuGlyArgHisValAlaPheTrpArgLysLeuArgLysAla 815
Qy      14421 CTGCTGATGGTAAATCATGGAATCCAGAAAGAAACATGGGATACAGATTCATTTGGCAG 14480
Db      816 LeuLeuAlaGlyLysProGlnSerProGlnGlyThrAlaAspAlaGlnThrAsnProGln 835
Qy      14481 GAAGCAATCT 14492
Db      836 GlnAlaThrThr 839

```

```

AC      06WCD4;
DT      05-JUL--2004 (TREMBlrel. 27, Created)
DT      05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT      05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE      Toll-Like receptor 4.
GN      Name=TLR4;
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.1333957100;
RA      White S.N., Taylor K.H., Abbey C.A., Gill C.A., Mornack J.B.;
RT      "Haplotype variation in bovine Toll-like receptor 4 and computational
RT      prediction of a positively selected ligand-binding domain.";
RL      Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
DR      EMBL, AY297043; AA062701.1; JOINED.
DR      EMBL, AY297041; AA062701.1; JOINED.
DR      EMBL, AY297042; AA062701.1; JOINED.
DR      GO, GO:0016020; C:membrane; IEA.
DR      GO, GO:004888; F:transmembrane receptor activity; IEA.
DR      InterPro, IPR001611; LRR.
DR      InterPro, IPR000483; LRR_Cterm.
DR      InterPro, IPR003885; LRR_Cyst.
DR      InterPro, IPR003591; LRR_Typ.
DR      InterPro, IPR000157; TIR.
DR      Pfam, PF01463; LRRCT; 1.
DR      Pfam, PF00560; LRR_1; 12.
DR      Pfam, PF01582; TIR; 1.
DR      PRINTS: PR00019; LEURICHRPT.
DR      SMART: SM00082; LRRCT; 1.
DR      SMART: SM00365; LRR_SD22; 6.
DR      SMART: SM00369; LRR_Typ; 13.
DR      SMART: SM00255; TIR; 1.
DR      PROSITE: PS50104; TIR; 1.
KW      Receptor.
SQ      SEQUENCE 841 AA; 95954 MW; AD6D06ACBF44CC91 CRC64;

Alignment Scores:
Pred. No.: 1,67e-229 Length: 841
Score: 2957,50 Matches: 591
Percent Similarity: 83,93% Conservative: 77
Best Local Similarity: 74,11% Mismatches: 115
Query Match: 8,94% Gaps: 11
DB: 2 Gaps: 4

US-09-396-985B-47 (1-18989) x 06WCD4 (1-841)
Qy      12165 CTAGAGTTTAATTTTC--TATTTAGTCTTATTGACGAGAAATATGATATCATG 12221
Db      59 LeuAspLeuSerPheAsnTyrLeuArgHisLeuGlySerHisAsnPhe-----Ser 75
Qy      12222 TCTTTTATTTTC-----TGAGGTGGAATCCAGCAATTTGAAGAT 12263
Db      76 SerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIleLysIleIleGlnAsp 95
Qy      12264 GGGGCAATATCAGAGCTTAAGCCACTCTCTTACTTAATATTTGACAGAAACCCCATCCAG 12323
Db      96 AspThrPheGlnGlnLysLeuAsnHisLeuSerThrLeuIleLeuThrGlnLysAsnProIleGln 115
Qy      12324 AGTTTGGCCCTGGGAGCCCTTTCTGCACTATCAAGTTTACAGAAAGCTGGTGGTGGAG 12383
Db      116 SerLeuAlaTrpGlyAlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGln 135
Qy      12384 ACAATCTAGACATCTCTAGAGAACTTCCCATTTGACATCTCCAAAATTGAAAGAACTT 12443
Db      136 ThrAsnLeuValSerLeuAsnAspPheProIleGlyHisLeuLysAsnLeuLysGlnLeu 155
Qy      12444 AATGTGGCTCACAACTTATCCAAATCTTTCAAATTAAGTGAATTTTCTGAATCTGACC 12503
Db      156 AsnValAlaHisAsnPheIleHisSerPheLysLeuPro*****PheSerAsnLeuPro 175

```


QY 12504 AATCTAGAGCACTTGGAACCTTTCCAGACAAGATTCAAGTATTATTTGACAGACTTG 12563
 DB 176 AsnLeuGlnHisLeuAspLeuSerAsnAsnLysIleGlnAsnIleTyrGluAspVal 195
 QY 12564 CGGGTTTACATCAAAATGCCCCCTACTCAATCTCTTTAGACCTTGCCCTGAACCTTAG 12623
 DB 196 LysValLeuHisIleGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeu 215
 QY 12624 AACTTATCCAAACCGAGTGCACTTTAAGAATTTAGGCTTCATAGCTGACTTAAGAAT 12683
 DB 216 AspPheIleGluProGlyThrPheLysGluIleLysLeuAsnGlyLeuThrLeuAsnSer 235
 QY 12684 AATTGTAGTATTAGTATAGTAAAGCTGTATTCAGAGCTGCGCTGTTTAGAAGTC 12743
 DB 236 AsnPheAsnSerSerHisValMetLysThrCysIleGlnGlyLeuAsnIleGlyLeuLysThr 255
 QY 12744 CATCGTTTGGTTCTTGAGGAATTTAGAAATGAGGAACTTGGAAGATTTGACAAATCT 12803
 DB 256 AsnArgLeuValIleGluGlyLysPheLysAsnGluArgLysLeuGlnArgPheAspArgSer 275
 QY 12804 GCTGAGAGGCGCTGCAATTTGACCAATTTGACCAATTTGCAATTTGCAATTTGCAATTTG 12863
 DB 276 PheLeuGluGlyLeuCysAsnLeuThrIleGluGlnPheArgIleAlaTyrLeuAspLys 295
 QY 12864 TACCTCGAT 12923
 DB 296 PheSerGlyAspAspThrAspLeuPheAsnCysLeuAlaAsnValSerValIleSerLeu 315
 QY 12924 GTGAGTGTACTATTTGAAAGGTTAAAGACTTTTCTTAATTTGAGTGGCAACTTTA 12983
 DB 316 LeuSerIleSerLeuGlySerLeuGlnAlaLeuLeuLysAspPheArgTyrGlnHisLeu 335
 QY 12984 GAATTAAGTAACTGTAATTTGACAGATTTCCACATTTGAAACTGAATCTCTCAAAAG 13043
 DB 336 GluIleIleAsnCysAspPheAspLysPheProAlaLeuLysLeuSerSerLeuLysLys 355
 QY 13044 CTTACTTCACTTCCAAAGGTGGAATGCTTTTCCAGAACTTGAATCTCAACCTT 13103
 DB 356 PheValPheThrAspAsnLysAspIleSerThrPheGlnGluPheGlnMetProSerLeu 375
 QY 13104 GAGTTTCTAGATCTCAGTAGAAATGCTGAGTTTCAAGGTGCTGTTCTCAAGTAT 13163
 DB 376 GlnTyrLeuAspLeuLysArgAsnHisLeuSerPheLysGlyCysCysSerHisThrAsp 395
 QY 13164 TTTGGGACACCAAGCTTAAATGATTATGATCTGAGCTTCATGCTGTTATTTACCAATG 13223
 DB 396 PheGlyThrThrAsnLeuLysHisLeuAspLeuSerPheAsnAspValIleThrLeuGly 415
 QY 13224 TCAAACTTGGGGCTTGAACAATAAGATCTGATTTCCAGATTTCCAAATTTGAAA 13283
 DB 416 SerAsnPheMetGlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLys 435
 QY 13284 CAATAGAGTGAATTTCAATCTTATCTACTCAAGAACTCATTTACTTCAATTTCT 13343
 DB 436 GlnIleAsnAlaPheSerAlaPheLeuSerLeuArgAsnLeuArgTyrLeuAspIleSer 455
 QY 13344 CATACTCACACCAAGTTGCTTTCAATGCAATCTTCAATGCTGCTGCTGCTGCAAGTC 13403
 DB 456 TyrThrAsnIleArgIleValPheHisGlyIlePheThrGlyLeuValSerLeuGlnThr 475
 QY 13404 TTGAAATGGCTGGCAATTTCTTCCAGGAAAGCTTCCAGATATCTTCCAGAGCTG 13463
 DB 476 LeuLysMetAlaGlyAsnSerPheGlnAsnAsnLeuLeuProAspIlePheThrGluLeu 495
 QY 13464 AGAAATTTGACCTTCTGAGACTCTCTGAGTGTCAATGAGCACTTGCTTCCAAAGCA 13523
 DB 496 ThrAsnLeuThrValLeuAspLeuSerLysCysGlnLeuGluGlnValAlaGlnThrAla 515
 QY 13524 TTTTAAGTACTCTGAGCTTCTGAGTATTAATATAGCCACACAACTTCTTTTCATG 13583
 DB 516 PheHisSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnLysLeuLeuSerLeu 535

QY 13584 GATACGTTTCTTATTAAGTGTGAACTCCCTCCAGGTTCTTGATTAAGTCTGATCAC 13643
 DB 536 AspThrPheLeuTyrGluProLeuHisSerLeuAsnArgIleLeuAspCysSerPheAsnArg 555
 QY 13644 ATTAATGACTTCCAAAACACAGAACTACAGCAATTTTCCAGATAGCTTACTTTCTTAAT 13703
 DB 556 IleMetAlaSerLysGluGlnGlnLeuGlnAsnLeuProArgSerLeuThrPheAsn 575
 QY 13704 CTTACTCAGAAATGACTTTGCTTGACTTGTAACAACAGAGTTTCCGCAATGATGATGAC 13763
 DB 576 LeuThrGlnAsnAlaPheAlaCysValCysGlnHisGlnSerPheLeuGlnThrValLys 595
 QY 13764 GACCAAGGACAGCTCTTGAGTGAAGTGAAGCAATGAGATGTGCAACACTTCAGATAG 13823
 DB 596 AspGlnArgGlnLeuLeuValGlyAlaGlnGlnMetCysAlaGluProLeuAspMet 615
 QY 13824 CAGGCAATGCTGCTGCTGAGTTG--AATATCACTGCTCAGATGATGAATGAACATCTT 13880
 DB 616 GluAspMetProValLeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrIle 635
 QY 13881 GGTGTGCGGCTCCAGTGCTGTAGTATCTGTTGACGAGTCTTGCTATTAAGTTC 13940
 DB 636 SerValSerValValThrValLeuLeuValSerValValGlyValLeuValTyrLysPhe 655
 QY 13941 TATTTTCACTGATGCTTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14000
 DB 656 TyrPheHisLeuMetLeuLeuAlaGlyCysLysLysTyrGlyArgGlyGluSerIleTyr 675
 QY 14001 GATGCTTTTGTATCTCAAGCCAGATGAGAGCTGGTGAAGATGAGTGAAGTGAAG 14060
 DB 676 AspAlaPheValIleTyrSerSerGlnAspLysPheValAlaArgAsnGluLeuValLys 695
 QY 14061 AATTGAAGAAGGGGCTCCCTCCATTTCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 14120
 DB 696 AsnLeuGluGlyValProProPheGlnLeuCysLeuHisTyrArgAspPheIleTyr 715
 QY 14121 GGTGTGCACTTGTGCAACATCATCATGAAGTTTCCATAAAGCCGAAGGTGATT 14180
 DB 716 GlyValAlaIleAlaAlaAsnIleIleGlnGlnLysPheHisLysSerArgLysValIle 735
 QY 14181 GTTGTGTGCTCCAGCACTTCATCAGAGCCGCTGTGTATCTTTGAATATGATTTGCT 14240
 DB 736 ValValAlaSerGlnHisPheIleGlnSerArgTyrCysIlePheGluTyrGluIleAla 755
 QY 14241 CAGACCTGGAGCTTCTGAGAGTCGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14300
 DB 756 GlnThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeu 775
 QY 14301 GAGAAACCTGCTCAGGACAGAGTGAAGCTGTGACCGCTTCTCAGAGGAAACCTTAC 14360
 DB 776 GluLysSerLeuLeuAlaGlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyr 795
 QY 14361 CTGAGTGGAGAGCACTGTCTTGAGGCGGCACTTCTTGAGAGCACTCAGAAAAGCC 14420
 DB 796 LeuGluTyrPheGluAspSerValLeuGlyArgHisValPheThrArgLysLeuArgAla 815
 QY 14421 CTGCTGATGCTTAATATGAAATCCAGAAAGAAACAGTGGGTACAGATGCAATTTGCGAG 14480
 DB 816 LeuLeuAlaGlyLysProGlnSerProGluGlyThrAlaAspAlaGluThrAsnProGln 835
 QY 14481 GAAGCAACATCT 14492
 DB 836 GluAlaThrThr 839

RESULT 11
 TLR4_FELCA STANDARD; PRT; 833 AA.
 ID TLR4_FELCA STANDARD; PRT; 833 AA.
 AC P58727;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;

OS	Felis silvestris catus (Cat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX	NCBI_TaxId=9685;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Yoshida N., Kano R.;
RT	"Fels catus Toll like receptor 4."
RL	Submitted (Apr-2001) to the EMBL/Genbank/DDBJ databases.
CC	-I- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via
CC	MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC	secretion and the inflammatory response (By similarity).
CC	-I- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC	multi-protein complex containing at least CD14, LY96 and TRAF4.
CC	Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
CC	their respective TIR domains (By similarity).
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	-I- SIMILARITY: Belongs to the Toll-like receptor family.
CC	-I- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC	-I- SIMILARITY: Contains 1 TIR domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AB060687; BAB43947.1; --
DR	HSSP; O60603; IFYX.
DR	GO; GO:0046696; Filippolysaccharide receptor complex; ISS.
DR	GO; GO:0010530; Filippolysaccharide binding; ISS.
DR	GO; GO:0004888; P-tranmembrane receptor activity; ISS.
DR	GO; GO:0007250; P-detection of NF-kappa-inducing kinase; ISS.
DR	GO; GO:0016046; P-detection of fungi; ISS.
DR	GO; GO:0009598; P-detection of pathogenic bacteria; ISS.
DR	GO; GO:0042116; P-macrophage activation; ISS.
DR	GO; GO:0045576; P-mast cell activation; ISS.
DR	GO; GO:0046671; P-negative regulation of osteoclast different. . ; ISS.
DR	GO; GO:0043364; P-positive regulation of interleukin-1 biosyn. . ; ISS.
DR	GO; GO:0045084; P-positive regulation of interleukin-12 biosy. . ; ISS.
DR	GO; GO:0045366; P-positive regulation of interleukin-13 biosy. . ; ISS.
DR	GO; GO:0045410; P-positive regulation of interleukin-6 biosyn. . ; ISS.
DR	GO; GO:0040881; P-T-helper 1 type immune response; ISS.
DR	InterPro; IPRO01611; LRR_Cterm.
DR	InterPro; IPRO00463; LRR_Cterm.
DR	InterPro; IPRO03591; LRR_Typ.
DR	InterPro; IPRO00157; TIR.
DR	Pfam; PF00560; LRR; 12.
DR	Pfam; PF01463; LRRCT; 1.
DR	Pfam; PF01582; TIR; 1.
DR	PRINTS; PRO0019; LEURICRPT.
DR	SMART; SM00369; LRR_TYP; 1.
DR	SMART; SM00082; LRRCT; 1.
DR	SMART; SM00255; TIR; 1.
DR	PROSITE; PS50104; TIR; 1.
KM	Glycoprotein; Immune response; Inflammatory response;
KM	Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
FT	SIGNAL 1 23 Potential.
FT	CHAIN 24 833 Toll-like receptor 4.
FT	DOMAIN 24 633 Extracellular (Potential).
FT	TRANSMEM 633 653 Potential.
FT	DOMAIN 654 833 Cytoplasmic (Potential).
FT	REPEAT 53 76 LRR 1.
FT	REPEAT 77 100 LRR 2.
FT	REPEAT 101 124 LRR 3.
FT	REPEAT 128 149 LRR 4.
FT	REPEAT 150 173 LRR 5.
FT	REPEAT 174 197 LRR 6.
FT	REPEAT 203 225 LRR 7.
FT	REPEAT 228 252 LRR 8.

FT	REPEAT	310	334	LRR 9.
FT	REPEAT	350	372	LRR 10.
FT	REPEAT	373	398	LRR 11.
FT	REPEAT	422	421	LRR 12.
FT	REPEAT	442	445	LRR 13.
FT	REPEAT	447	469	LRR 14.
FT	REPEAT	470	494	LRR 15.
FT	REPEAT	495	518	LRR 16.
FT	REPEAT	520	542	LRR 17.
FT	REPEAT	544	566	LRR 18.
FT	REPEAT	568	592	LRR 19.
FT	DOMAIN	673	819	TIR.
FT	CARBOHYD	35	35	N-linked (GLcNAc. .) (Potential).
FT	CARBOHYD	173	173	N-linked (GLcNAc. .) (Potential).
FT	CARBOHYD	205	205	N-linked (GLcNAc. .) (Potential).
FT	CARBOHYD	238	238	N-linked (GLcNAc. .) (Potential).
FT	CARBOHYD	309	309	N-linked (GLcNAc. .) (Potential).
FT	CARBOHYD	497	497	N-linked (GLcNAc. .) (Potential).
FT	CARBOHYD	526	526	N-linked (GLcNAc. .) (Potential).
FT	CARBOHYD	570	570	N-linked (GLcNAc. .) (Potential).
FT	CARBOHYD	575	575	N-linked (GLcNAc. .) (Potential).
FT	CARBOHYD	625	625	N-linked (GLcNAc. .) (Potential).
SEQ	SEQUENCE	833 AA;	95592 MW; 3E3A84F2BB8A55EA CRC64;	
 Alignment Scores:				
Pred. No.:	7.58e-228	Length:	833	
Score:	2937.00	Matches:	587	
Percent Similarity:	81.33%	Conservative:	88	
Best Local Similarity:	70.72%	Mismatches:	115	
Query Match:	8.88%	Indels:	40	
DB:	1	Gaps:	6	
 US-09-396-985B-47 (1-18989) x TLR4_FEICA (1-833)				
OY	11992 TGCTTATCAGTGATGCGTTACAGCAAAAAGAAGCGGTATCATTCGAGCGCAGATTGATA	12051		
Db	29 CysValGluValValProAsnIleThrTYrGlnCysMetAspLeuAsn-----	44		
OY	12052 TACTCAGCTGTGGGGCTTCTTAATTGCCTT-----ATTCCATCATCA	12093		
Db	45 -----LeuHisLysIleProAsnArgIleProSerSer	55		
OY	12094 TCCTGTCTGCTTGATGTCTTTGGCGTTAGCAATCATATGACCACATCATCTGTATGAA	12153		
Db	56 ThrIysAspLeuAspMet-----SerPheAsnPro-----	65		
OY	12154 GAGCTGATGACATGAGATTAAATTCATTTTAGAGTTTATATCA---GCCAAAAATTGA	12210		
Db	66 -----LeuArgAsnLengIlySerHisSerPheAsnPhePro	78		
OY	12211 GATATCAATATGCTTTTTTATTTCTGTAGTGATGAATTCAGACAATTGAAGATGGGGCAT	12270		
Db	79 GluLeuGlnValLeuAspLeu--SerArgCysGluIleGlnIleIleGlnIleAspAspAlaT	98		
OY	12271 ATCAGAGCTTAAGCCAGCCTCTTACCTTAATATTGACAGAAACCCCATCCAGAGTTTAA	12330		
Db	98 YrGInGlyLeuAsnHisLeuSerIleLeuIleLeuThrGlyAsnProIleGlnArgLeuP	118		
OY	12331 CCCCTGGAGAGCTTTTCTGCACTATCAAGTTTACAGAAAGCTGGCGCTGTGGAGACAATTC	12399		
Db	118 heProGlyAlaRheSerGlyLeuSerSerLeuGlnThrLeuValAlaValGluThraAsnI	138		
OY	12391 TAGCACTGTAGAGACCTCCCCCTTGGACATGCTCAAACTTTGAAGAATCTTAATGTGG	12455		
Db	138 IeAlaSerLeuGlnAspPheProIleGlyIleLeuYsthrLeuYsthrLeuAsnValAla	158		
OY	12451 CTCACAATCTTATCCAACTTTTCAAAATTACCTGAGATTATTTTCTTAATGACCAATCTAG	12510		
Db	158 IaHlaEnaIleuIleHisSerPheLeuYeurProGluYrPheSerAsnMetSerAsnLeuG	178		
OY	12511 AGCACTTGACCTTTTCCAGGACACAGATTAAAGTATTATTGACACAGACTTGGGGTTTC	12570		
Db	178 LuYrYleAspLeuSerAsnAsnIlysiIleGlnIleAsnIleYrHiSlyAspLeuGlnValI	198		

QY 12571 TACATCAAAATCCCTCAATCTCTTTAGACCTGCTCCCTGAACCCATTAATCTTAC 12630
 DB 198 EHHISGlnlyProleuLeuSnmleuSerleuAapleuSerleuAapleuSerleuAapleu 218
 QY 12631 TCACACAGGTGATTAAGAAATTAAGGCTTCAATAGCTGATTAAGAAATTAATTTG 12690
 DB 218 IeGlnProGlyAlaPheleuSgluValylleuAargluLeuThrleuAargSerleuPheA 238
 QY 12691 ATACTTAATTAATGAAGAAATCTGTATTCAGAGCTGCTGCTTGAATCCATGCTT 12750
 DB 238 SnsrThrAapValMetlyAlaSerlleGlnGlyleuAlaGlyleuGlnlleHISGlnL 258
 QY 12751 TGGTCTGGGAGATTAAGAAATTAAGAAATCTGAAAGATTTGAACAATCTGCTAG 12810
 DB 258 euValleuGlyGluPheleuAapleuAargleuAapleuAargleuAapleuSerlleu 278
 QY 12811 AGGCGCTGTGCAATTTGACATTAAGAAATTCGATTAAGCTTGAATTAAGCTTGC 12870
 DB 278 IuGlyleuCyAapleuIlelleGlyleuPheAarglleAlaTyPheAapleuPheSerG 298
 QY 12871 ATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 12930
 DB 298 IuAapValleAapSerPheAapleuAapleuAapleuAapleuAapleuAapleuAap 318
 QY 12931 TGACTTAATTAAGAAATTAAGAAATCTTTCTTAATTAATTAATTAATTAATTAATTA 12990
 DB 318 euTyPheleuSgluPheleuSgluLeuProlyAapleuGlyTTPGlnIuGlyleuGly 338
 QY 12991 TTAATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 13050
 DB 338 AlaAapleuSgluPheleuSgluPheleuProthrIleuAapleuProleuSgluValP 358
 QY 13051 TCATCTTCAACAAGGTGGAATGCTTTTTCAGAAATGATTAATTAATTAATTAATTAAT 13110
 DB 358 HeSerAlaAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleuAap 378
 QY 13111 TAGATCTCAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13170
 DB 378 euAapleuSerThrAapleuPheSerleuSgluSgluSgluSgluSgluSgluSgluSglu 398
 QY 13171 CAACAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 13230
 DB 398 HThrAargleuLysIleuAapleuSerleuAapleuAapleuAapleuAapleuAapleu 418
 QY 13231 TCTTGGGCTTGAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13290
 DB 418 HeleuGlyleuGlyleuGlyleuGlyleuGlyleuGlyleuGlyleuGlyleuGlyleu 438
 QY 13291 GTGAGTTTCAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 13350
 DB 438 eAapleuSerleuAapleuProleuSgluSgluSgluSgluSgluSgluSgluSgluSglu 458
 QY 13351 ACACAGAGTGTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13410
 DB 458 IeThrGlnValAlaPheIleGlyllePheAapleuGlyleuIleSerleuGlnlleuLeu 478
 QY 13411 TGGTGGCAATTTTTCAGAAATCTTCTTCAATTAATTAATTAATTAATTAATTAATTA 13470
 DB 478 eAlaGlyAapleuSerPheGlnAapleuPheleuProAapleuPheleuGlyleuThrAap 498
 QY 13471 TGAACCTTCAAGTGTCTTCAAGTGTCAATTAATTAATTAATTAATTAATTAATTAATTA 13530
 DB 498 euThrIleleuAapleuSerPheSgluSgluSgluSgluSgluSgluSgluSgluSglu 518
 QY 13531 CACTCTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGT 13590
 DB 518 eAapleuProlyleuGlnleuLeuSnmleuSerIleAapleuSgluSgluSgluSgluSglu 538
 QY 13591 TTCTTTTAAGTGTCTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCAAG 13650
 DB 538 euProTyPheleuIleSerleuGlnIleThrleuAapleuCySerPheAapleuAapleuAap 558

QY 13651 CTTCACAAAAACAGAACTACAGATTTTCAAGTCTTCAAGTCTTCAAGTCTTCAAGTCTTCA 13710
 DB 558 IeSerleuSgluGlnleuAapleuAapleuAapleuAapleuAapleuAapleuAapleuAap 578
 QY 13711 AGAATGACTTTTCTTGTGATTTTGAACACAGATTTTCTGCAATTAATTAATTAATTAAT 13770
 DB 578 rAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleu 598
 QY 13771 GGCAGCTCTTGGGAGGATTAAGCAATTAAGTGAATTAAGTGAATTAAGTGAATTAAGTGA 13830
 DB 598 rGlnleuLeuValGlnValGlnValGlnValGlnValGlnValGlnValGlnValGlnVal 618
 QY 13831 TGCCTGTGCTGATTTG---AATATCACTGTGCAAGATTAAGTGAATTAAGTGAATTAAG 13887
 DB 618 eAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleu 638
 QY 13888 CGGTCTCAAGTGTCTTGTGATTTGATTAAGTGAATTAAGTGAATTAAGTGAATTAAGTGA 13947
 DB 638 eValPheThrValleuLeuValPheleuValPheleuValPheleuValPheleuValPhe 658
 QY 13948 ACCGTGAGCTTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14007
 DB 658 IeLeuMetleuLeuAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleu 678
 QY 14008 TTGTTATCTACTACAGCAGATTAAGTGAATTAAGTGAATTAAGTGAATTAAGTGAATTAAG 14067
 DB 678 HeValleuIleTyPheSerleuAapleuAapleuAapleuAapleuAapleuAapleuAap 698
 QY 14068 AAGAAAGGCTGCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14127
 DB 698 IuGlnGlyValPheProPheGlnleuCySgluSgluSgluSgluSgluSgluSgluSglu 718
 QY 14128 CCAATGCTGCAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14187
 DB 718 IAlaIleAlaAapleuIlelleGlnGlyleuPheSgluSgluSgluSgluSgluSgluSglu 738
 QY 14188 TGTCACAGACTTCAATCAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14247
 DB 738 AlSerGlnIlePheIleGlnSerAargIlePheIleGlnIleGlnIleGlnIleGlnIle 758
 QY 14248 GGCAGTCTTCAAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14307
 DB 758 rGlnPheleuSerleuAapleuAapleuAapleuAapleuAapleuAapleuAapleuAap 778
 QY 14308 CCTGTCTCAAGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14367
 DB 778 eAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleu 798
 QY 14368 GGCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14427
 DB 798 rPheleuSerleuAapleuAapleuAapleuAapleuAapleuAapleuAapleuAapleu 818
 QY 14428 ATGTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 14487
 DB 818 SgluGlyPheProAapleuCySgluGly 826
 RESULT 12
 TLR4_PIG STANDARD; PRT; 841 AA.
 AC 068Y56;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DS Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Alveolus;
 RA Shinkai H., Uemishi H.;


```

QY 13120 GTAAATGCGTTGAGTTTCAAGGTTGCTGTTCTCAAGTGAATTTGGACAACACCC 13179
DB 381 ergLysenHieLseuSerHelysGlyCyseSerHieAangLidPhelYlthrlhrySL 401
QY 13180 TAAAGTATTGATGTAGCTTCAATGGGTATTATTCATGATGATCAATCTTGGGCT 13239
DB 401 euLysHieLseuSerHieAangLidPhelYlthrlhrySL 421
QY 13240 TAGAACAATGATGATGATTTCCAGATTCCTCAATTTGAAACAATGATGATTT 13299
DB 421 euGlnGlnLeuGlnLysLeuSerHieAangLidPhelYlthrlhrySL 441
QY 13300 CAGTATTCCTTCACTCAAGAAACCTCAATTTCTTCAATTTCTCACTCACTCAAG 13359
DB 441 erLlePhelLeuSerHieAangLidPhelYlthrlhrySL 461
QY 13360 TTGCTTCAATGATGATGATTTCCAGATTCCTCAAGTCTTGAAGTCTTGAAGTCTTGA 13419
DB 461 alValPheArgGlyLlePheAlaGlyLeuValSerLeuGlnThrLeuLysMetAlaGly 481
QY 13420 ATTCTTCCAGAAACCTTCCAGATTCCTCAAGTCTTGAAGTCTTGAAGTCTTGA 13479
DB 481 snSerPheGlnAsnAsnLeuLeuProAspValPheThrAspLeuThrAsnLeuLeuL 501
QY 13480 TGGAACCTCTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13539
DB 501 euAspLeuSerLysCyseGlnLeuGlnValSerGlnAlaPheHieSerLeuPro 521
QY 13540 GTCTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13599
DB 521 rglLeuGlnValLeuAsnMetSerHieAangLidPhelYlthrlhrySL 541
QY 13600 AGTGTGAAATCCCTCCAGTCTTGAATTCAGTCTCAATCAATCAATCAATCAATCAAT 13659
DB 541 yspProLeuHieSerLeuArgLleLeuSerCyseSerYAsnLeuLleValAlaSerLysG 561
QY 13660 AACGAACTACAGCAATTTTCAAGTCTTGAATTTCTTCAATTTCTTCAATTTCTTCA 13719
DB 561 lueGlnGlnLeuGlnHieLeuProArgSerLeuAlaPheLeuAsnLeuThrLysAsnAsp 581
QY 13720 TTGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13779
DB 581 heserCyAlaCyseGlnHieGlnThrPheLeuGlnThrValAlaAspLidPhelGlnLeuL 601
QY 13780 TGTGGAAGTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13839
DB 601 euValGlyAlaGlnGlnMetValCyseThrGlnProLeuGlnMetGlnAspLeuProVal 621
QY 13840 TGAATTTG---AATATCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 13896
DB 621 euSerPheAlaGlnAlaThrCyseGlnHieSerGlnAlaValAlaSerAlaSerValLeuL 641
QY 13897 GTGTGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13956
DB 641 hrPheLeuLeuValSerValAlaGlyLleLeuValYlYlYlPheHieLeuLeuL 661
QY 13957 TTCTGCTGCTGCTGATGAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 14016
DB 661 euPheValGlyCyseLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysL 681
QY 14017 ACTCAAGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 14076
DB 681 yspSerSerGlnAspGlnAspTrpValAlaArgAsnGlnLeuValLysAsnLeuGlnLidLys 701
QY 14077 TGCCTCAATTTCACTGCTGCTTCACTCACTCACTCACTCACTCACTCACTCACTCACT 14136
DB 701 alPropPheHieLeuCyseLysHieLysLysLysLysLysLysLysLysLysLysLysL 721
QY 14137 CCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 14196
DB 721 laaenLleLleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 741

```

```

QY 14197 ACTTCATCCAGAGCCGCTGCTGATCTTTGATATGATGATGATGATGATGATGATGATGAT 14256
DB 741 isPheLleGlnSerArgTrpCyseLlePheGlnLysLysLysLysLysLysLysLysLysL 761
QY 14257 TGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14316
DB 761 euArgSerHieAlaGlyLleLlePheLleValLeuGlnLysLysLysLysLysLysLysL 781
QY 14317 GGCAGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 14376
DB 781 rglGlnGlnValGlnLeuLysLysLysLysLysLysLysLysLysLysLysLysLysLysL 801
QY 14377 GTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAT 14436
DB 801 erValLeuGlnYlArgHieLlePheThrArgLysLysLysLysLysLysLysLysLysL 821
QY 14437 CATGAAATCCAGAAACGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 14492
DB 821 rotPserProGlnGlnLysLysLysLysLysLysLysLysLysLysLysLysLysL 839

RESULT 13
ID 08MIQ2 PRELIMINARY; PRT; 839 AA.
AC 08MIQ2;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Toll-like receptor 4.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Kajikawa O., Fievert C.W., Goodman R.B., Wong V.A., Martin T.R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY101394; AAM50060.1; -.
DR HSSP; O60603; 1077.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_Lyp.
DR InterPro; IPR000157; TIR.
DR Pfam; PF00560; LRR_1; 11.
DR Pfam; PF01582; TIR_1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00369; LRR_TYP; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PSS0104; TIR; 1.
KW Receptor.
SQ SEQUENCE 839 AA; 96338 MW; 09F7D401EC14B6A CRC64;

Alignment Scores:
Pred. No.: 5,16e-213 Length: 839
Score: 2753.50 Matches: 544
Percent Similarity: 82.65% Conservative: 80
Best Local Similarity: 72.05% Mismatches: 126
Query Match: 8.33% Indels: 5
DB: Gaps: 3

US-09-396-985b-47 (1-18989) x 08MIQ2 (1-839)
QY 12237 AGGTGGAATTCAGACATTTGAAGATGGGGCATATCAGACCTTAAGCACTTCTTACC 12296
DB 87 ArgCyseLysLleHieThrLleGlnAspAspAlaLysLidLysLysLysLysLysLysL 106
QY 12297 TTAATATTCAGAGAAACCCATCCAGATTTAGCCCTGGAGACCTTTTGTGACTATCA 12356
DB 107 LeuLleLeuThrGlnYanProLleGlnSerLeuSerProGlnAlaPheSerGlyLeuSer 126
QY 12357 AGTTTACAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12416

```

```

Db 127 AsnLeuGlnIysLeuValAlaValGluThrHisLeuThrSerLeuGlnIysAspPheProIle 146
Qy 12417 GGACATCTCAAAACTTTGAAAGAACTTAAGTGGCTGACAACTCTTAATCCATCTTTGAAA 12476
Db 147 GlnHisLeuIysThrLeuGlnLeuAsnValAlaHisAsnLeuIleHisSerPheSer 166
Qy 12477 TTACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTGACCTTTCCAGCAACAG 12536
Db 167 IleProAspTyrPheSerAsnLeuSerSerLeuGlnHisLeuAspLeuSerAsnAsnIys 186
Qy 12537 ATTCAAAGTATTTAATTGACACACTTGGGGTTTACATCAAAATGCCCTTACTCAATCTC 12596
Db 187 IleGlnSerIleTyrHisIysAspLeuArgValLeuHisGlnMetProLeuGlnThrLeu 206
Qy 12597 TCTTTAAGCTGTCCCTGAAACCTTATGAATTTTCCAAACGAGTGCATTTAAAGAAATT 12656
Db 207 SerLeuAspLeuAlaLeuAsnProIleAspPheIleProProGlnAlaPheGlnAlaIle 226
Qy 12657 AGGCTTCATAGCTGACTTTAAGAAATTAATTGATGTTTAATTAATGAAGAAACTGT 12716
Db 227 ArgLeuHisGlnLeuIleLeuIysSerAsnPheIysSerThrAsnIleMetIysIleCys 246
Qy 12717 ATTCAGAGCTGCTGCTGTTTGAAGTCCATGCTTGGTTCTGGAGAAATTGAAATGAA 12776
Db 247 IleGlnGlnLeuSerGlnLeuGlnValHisArgLeuValLeuGlnGlnPheIysAsnGln 266
Qy 12777 GGAACCTTGAAAGATTGACAAATCTGCTTAAGAGGCTGTGCAATTTGACCATTTGAA 12836
Db 267 ArgAsnMetIysAsnPheAspIysSerAlaLeuGlnGlnLeuCysAsnLeuAlaIleGln 286
Qy 12837 GAATTCGATAGTATGACTTGTGACTACTGACTCGATGATTAATTAATTAATTTGAT 12896
Db 287 GluPheArgLeuAlaTyrIleAspAspLeuGlnGlnIysAsnIleThrAspLeuPheAspCys 306
Qy 12897 TTGCAAAATGTTTCTTCATTTCCCTGAGTGTGACTGATTAAGAAAGGTAAAGACTTT 12956
Db 307 LeuGlnAsnValSerValMetAlaLeuValHisMetTyrIleAspAsnGlnIleIlePhe 326
Qy 12957 TCTTATTAATTTGGATGGCAACATTTAGATTAATTAATTAATTTGACAG---TTT 13013
Db 327 ProIysAspPheSerTyrIysSerLeuGlnPheIleAsnGlnPheSerGlnAsnIle 346
Qy 13014 CCCGATTTGAAACCTCAATCTCTCAAAAGGCTTACTTCACTTCCAAACAAAGGTGGAGAT 13073
Db 347 PhePheLeuIysLeuSerSerLeuArgLeuIlePheThrAlaAsnIysGlnValArg 366
Qy 13074 GCTTTTTCAGAGTGTACTACCAAGCTTGAGTTTCTAGATCTCAGTAAATAGGCTTG 13133
Db 367 ThrPheProGlnLeuAsnThrProSerLeuGlnIupheLeuAspIleSerAsnAsnGlnLeu 386
Qy 13134 AGTTTCAAAAGTGTCTGTTCTCAAAAGTATTTGGGACACACGCTTAAGATTTTATGAT 13193
Db 387 SerLeuAsnIserCysCysSerValAsnSerLeuArgLeuThrGlnLeuIysHisLeuAsn 406
Qy 13194 CTGAGCTTCAATGGGTATTAATACCATGATCAAACTTCTGGGCTTAGAACTTAAGAA 13253
Db 407 LeuSerPheAsnGlnValIleThrMetThrSerAsnPheValGlnLeuGlnIupheGln 426
Qy 13254 CATTCGATTTTCAGCACTTCCAAATTTGAAACAAATGAGTGAAGTTTTCAGATCTTCA 13313
Db 427 HisLeuTyrPheGlnHisSerAsnLeuArgAsnIleAsnGlnPheSerIlePheLeuSer 446
Qy 13314 CTCGAAACCTCATTTACTTGACATTTCTCATCTCACACCAAGATTTGCAATGGC 13373
Db 447 LeuAsnAsnLeuLeuTyrLeuAspIleSerTyrThrHisIleArgValAlaPheArgGln 466
Qy 13374 ATCTTCATGGCTGTCCAGCTCGAAGCTTGAAGAAATGGCTGCAATTTCTTCCAGGAA 13433
Db 467 IlePheAspGlnIysLeuTyrSerLeuArgValIleuIysPheAlaGlnAsnAlaPheGlnAsp 486
Qy 13434 AACTTCCTTCAGATATCTTCACAGAGCTGAAACTTGACCTTCTCGACCTCTCAG 13493

```

```

Db 487 AsnArgLeuLeuAsnIlePheThrGlnMetThrSerLeuThrThrLeuAspLeuSerSer 506
Qy 13494 TGTCACTGGAGAGAGTTGTCTCCAAACGATTTAACTCACTCCAGCTTCCAGTACTA 13553
Db 507 CysGlnLeuGlnIupheValTyrGlnGlnAlaPheGlnSerLeuProArgLeuGlnSerLeu 526
Qy 13554 AATATGAGCCACAACAACTTCTTTCATTTGATGATACCTTCTTATTAAGTCTGAACTCC 13613
Db 527 AsnMetSerHisAsnAsnLeuLeuValLeuAspThrLeuThrTyrIysCysLeuTyrSer 546
Qy 13614 CTCGAGGTTCTTGATTAACACTTCATTCATCAATATGACTTCCAAAACAGAACTTACAG 13673
Db 547 LeuGlnValLeuAspLeuSerPheAsnHisIleGlnIysAsnIleThrGlnProGlnGln 566
Qy 13674 CATTTTCCAGTATGCTGCTTCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13733
Db 567 HisPheProSerAsnLeuThrLeuLeuHisIleThrIysAsnAlaPheValCysAspCys 586
Qy 13734 GAACACGAGTTTCTGCAATGATCAAGACCAAGACGAGCTTGTGGAAGTTGAA 13793
Db 587 GlnHisGlnIlePheMetGlnTyrIleIysAspGlnArgArgLeuLeuValGlnValGln 606
Qy 13794 CGAATGGAATGTGCAACACTTTCAGATTAACGACGCAATGCTGTGCTGACTTGG---AAT 13850
Db 607 GlnMetValCysIleThrProProAsn-----MetProValLeuSerPheThrAsn 623
Qy 13851 ATCACTCTTCAGATGAATTAAGCATCAATTTGATGCTGTGCTGCTCTCACTGCTTGA 13910
Db 624 AlaThrCysGlnIleSerIysThrIleIleSerValSerValPheSerValLeuValVal 643
Qy 13911 TCTGTTGATCAAGTCTGCTGCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 13970
Db 644 SerPheAlaValAlaLeuValTyrIysPheTyrPheProIleMetLeuLeuValGlnArg 663
Qy 13971 ATAAAGTATGTAAGAGTGAAGAAATCTATGATGCTCTTGTATCTTACTAAGCCAGAT 14030
Db 664 ArgIysTyrGlnArgGlnIysSerValTyrAspAlaPheValIleTyrSerSerGlnAsp 683
Qy 14031 GAGGACCTGGGTAAGAAATGACATGACATTAAGAAATTTGAAAGAGGGCTCCATTTTCA 14090
Db 684 GluAspTyrAlaArgAsnGlnLeuValIysAsnLeuGlnIupheValProProPheArg 703
Qy 14091 CTCTGCTTCACTACAGAGACTTAAATCCCGGTGGCCATTTGCTGCAACATCATTCAT 14150
Db 704 LeuCysLeuHisIysTyrArgAspPheIleProGlnValAlaIleAlaAsnIleIleGln 723
Qy 14151 GAAGTTTCCATTAAGCCGAAAGGTGATTTGTGTGCTGCCAGCATTCATTCAGAGC 14210
Db 724 GluGlnIysPheHisIysSerArgIysValIleValValIysSerGlnHisPheIleGlnSer 743
Qy 14211 CGCTGCTGATCTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 14270
Db 744 ArgTyrPheIlePheGlnTyrGlnIleAlaGlnThrTyrPheIleLeuSerSerHisAla 763
Qy 14271 GGTATCATCTTCAATTTGCTGCAAGAGTGAAGAAAGCTTGTCTGAGGCAAGCTGAG 14330
Db 764 GlnIleIlePheIleValLeuGlnIysValGlnIysSerLeuMetArgIlnArgValGln 783
Qy 14331 CTGTACCGCTTCTTCAGACAGAACTTACCTGAGTGGAGAGCACTGTCTCGGGCGG 14390
Db 784 LeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnIupheIleAspThrValLeuGlnArg 803
Qy 14391 CACATCTTTCGAGAGCACTCAGAAAAGCCCTGCTGATGCTTAATTAATTAATTAATTAAT 14450
Db 804 HisIlePheThrArgAsnArgIysValAlaLeuLeuAspIlyIysThrLeuSerProGln 823
Qy 14451 GGAACAGTGGGTACAGGATGCAATTTGACGAGAAAGCAATCATTTATC 14495
Db 824 GlnMetAlaArgAlaGlnAsnAsnGlnGlnIupheAlaMetThrLeu 838

```

RESULT 14
TLR4_CRIGR STANDARD; PRT; 838 AA.

AC Q9WV82; 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS *Cricetulus griseus* (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC *Cricetulus*.
 NC NCBT_TaxID=10029;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Macrophage;
 RX MEDLINE=20148868; PubMed=10683379;
 RA Lien E., Means T.K., Heine H., Yoshimura A., Kusumoto S., Fukase K.,
 RA Ingalls R.R., Goldenhock D.T.;
 RT "Toll-like receptor 4 impacts ligand-specific recognition of bacterial
 RT lipopolysaccharide.";
 RL J. Clin. Invest. 105:497-504(2000).
 CC -I- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -I- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TIRAP.
 CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
 CC their respective TIR domains.
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -I- TISSUE SPECIFICITY: Detected in macrophages and the Chinese
 CC hamster ovary fibroblast cell line.
 CC -I- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -I- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
 CC -I- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF153676; AAD41891.1; -
 DR HSPB; Q15399; 1FV.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR000157; TIR.
 DR Pfam: PF00560; LRR; 8.
 DR Pfam: PF01582; TIR; 1.
 DR PRINTS: PRO0019; LEURICRPT.
 DR SMART: SMO0082; LRRCT; 1.
 DR SMART: SMO0369; LRR_Typ; 1.
 DR SMART: SMO0255; TIR; 1.
 DR PROSITE: PS50104; TIR; 1.
 KW Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 25
 FT CHAIN 26 629
 FT TRANSMEM 630 650
 FT DOMAIN 651 838
 FT REPEAT 31 52
 FT REPEAT 53 75
 FT REPEAT 76 99
 FT REPEAT 100 123
 FT REPEAT 127 148
 FT REPEAT 149 172
 FT REPEAT 173 196
 FT REPEAT 200 224
 FT REPEAT 227 251

FT REPEAT 305 330 LRR 10.
 FT REPEAT 351 370 LRR 11.
 FT REPEAT 371 393 LRR 12.
 FT REPEAT 396 419 LRR 13.
 FT REPEAT 420 443 LRR 14.
 FT REPEAT 448 468 LRR 15.
 FT REPEAT 494 516 LRR 16.
 FT REPEAT 517 538 LRR 17.
 FT REPEAT 541 563 LRR 18.
 FT REPEAT 565 589 LRR 19.
 FT DOMAIN 670 816
 FT CARBOHYD 34 34 N-linked (GlcNAc...)
 FT CARBOHYD 115 115 N-linked (GlcNAc...)
 FT CARBOHYD 172 172 N-linked (GlcNAc...)
 FT CARBOHYD 204 204 N-linked (GlcNAc...)
 FT CARBOHYD 237 237 N-linked (GlcNAc...)
 FT CARBOHYD 307 307 N-linked (GlcNAc...)
 FT CARBOHYD 492 492 N-linked (GlcNAc...)
 FT CARBOHYD 495 495 N-linked (GlcNAc...)
 FT CARBOHYD 524 524 N-linked (GlcNAc...)
 FT CARBOHYD 572 572 N-linked (GlcNAc...)
 FT CARBOHYD 622 622 N-linked (GlcNAc...)
 SQ SEQUENCE 838 AA; 96277 MW; 129B33596EB908B48 CRC64;
 Alignment Scores:
 Pred. No.: 9,236-212 Length: 838
 Score: 2738.00 Matches: 528
 Percent Similarity: 81.66% Conservative: 100
 Best Local Similarity: 68.66% Mismatches: 129
 Query Match: 8.28% Indels: 12
 DB: 1 Gaps: 4
 US-09-396-985b-47 (1-18989) x TLR4_CRIGR (1-838)
 QY 12216 TCAATGCTTTTATTCCTCTAGAGTCTGGAATC 12248
 DB 70 SerHisSerPhePheAsnPheProGluLeuLysLeuLeuAspLeuSerArgCysGluIle 89
 QY 12249 CAGCAATTTGAAGTGGGATATGACGCTTACGACCTCTTACTTAAATTGACA 12308
 DB 90 GluThrIleGluAspLysAlaIleGlyGlyLeuHisGlnLeuThrIleLeuThr 109
 QY 12309 GAAACCCCATCCAGAGTTTACGCTGAGACCTTTCTGACATGATGAGTTACAGAG 12368
 DB 110 GlyAsnProIleGlnAsnLeuSerLysGlyThrPheSerGlyLeuAlaAsnLeuGlnAsn 129
 QY 12369 CTGGTGGCTGTGAGACAAATCTAGCATCTCTAGAGAACTTCCCATTTGACATCTGAAA 12428
 DB 130 LeuValAlaValGluIleLysLeuAlaSerLeuAspSerLeuProIleGlyHisLeuVal 149
 QY 12429 ACTTTGAAGAACTTAATGTGGCTCACAAATCTTATCCAAATCTTTCAATTAAGTGAAT 12488
 DB 150 ThrLeuLysLysLeuAsnValAlaHisAsnLeuLeuHisSerPheLysLeuProGluLys 169
 QY 12489 TTTTCTATCTGACCAATCTAGAGCACTTGGACCTTTCTGACAAAGAAATTCAGATAT 12548
 DB 170 PheSerAsnLeuThrAsnLeuGluHisLysLeuAspLeuSerAsnLysLysIleGlnThrIle 189
 QY 12549 TATTTGACAGACTTGGCGGTTTACATCAATGCGCCCTACTCATCTCTTTAGACCTG 12608
 DB 190 TyrTyrThrAspLeuGlnIleThrLysArgGluAsnProGlnLeuAsnLysSerLeuGluLeu 209
 QY 12609 TCCCTGAACCTTATGAACTTTATTCACACGCTGACATTTAAAGAAATTTAGCTTCAAG 12668
 DB 210 SerLeuAsnProIleAspPheIleGlnProGlyAlaIleGlnGlyIleArgLeuHisGlu 229
 QY 12669 CTGACTTGAAGAAATTAATTTGATAGTTTAATGATTAAGAAATTTGATTAAGAGTCTG 12728
 DB 230 LeuThrLeuArgSerAsnPheAsnSerThrAsnValMetLysThrCysIleHisAsnLeu 249
 QY 12729 GCTGGTTTGAAGTCCATCGTTGGTTCTTGGAGAAATTTGAAATGAAGAAATTTGAA 12788
 DB 250 AspLysLeuGlnValHisArgLeuIleLeuGlyGluIleLysAsnGlnValArgAsnValGlu 269

QY 12789 AAGTTGCAAAATGCTGCTTAAGGCGCTGNGCAATTGACCATTTGAAGAAATTCGGATTA 12848
 DB 270 ArgPheAspArgIYValIIeGluGlyLeuCybLysValThrIIeGluGluPheArgPhe 289
 QY 12849 GCATACCTTAGACTCTACCTCGATGATATATATGACTATATTAATGTTTGAACAAAGTTT 12908
 DB 290 ThrIYrIaIaenGluPheSerGluAspIIeThrAsp---PheAspCybLeuAlaIaenVal 308
 QY 12909 TCTTCATTTTCCCTGGAGCTGAGCTGATTCAGTAAGGGTAAAGACTTTTCTTAATATTC 12968
 DB 309 SerIaMetSerLeuAlaAsnValIYrLeuIYsArgLeuGluAspIIeProIYsIYrPhe 328
 QY 12969 GGATGGCAACTTTAGATTGATTAACGTAAATTTGGACAGCTTTCCCACTGAAATCTC 13028
 DB 329 LysIYrGlnThrLeuAlaValIIeArgGlyLeuIYsGlnPheProIYsLeuGluLeu 348
 QY 13029 AAATCTCTCAAAAGGCTTACTTCTTCACTTCACAAAGGAGGGAATGCTTTTTCAGAAATT 13088
 DB 349 ProPheLeuIYsArgLeuIIePheIIeThrAsnIYsGlyAlaThrSerPheProGluVal 368
 QY 13089 GATTCACCAAGCTTGTGAGTTTCTAGATCTCAGTAAAGGCTTGAAGTTTCAAGTTTC 13148
 DB 369 AsnLeuProSerLeuThrPheLeuAspLeuSerGlyAsnGlyMetSerPheArgGlyCys 388
 QY 13149 TGTCTCTCAAAAGTGTTTGGGACAAACAGCCTAAAGTATTTAGATCTGAGCTTCAATGCT 13208
 DB 389 CysSerIYrThrAspLeuGlyAlaArgSerLeuIYsHsIeLeuAspLeuSerPheAsnGly 408
 QY 13209 GTATTAACCATGAGTTCAAACTTCTGGGCTTAGAACAACTGAAACTGGAATTTTCAG 13268
 DB 409 ValIleSerMetSerGluAsnPheMetGlyLeuGlnIleuGluIYrIYrLeuAspPheGln 428
 QY 13269 CATTCGAATTTGAAACAAATAGTGAAGTTTCACTGATCTCATCTGCAAACTCATTT 13328
 DB 429 HisSerThrLeuIYsIYsAlaThrGluPheSerMetPheLeuProLeuGluIYsLeuLeu 448
 QY 13329 TACCTGACATTTTCTCTACTACACACAGAGTGTGCTTCAATGACATCTTCAATGGCTTG 13388
 DB 449 TyrLeuAspIleSerIYrThrAsnThrIYsIleAsnPheAsnGlyIlePhePheGlyLeu 468
 QY 13389 TCCAGTCTCGAAGTCTTGAAATGGCTGGCAATTTCTTCCAGAAACTTCTTCCAGAT 13448
 DB 469 ThrSerLeuAsnThrIYsLeuIYsMetAlaGlyAsnSerPheIYsAspAsnIIeLeuSerAsn 488
 QY 13449 ATCTTCACAGAGCTGAGAAACTTGAACCTTCTGACCTCTCTGAGTGTCAACTGAGCAG 13508
 DB 489 ValPheThrAsnThrIYsAsnLeuThrPheLeuAspIleSerIYsCybGlnLeuGlnGln 508
 QY 13509 TTGCTCCAAAGCATTTAACTCTCCAGTCTTCAAGTATTAATATGAGCACAAC 13568
 DB 509 ValSerIYrGlyValPheAspThrLeuIYsHsIeArgLeuGluLeuLeuMetSerHsIeAsn 528
 QY 13569 AACTTCTTTCATGATGATACCTTTCTTAAAGTGTGAAGTCTCCCTCCAGAGTTCTTGAT 13628
 DB 529 AsnLeuLeuLeuLeuAspLeuPheHsIeIYrIYsGlnLeuHsIeSerLeuIYsThrLeuAsp 548
 QY 13629 TACAGTCTCAATCACATATGACTTCCAAAAACAGAACTACAGACTTTTTCAGATGCT 13688
 DB 549 CysSerPheAsnHsIeIleGluThrSer---IYsGlyIleMetGlnHsIePheProIYsSer 567
 QY 13689 CTAGCTTTCTTAATCTTACTACAGATGACTTTGCTGTGATCTTGGACACACAGAGTTTC 13748
 DB 568 LeuAlaPheLeuAsnLeuThrAsnAsnProPheAlaCybIIeCybGlnHsIeGlnAsnHe 587
 QY 13749 CTGCAATGATCAAGACAGACAGGAGCTTGTGATGAGTTGAACGATGAAATGTGCA 13808
 DB 588 LeuGlnIYrValIYsAspGlnArgLeuPheLeuValIYsThrGlnGlnMetThrCybAla 607
 QY 13809 AACCTTCAGATTAAGCAGGAGCAGTGCCTGTGCTGAGTTG---AATATCACTGTGCAGATG 13865
 DB 608 ThrProValGluMetIYsAspSerLeuValIYsAspPheArgAsnAlaThrCybIYrVal 627

QY 13866 AATAAGACCATCATGTTGGTGTGCTGCTCACTGATGCTTGTAGTATCTGTGTGACAGTT 13925
 DB 628 GlnIYrThrIleIleSerValIleSerValIleSerValIleValIleValIleAlaPhe 647
 QY 13926 CTGGCTTAATAGTTCTATTTTCACTGATGCTTCTTGTGGCTGCAATTAAGTATGCTA 13985
 DB 648 LeuValIYrIYsPheIYrPheHsIeIleIleValIleAlaGlyCybIYsIYrIYsSerArg 667
 QY 13986 GGTGAAACATCTATGATGCTTGTATCTACTCAAGCAGAGATGAGGCTGGTGAAG 14045
 DB 668 GlyGluSerIleIYrAspAlaPheValIIeIYrSerSerGlnAspGluAspIYrValArg 687
 QY 14046 AATGAGCTAGTAAAGATTTAGAAAGAGGAGTGCCTTCATTTCAAGCTGTGCTTCACT 14105
 DB 688 AsnGluLeuValIYsAsnLeuGluGluGlyValProProPheGlnIleuCybLeuHsIeIYr 707
 QY 14106 AGAGACTTATTTCCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14165
 DB 708 ArgAspPheIleProGlyValAlaIleAlaIleAlaAsnIleIleGlnIYsPheHsIeIYs 727
 QY 14166 AGCCGAAAGGATGTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 14225
 DB 728 SerArgIYsValIleValIleValIleValIleSerArgHsPheIleGlnSerArgIYrIYsIlePhe 747
 QY 14226 GAATATGAGATGCTGACACTGCTGAGCTTCTGAGCAGTGTGCTGATCATCTTCATT 14285
 DB 748 GluIYrGluIleAlaGlnThrIYrGlnPheLeuSerHsIeSerGlyIleIlePheIle 767
 QY 14286 GTCTTGAGAAAGGTGAGAAAGACCTGCTGAGCAGCAGAGGTGAGCTGTACCGCTTCTC 14345
 DB 768 ValLeuGluIYsValGluIYsSerLeuIYsGlnGlnIYsValGluIYrIYrArgLeuLeu 787
 QY 14346 AGCAGAAACCTTACTGAGTGGAGGAGACAGTGTCTGGGGGAGCACTTCTTGAGA 14405
 DB 788 SerArgAsnThrIYrIYsGluIYrGluIYsAspAlaIleuIYsArgHsIeIlePheIYrArg 807
 QY 14406 CGACTCGAAAGACCTGCTGATGATGATGAATTCAGAAATCCAGAAAGACAGTGGGTACA 14465
 DB 808 ArgLeuIYsIYsAlaLeuLeuAspGlyArgAlaITrAsnProGluIYsAlaThrGluAla 827
 QY 14466 GGATGCAATGGCAGAGACCAATCT 14492
 DB 828 GluAsnAsnGlnIYsGluIYrThrThr 836
 DB 836
 RESULT 15
 ID Q8K2T5 PRELIMINARY; PRT; 835 AA.
 AC Q8K2T5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP
 RC SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J, TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dere J.G.,
 RA Klusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Helel F.,
 RA DiCicco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stedman M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebli T.B., Toobyuk S., Carninci P., Prange C.,
 RA Rata S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiy S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,


```
Db 498 heLeuAryLeuSerLysCysGlnLeuGlnIleSerTrpGlyValPheAspThrLeuH 518
QY 13537 CAGCTTTCAGGTAATAATATAGCCACAACAATTCTTTCATGTGATACGTTTCCTT 13596
Db 518 IsArgLeuGlnLeuAsnMetSerHisAsnAsnLeuPheLeuAspSerHisIer 538
QY 13597 ATAAGTGTCCGAACTCCCTCCAGGTTCTTATTAACAGTCCAAATCAATCAATATGACTTCCA 13656
Db 538 yrnGlnLeuIYrSerLeuSerThrLeuAspCysSerPheAsnArgIleGlnThrSer- 557
QY 13657 AAAAACAGAACTTACAGACATTTTCCAAAGTAGCTAGCTTTCTTAATCTTATTCAGATG 13716
Db 558 --LysGlyIleLeuGlnHisPheProLysSerLeuAlaPhePheAsnLeuThrAsnAsn 577
QY 13717 ACTTGTCTGTACTTGTGAACACCAAGATTCTCTGCAATGATCAGACCAAGGAGCAGC 13776
Db 577 erValAlaCysIleCysGlnHisIleGlnLysPheLeuGlnTrpValLysAspGlnLysGlnP 597
QY 13777 TCTTGTGGAAGTTGAACGAATGGATGTGCAACACCTTCAGATTAAGCAGGAGCATGCTG 13836
Db 597 heLeuValAsnValGlnGlnMetThrCysAlaThrProValGlnMetAsnThrSerLeuV 617
QY 13837 TGCTGAGTTTG--AATATCACTGTGCAATGAATAAGACCATCATTTGTTGTGCTGCC 13893
Db 617 alLeuAspPheAsnAsnSerThrCysGlyMetGlyLysThrIleIleSerValSerValI 637
QY 13894 TCACTGTCTGTATGATCTGTTGTAGACAGTCTGTCTATTAAGTTCTATTTTCACTGA 13953
Db 637 leSerValIleValIleSerThrValAlaPheLeuIleTyHisPheTyrrPheHisIleuI 657
QY 13954 TGCTTCTGTGCTGCTGATGAAGTATGATGATGAGGTAAGGTAACATGATGACCTTGTTA 14013
Db 657 leLeuIleAlaGlyCysLysLysTyrrSerArgGlyGlnSerIleTyrrAspAlaPheValI 677
QY 14014 TCTACTAAGCCAGATAGAGTACGCTGCTGAAGATGAGTATGAAGATTTAGAAAG 14073
Db 677 leTyrrSerSerGlnAsnGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGln 697
QY 14074 GGGTGCCTCCATTCACTGCTGCTTCACTACAGAACTTATTCCTGGTGTGCTGCTG 14133
Db 697 LysValProArgPheHisIleuCyLeuHisIleTyrrArgAspPheIleProGlyValAlaIleAla 717
QY 14134 CTGCAACATCATCATGATGAAGGTTTCCATAAAGCCGAAAGGATGTTGTTGTGTTGCC 14193
Db 717 laAlaAsnIleIleGlnGlnIlePheHisLysSerArgLysValIleValValIleSerA 737
QY 14194 AGCACTTCATCCAGAGCCGCTGATGATCTTTGAATATGAGATTGTCAGACCTGCGAGT 14253
Db 737 rGHisPheIleGlnSerArgTrpCysIlePheGlnIleGlnIleAlaGlnThrTrpGlnP 757
QY 14254 TTCTGAGCAGTCTGCTGCTGATTCATCTTCATTTGCTGCAAGAGTGGAGAAACCTGCC 14313
Db 757 heLeuSerSerArgSerGlyIleIlePheIleValLeuGlnLysValGlnLysSerLeuL 777
QY 14314 TCAGCAGCAGGCTGAGCTGATGACGCTTCCAGACGGAACACTTACCTGAGTGGGAGG 14373
Db 777 euArgGlnGlnValGlnLeuTyrrArgLeuLeuSerArgAsnThrTyrrLeuGlnTrpGlnA 797
QY 14374 ACAAGTCTCTGGGCGGCGACATCTTCTGAGACGACTCAGAAAAGCCCTGCTGATGGTA 14433
Db 797 sPAsnProLeuGlyArgHisIleIlePheTrpArgGlyLeuLysValAlaLeuLeuAspGlyL 817
QY 14434 AATCATGGAATCCGAAAGAAC 14456
Db 817 ysaIleSerAsnProGlnGlnThr 824
```

Search completed: March 29, 2005, 19:41:11
Job time : 1213.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_nbp model

Run on: March 29, 2005, 09:56:53 ; Search time 2221.5 Seconds
(without alignments)
17409.875 Million cell updates/sec

Title: US-09-396-985B-48

Perfect score: 86900
Sequence: 1 ttccatcatcatgtagtgc.....catttagtatttccaga 50000

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 8422768

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ndp_model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09396985/runat_28032005_155742_21135/app_query.fasta_1.85098
-DB=Geneseq_16Dec04 -QMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOFCU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR=MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptco -NORC=ext -HEAPSIZE=500 -MITLEN=0 -MAXLEN=2000000000
-USER=US09396985 @CGN_1_1_4007 @runat_28032005_155742_21135 -NCPU=6 -ICPU=3
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -WAIT -DSPLOCK=100 -LONGLOG
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*\n2: geneseqp1980s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2607	3.0	839	6	ABU04773 Human exp
2	2607	3.0	839	6	ABU04774 Human exp
3	2607	3.0	839	6	ABU04775 Human exp
4	2607	3.0	839	7	AD078785 Human PRO
5	2607	3.0	839	7	AD048826 Human PRO
6	2600.5	3.0	837	2	AAW86361 Human DNA
7	2600.5	3.0	837	2	AAE16102 Human DNA
8	2600.5	3.0	837	6	ABU04776 Human exp
9	2599	3.0	795	8	AD057791 Rheus mo
10	2596	3.0	808	8	AD057803 Chimpanze

11	2594	3.0	801	8	AD057797
12	2593.5	3.0	837	5	AAE16116
13	2592	3.0	808	8	AD057782
14	2591	3.0	799	2	AAW86352
15	2591	3.0	799	5	AAE16093
16	2591	3.0	799	5	ABB83162
17	2591	3.0	799	6	ABR42963
18	2591	3.0	799	7	ADB39121
19	2591	3.0	799	8	ADP56556
20	2591	3.0	799	8	ADP48597
21	2582	3.0	795	8	AD057800
22	2574	3.0	808	8	AD057785
23	2558	2.9	801	8	AD057788
24	2548.5	2.9	745	8	AD057794
25	2547.5	2.9	738	8	ADP29455
26	942	1.1	179	7	AD042707
27	886	1.0	208	3	AAW86059
28	748	0.9	178	8	ADN12270
29	727	0.8	1300	7	ADP63060
30	701.5	0.8	1300	7	ADP63060
31	598.5	0.7	1658	4	ABG06940
32	581.5	0.7	994	4	ABG14604
33	581.5	0.7	994	4	ABG07468
34	581.5	0.7	994	4	ABG19901
35	581.5	0.7	994	4	ABG14924
36	582	0.7	1318	7	ABG12875
37	568.5	0.7	513	7	ADP63833
38	580	0.7	879	4	ABG12671
39	577.5	0.7	721	4	ABG13961
40	575.5	0.7	641	4	ABG08128
41	575.5	0.7	641	7	ADJ68375
42	575.5	0.7	1224	4	ABG03861
43	575.5	0.7	1284	4	ABG10795
44	575.5	0.7	1284	4	ABG06053
45	575.5	0.7	1284	4	ABG09636

ALIGNMENTS

RESULT 1	ABU04773	standard; protein; 839 AA.
AC	ABU04773;	
DT	29-JAN-2003	(first entry)
DE	Human expressed protein tag (EPT) #1439.	
XX	Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.	
XX	Homo sapiens.	
OS	W0200278524-A2.	
XX	10-OCT-2002.	
PD	28-MAR-2002; 2002WO-US009671.	
XX	28-MAR-2001; 2001US-0279495P.	
PR	21-MAY-2001; 2001US-0292544P.	
PR	08-AUG-2001; 2001US-0310801P.	
PR	01-OCT-2001; 2001US-0326780P.	
PR	04-DEC-2001; 2001US-0336780P.	
PR	20-FEB-2002; 2002US-0358965P.	
XX	(ZYCO-) ZYCOs INC.	
PA	Chicz RM, Tomlinson AJ, Urban RG;	
XX		
PI		

XX WPI; 2003-040607/03.
DR

PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.

PS Example 2; SEQ ID NO 1439; 134pp; English.

The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting an immune or immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPRO at http://wipro.int/pub/published_pct_sequences

SQ Sequence 839 AA;

Alignment Scores:

Pred. No.:	2.37-234	Length:	839
Score:	267.00	Matches:	526
Percent Similarity:	73.68%	Conservative:	101
Best Local Similarity:	61.81%	Mismatches:	172
Query Match:	3.00%	Indels:	52
DB:	6	Gaps:	8

US-09-396-985B-48 (1-50000) X ABU04773 (1-839)

[illegible]

Db	137	AsnLeuLaserLeuGluAenPheProIleGluHisbLeuLySThrLeuLySgluAen	156
QY	37940	GTGGCTCAAAATTTATACATTCCTGTAAAGTTACSTGCATATTTTCSAATGSAAGAC	37999
Db	157	ValAlaHisAsnLeuIleGlnSerPheLySLeuProGluTyrPheSerAsnLeuThrAen	176
QY	38000	CTACTAATGSGATCTTTTATTAACTATATCTAAACATTAAGTACGACATCTTAAG	38059
Db	177	LeuGluHisLeuAspLeuSerSerAsnLySLeIleGlnSerIleTyrCySThrAspLeuAag	196
QY	38060	TTTCTAGCGAAAAATCSACAAAGTCATCTCTTTAGACATGCTTTGAACCCCAATGAC	38119
Db	197	ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAen	216
QY	38120	TTTCATTCAGACCAAGCCCTTTACAGGAATTTAAAGCTTCATGAATGCTTAAGAGTAAT	38179
Db	217	PheIleGlnProGluAlaPheLySgluIleArgLeuHisbLeuLySLeuThrLeuArgAen	236
QY	38180	TTTAAATGCTCAAAATATATGAAGAACTTGCTTCAAAACCTGGCTGTTCACGCTCCAT	38239
Db	237	PheAspSerLeuAsnValMetLySThrCySLeIleGlnLyLeuAlaGluValHis	256
QY	38240	CGGTATCTTTGGGAGAAATTTAAAGATGAAGAAAGCATGGAATTTTGAACCCCTATAC	38299
Db	257	ArgLeuValLeuGluGluPheArgAsnGluGlyAsnLeuGluLyPheAspLySLeAla	276
QY	38300	ATGGAGAGCATATGTGTATGACACCATGTATGAAGTTACAGGTTACATATCAATGATTTT	38359
Db	277	LeuGluGluLySLeuCySAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyr	296
QY	38360	TCAGATCATTTGTGTAA--TTCCATCTGTGGGCAATGTTTCTGCATATGCTCTGGCA	38416
Db	297	LeuAspAspIleIleLeAspLeuPheAsnCySLeuThrAsnValSerSerPheSerLeuVal	316
QY	38417	GGGTATCTTAATAAATCTAGAAAGATGGTTCSTAAACATTTGAAAAGGAACCTTATGA	38476
Db	317	SerValThrIleGluArgValLySAspPheSerTyrAsnPheGlyTyrGlnHisbLeuGlu	336
QY	38477	ATCATTTAGATGCAACTTAAGCAAGTTCSCAATCTGGAATCAACCTTTGTTAAAGTTTG	38538
Db	337	LeuValAsnLySbysPheGluGlnPheProThrLeuLySLeuLySLeuSerLeuLySArgLeu	356
QY	38537	ACTTTAATCTATGAACAAAGGCTCTATCAGTTTAAAAAGTGCCCTCAACAAAGTCTCAGC	38596
Db	357	ThrPheThrSerAsnLySgluYAlaAsnAlaPheSerGluValAspLeuProSerLeuGlu	376
QY	38597	TATCTAATCTTATGATAAATGACATCGAGCTTTAAGTGTTGCGTCTTATTTCTGATTTG	38656
Db	377	PheLeuAspLeuSerAlaArgAsnGlyLeuSerPheLySgluCySAspSerGlnSerAspPhe	396
QY	38657	GGAAACAAACAGCCGTGACACTTAAGCACTGACGTTCAATGAAGTGCCCATTTATGAGTGC	38716
Db	397	GlyThrThrSerLeuLySbysTyrLeuAspLeuSerPheAsnGlyValIleHisMetSerSer	416
QY	38717	AATTTCAATGGGCTAGAAAGAGCTGCACACCTGATTTTACAGACCTTACATTTAAAGG	38776
Db	417	AsnPheLeuGluGluGlnGlnLeuGluHisbLeuAspPheGlnHisSerAsnLeuLySgln	436
QY	38777	GTCACAGAAATTTACAGGTTCTTATCCCTTGAAGACCTATTTACTTGAATCTTCTAT	38836
Db	437	MetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHis	456
QY	38837	ACTAAACCAAAATGTCATCGAATGGATATTTCTTGAGTGAACAGCTGCACAAACATTA	38896
Db	457	ThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeu	476
QY	38897	AAATGCGCTGGCAATCTTTCAAGACCAACACCTTTCAATGATGCTTTGCAACACACCA	38956
Db	477	LySLeuThrAlaGlyAsnSerPheGlnGluAenPheLeuProAspIlePheThrGluLeuArg	496
QY	38957	AACCTGACATTTCTGATCTTTTAAATGTCATTTGAAACAAATATCTTGGGGGCTATTT	39016

Db 40 CysMetGluLeuAenPheTyrLysIleProAspAenLeuPro----- 53
 Qy 37520 ATCATCACTGTAGCAAGTGTGAAATATGCACAAATCTGCAGAGTCTCTCTCTGCTCACACC 37579
 Db 54 -----PheSerThrLysAsnLeuAspLeuSerPheAsnProLeuArgHis--- 68
 Qy 37580 ATCATCACTGTGTTTGTCTGTGTATCTCTTTCACAAATATACATGATATATCATATCT 37639
 Db 69 -----LeuGlySerTyrSerPhe----- 74
 Qy 37640 GTTTGTATCATATGATAGTGGAGCACTGTATGATTAGTAAAGGGTTTTTTTTTTCAGCAA 37699
 Db 75 -----PheSerPheProGlu 79
 Qy 37700 AAATACATAATTTGGTATCTCTTTTGGCCATGATGTGATAATTTGAACATTTGAAGACAG 37759
 Db 80 LeuGlnValLeuAspLeuSer-----ArgCysGlnIleGlnThrIleGlnAspGly 96
 Qy 37760 GCATGGCATGGCTTACACACACCTCTCAAACTTGTATCTGACAGAGAAACCTATCCAGAGT 37819
 Db 97 AlaTyrGlnSerLeuSerHisLeuSerThrLeuIleuThrGlyAsnProIleGlnSer 116
 Qy 37820 TTTTCCCAAGAACTTCTCTGTGACTAACAAATTTAGAAATCTGTGCTGTGGAGACA 37879
 Db 117 LeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThr 136
 Qy 37880 AAATTTGGCTCTCTAGAAAGTTCCTTATTTGACAGCTTATTAACCTTAAAGAACTCAAT 37939
 Db 137 AsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGlnLeuAsn 156
 Qy 37940 GTGGCTCACAATTTTATCATCTCTGTAGAGTTTACCTGCATATTTTCCAACTGACAGAC 37999
 Db 157 ValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsn 176
 Qy 38000 CTAGTACATGTGATCTTTCTTATTAATAATTAACATTAATTTACTGTCAACGACTTACAG 38059
 Db 177 LeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArg 196
 Qy 38060 TTTTACGTGAAATCCACAGTCAATCTCTTTTGAACAGTCTTTTGAACCCCAATTGAC 38119
 Db 197 ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsn 216
 Qy 38120 TTTCAATCAAGACCAACCTTTCAAGGAAATTAAGTCCATGACACTGATCAAGATATAT 38179
 Db 217 PheIleGlnProGlyAlaPheLysGlnIleArgLeuHisLysLeuThrLeuArgAsnAsn 236
 Qy 38180 TTTAATAGCTCAAAATATATATGAAAACTTGCCTTCAAACTGGCTGTGTTACACGTCAT 38239
 Db 237 PheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHis 256
 Qy 38240 CGGTGATCTTGGAGAAATTTAAGATGAAAGAACTGGAATTTTGAACCTCTATC 38299
 Db 257 ArgLeuValLeuGlnLysPheArgAsnGlnLysAsnLeuGlnLysPheAspLysSerIle 276
 Qy 38300 ATGGAAGCACTATGTATGATGACCAATGATGATGATGATGATGATGATGATGATGAT 38359
 Db 277 LeuGlnGlyLeuCysAsnLeuThrIleGlnLysPheArgLeuAlaTyrLeuAspTyrTyr 296
 Qy 38360 TCAGATGATATTTGTAAG--TTCCATGCTTGGCGAAATGTTTGTCAATGCTCTTGCA 38416
 Db 297 LeuAspSerIleIleLeuAspLeuPheAsnLysLeuThrAsnValSerSerPheSerLeuVal 316
 Qy 38417 GGTTATCTATTAATAATCTAGAAAGTGTCTTAAACATTTCAATGGCAATCTTATCA 38476
 Db 317 SerAlaThrIleGlnLysValLysAspPheSerTyrAsnPheGlyTyrGlnHisLeuGln 336
 Qy 38477 ATCATAGATGTCACTTAAGCAAGTTTCAACTGATGATCAACCTTTCTTAAAGTTT 38536
 Db 337 LeuValaLysCysLysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeu 356
 Qy 38537 ACTTAACTATGAAACAAGGCTATATCAGTTTAAAAAGTGGCCCTTACCAAGTCTCAGC 38596
 Db 357 ThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGln 376

Qy 38597 TATCTAGATCTTGTAGAAATGCACTGAGCTTTAGTGGTTGCTGTTCTTATCTGATTTG 38656
 Db 377 PheLeuAspLeuSerTyrGlnGlyLysLeuSerPheLysGlyCysCysSerGlnSerAspPhe 396
 Qy 38657 GGAACAACAACCTGTAGACACTTATGACCTTCACTGATGATGATGATGATGATGATGATGAT 38716
 Db 397 GlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSer 416
 Qy 38717 AATTTCATGGGCTTATGAAAGCTGCAGACCTTGGATTTTACAGACTTCTATTTAAAAAG 38776
 Db 417 AsnPheLeuGlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGln 436
 Qy 38777 GTCAAGAAATTCCTCAGGCTCTTATCCCTTGAAGAAGTACTTACCTTACCTCTCTAT 38836
 Db 437 MetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHis 456
 Qy 38837 ACTTACACCAAAATGCACTTGTGATATATTTCTTGGCTTGAACAATCTTCAACATTA 38896
 Db 457 ThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeu 476
 Qy 38897 AAAATGGCTGGCAATCTTTTCAAAAGACACACCTTTCAAAATGCTTTTGCAAAACACA 38956
 Db 477 LysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGluLeuArg 496
 Qy 38957 AACTTGACATTCCTGGATCTTTCTTAAATGTCATTTGGAACAAATATCTGGGGGTATT 39016
 Db 497 AsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnIleLeuSerProThrAlaPhe 516
 Qy 39017 GACACCTTCATAGACTTCAATATTAATATATGATGATGACACAAATCTATTTGTTTGAT 39076
 Db 517 AsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeuAsp 536
 Qy 39077 TCATCCATTAATACAGCTGTATCTCTCAGACCTTATTTGAGATTTCATATCGATA 39136
 Db 537 ThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIle 556
 Qy 39137 GAGACATCT--AAAGAAATATGCAACATTTTCCAAAGAGCTTAGGCTTCTCAATCTT 39193
 Db 557 MetThrSerLysLysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 576
 Qy 39194 ACTTACAAATCTGTGCTTATATATGTAACATCAGAAATCTCTGACGTGGTCAAGAA 39253
 Db 577 ThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrrIleLysAsp 596
 Qy 39254 CAGAGCACTTCTTGGTGAATGTTGAACAATGACATGCTGACACCTGTAGAGATGAAT 39313
 Db 597 GlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGln 616
 Qy 39314 ACCTCCTTAGTGGATTTAATTAATTTTACCTGATATATGTAACAAGATCATCAGT 39373
 Db 617 GlyMetProValLeuSerLeu--AsnIleThrCysGlnMetCysAsnLysThrIleIleGly 635
 Qy 39374 GTGTCACTGTGCACTGTATGTGTGATTCACCTGTATGATCTTGTATATCAACTTAT 39433
 Db 636 ValSerValLeuSerValLeuValIleSerValValAlaValLeuValTyrLysPheTyr 655
 Qy 39434 TTTTACCTGATCTTATTTGCTGTGCTGTTAAAAAGTACAGAGAAAGAAAGCTTATGAT 39493
 Db 656 PheHisLeuMetLeuLeuAlaGlyCysIleLysTyrIleLysArgGlyLysAsnIleTyrAsp 675
 Qy 39494 GCATTTGTATCTTACCTGAGTCAAGTGAAGAGACCTGGGTGAAGAAATGAGCTGTAAAGAT 39553
 Db 676 AlaPheValIleTyrSerSerGlnAspGlnAspTrrAlaArgAsnGlnLeuValLysAsn 695
 Qy 39554 TTAGAAAGAGAGTCCCGCTTTCACCTCTGCTTCACTACATGACAGACTTATTTCTGCT 39613
 Db 696 LeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrThrArgAspPheIleProGly 715
 Qy 39614 GTAGCCATTTGCTGCAACATCATCTACAGAAAGCTTCCACAAGACCGGAAAGCTTATTTG 39673
 Db 716 ValAlaIleIleAlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleVal 735

QY 39674 GTAGTCTACAGACATTATTCAGAGCCGCTGATCTTGAATATGAGATTCCTCAA 39733
 DB ValValSerGlnHisPheIleGlnSerIleArgTrpCysIlePheGluTrpGlnIleAlaGln 755
 QY 39734 ACATGACGATTTCTGAGCAGCCGCTCTGACATCATCTTCAATGTTCTTGAGAGGTTGAG 39793
 DB ThrTrpGlnPheLeuSerSerArgIleAlaGlnIlePheIleValLeuGlnIleValGlu 775
 QY 39794 AAGTCCCTGAGGACAGGACGATGGAATGTATGSCCTCTTGAAGAAACACCTACTG 39853
 DB LysThrLeuLeuArgGlnGlnIleValGlnLeuTrpArgLeuLeuSerArgAsnThrTrpLeu 795
 QY 39854 GAATGAGAGACAAATCTCTGAGGAGACATCTTCTGAGAAAGATTAAATGCCCCCTA 39913
 DB GluTrpGlnAspSerValLeuGlnIleArgIleIlePheTrpArgArgLeuArgIleAlaLeu 815
 QY 39914 TTGATGGAAGAACCTCGAATCTCTGAGCAACA 39946
 DB LeuAspGlyLysSerTrpAsnProGluGlyThr 826
 RESULT 3
 AB04775
 ID AB04775 standard; protein; 839 AA.
 AC AB04775;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #1441.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCO INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1441; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and

CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 839 AA;
 Alignment Scores:
 Pred. No.: 2,33e-234 Length: 839
 Score: 2607.00 Matches: 526
 Percent Similarity: 73.68% Conservative: 101
 Best Local Similarity: 61.81% Mismatches: 172
 Query Match: 3.00% Indels: 52
 DB: Gaps: 8
 US-09-396-985b-48 (1-50000) x AB04775 (1-839)
 QY 37400 TGGAAAAATGCAATAATTAATCAAGACTATCACTGCTTTATGACCCA 37459
 DB 26 TrpGluProCysValGluValAlaProAsnIleThrTyrosin----- 39
 QY 37460 GTTATGATCTTGAATGATTTTCTAATGAGATTGCGCTGACATAGTGTAGATT 37519
 DB 40 CysMetGluLeuAsnPheTrpLysIleProAspAsnLeuPro----- 53
 QY 37520 ATCATCACTGAGCAAGTGTGAAATGACAAATCTGCAAGTTCTCTCTGACACC 37579
 DB 54 -----PheSerThrLysAsnLeuAspLeuSerPheAsnProLeuArgHis--- 68
 QY 37580 ATCATCACTGTTTGTCTGTCGACAGTTTCTCTTCAATACATGATATATCT 37639
 DB 69 -----LeuGlySerTyrosPhe----- 74
 QY 37640 GTTTGTATCATAGTATGAGGACGCTGTTATGATTAGAAAGGTTTTTTTACGAA 37699
 DB 75 -----PheSerPheProGlu 79
 QY 37700 AATATCAATAATGATATCTTTTCCCATAGTGTGAAATGAAACATTTGAAGACAG 37759
 DB 80 LeuGlnValLeuAspLeuSer-----ArgCysGlnIleGlnThrIleGluAspGly 96
 QY 37760 GCATGCAATGCTTACACCACTCTGAACTTGATCTGACAGAAACCTATCCAGACT 37819
 DB 97 AlaTyrosIleSerLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSer 116
 QY 37820 TTTTCCCGAGAAAGTTTCTGCACTPAACAAGTTTAGAAATCTGGGCTGGAGACA 37879
 DB 117 LeuAlaLeuGlnAlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGlnThr 136
 QY 37880 AATTTGCTCTCTAGAAAGCTTCCCTATTGACAGCTTAACTTAAAGAACTCAAT 37939
 DB 137 AsnLeuAlaSerLeuGlnLeuAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsn 156
 QY 37940 GTGGCTCACAATTTTATACATCTCTGTAAGTTACTGTCATATTTTCCATCTGACGAC 37999
 DB 157 ValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTrpPheSerAsnLeuThrAsn 176
 QY 38000 CTAGTACATGATGATCTTTCTTAATACTATTAATCAACTTATGTCACAGACTTACG 38059
 DB 177 LeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIleTrpCysThrAspLeuArg 196
 QY 38060 TTTTACGTGAAATCAACAAGTCAATCTCTTTAGACATGTCTTTGAACCCATTTGAC 38119
 DB 197 ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAsnLeuSerLeuAsnProMetAsn 216
 QY 38120 TTCAATTAAGACCAAGCTTTCAAGGGAATTAGCTCCATGACTGACTTGAAGGTTAT 38179
 DB 217 PheIleGlnProGlyAlaPheLysGluIleArgSerHisLysLeuThrLeuArgAsnAsn 236

QY	38180	TTTATATAGCTCAATATATATAGAAAACCTGGCTTCAAAACCTGGCTGGTTTATACAGTCCAT	382823
Db	237	PheAspSerLeuSeruValMetIyLThrCysIleGlnGlyLeuAlaGlyLeuGluValHis	256
QY	38240	CGGTTGATCTGGGAGAAATTTTAAAGATGAAGAAAGAAATCTGGAAATTTTGACCCCTCTATC	38299
Db	257	ArgLeuValLeuGlyGluPheArgAsnGlyGlyAsnLeuGlyLysPheAspLysSerAla	276
QY	38300	ATGGAAGACATATGTGATGTGACCATTTGATGAGTTACAGTTTACATATACAAATGATTTT	38359
Db	277	LeuGluGlyLeuCysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyr	296
QY	38360	TCAAGTATATGTTAA--TTCCATCTGTTGGCCGAATGTTTCGCAATGTCCTGGCA	38416
Db	297	LeuAspAspIleIleAspLeuPheAsnGlyLeuThrAsnValSerSerPheSerLeuVal	316
QY	38417	GGTGTATCTATTAATAATATCTAGAAAGATGTTCCATAATTCCTAAAGGCAATCCATTATCA	38476
Db	317	SerValThrIleGluArgValLysAspPheSerTyrAsnIleGlyTyrGlnHisLeuGlu	336
QY	38477	ATCATATAGATGTCAATTAAGACAGTTTCCAACTGGATCTACCTTTCTTAAAGTTTG	38536
Db	337	LeuValAsnLysLysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeu	356
QY	38537	ACTTAACTATGAACAAGAGGTATCATGTTTAAAAAGTGGCCCTTACCAAGTCTCAC	38596
Db	357	ThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGlyValAspLeuProSerLeuGlu	376
QY	38597	TATCTAGATCTTATAGAAATGACATGAGCTTTAGTGTGGCTGCTTATCTGATTTG	38656
Db	377	PheLeuAspLeuSerAlaArgAsnGlyLeuSerPheLysGlyCysAspSerGlnSerAspPhe	396
QY	38657	GGAACAAACAGCCCTGAGACACTTACAGCTTCAATGTCGCTCACTTATATGAGTGC	38716
Db	397	GlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnGlyAlaIleThrMetSerSer	416
QY	38717	AATTTCATGGGCTTAGAAGACCTGACACCTGGATTTTCAGACCTTCACTTTAAAAAG	38776
Db	417	AsnPheLeuGlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGln	436
QY	38777	GTCACAGAACTTCAGAGGCTTATCCCTTGAAAGGATCTTACCTGACATCTCTAT	38836
Db	437	MetSerGlnPheSerValPheLeuSerLeuArgAsnLeuLysTyrLeuAspIleSerHis	456
QY	38837	ACTAACAACAATATGAATCTGCATGATATATTTCTTGAGCTTGACAGTCTCAACATAT	38896
Db	457	ThrIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeu	476
QY	38897	AAATGCTGGCAATCTTTCAAGACACACACCTTTCAATATGTTTGCAACACACACA	38956
Db	477	LysMetAlaGlyAsnSerPheGlnGlnHisAsnPheLeuProAspIlePheThrGluLeuArg	496
QY	38957	AACTTGACATCTCCGATCTTTCTTAATATGCATATGAAACAATATCTTGGGGGGATTT	39016
Db	497	AsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnLeuLeuSerProThrAlaPhe	516
QY	39017	GACACCCCTCCATAGACTTCAATTTTAAATATGAGTACACAACAATCATATGTTTGGAT	39076
Db	517	AsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAsp	536
QY	39077	TCATCCCATTAACAACAGCTGATTTCCCTGACACCTTGATTTGACAGTTTACATGCGATA	39136
Db	537	ThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIle	556
QY	39137	GAGACATCT--AAAGAAATCTGCAACATTTTCCAAAGAGTCTAGCTTTTCAATCTT	39193
Db	557	MetThrSerLysLysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeu	576
QY	39194	ACTAACAATTCGTGCTTGTATATGACATACAGAAATTCCTGACAGTGGGACGAGA	39253
Db	577	ThrGlnAsnAspPheAlaCysThrCysGluHisGlnSerPheLeuGlnTrrIleLysAsp	596
QY	39254	CAGAAGCAGTCTCTGGTGAATGTGAAACAATGACATGTGCAACACCTGTAGATGAAT	39313

Db	597	GLNATGSLINLEUVALGLIUALGUAAGMEGLUCYALATHProSerAspLysGln	616
QY	39314	ACCCCTTATGCTGGATTTTAAATGATATCTACCTGTATATATGATACAAATCATCACT	39373
Db	617	GLYMERProValLeuSerLeu---AanILethrCysGlnMetAsnLysThrIleIleGly	635
QY	39374	GTCGACGTGCTCAGTGTGATGTGTGATGCACTGTAAGCACTTTCTGTATATACACTTTCTAT	39433
Db	636	ValSerValLeuSerValLeuValValSerValValAlaValLeuValValLysPheTyr	655
QY	39434	TTTCAACCTGATCTTATATGCTGCTGTATAAAGTAAAGACAGAGAGAAAGCATCTATGAT	39493
Db	656	PheHISLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGlyGlyAsnIleTyrAsp	675
QY	39494	GCATTTTGTATCTACTGCACTGATGAGATGAGATGAGACTGCGTGAAGAAATGACCTGGTAAAGAT	39553
Db	676	AlaPheValIleIleTyrSerSerGlnAspGlyAspTyrValArgAsnIleuValLysAsn	695
QY	39554	TTAGAAAGAGAGTGCCTCCGCTTTCACCTCTGCTTCACTACAGACATTTATTCCTGCT	39613
Db	696	LeuGluGluGlyValAlaProPheGlnLeuCysLeuHISLysArgAspPheIleProGly	715
QY	39614	GTACCCATTCCTGCGCAATCATCAACAGAAAGCTTCCSAAAGCCGGAAGGTTATGTG	39673
Db	716	ValAlaIleAlaIleAsnIleIleHISGluGlyPheHISLysSerArgLysValIleVal	735
QY	39674	GTAGTGTCTAGACACTTTATTCAGACCCGTTGCTATCTTTGAAATGATGAGATTGCTCA	39733
Db	736	ValValSerGlnHISpHeIleGlnSerHISArgTyrCysIlePheGluTyrGluIleAlaGln	755
QY	39734	ACATGCGAGTTTCTGAGACAGCCGCTCTGCGCATCATCTTCAATGTCTCTTGAGAAAGTTGAG	39793
Db	756	ThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGln	775
QY	39794	AAGTCCCTGCTGAGGCGAGCGGTGGAATTATGCGCTTTAGAGAGAAACCTACCTG	39853
Db	776	LysThrLeuLeuArgGlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyrLeu	795
QY	39854	GAATGCGAGACACTCTCTGGGAGAGACATCTTCTGAGAAAGATTTAAATGCGCTTA	39913
Db	796	GluTyrGlnAspSerValLeuGlyArgHISIlePheThrArgArgLeuArgLysAlaLeu	815
QY	39914	TTGGATGAAAAAGCTCGAATCCTGAGCAACA	39946
Db	816	LeuAspGlyLysSerTyrAsnProGluGlyThr	826
RESULT 4			
ADCT8785	ID	ADCT8785 standard; protein; 839 AA.	
XX	AC	ADCT8785;	
XX	DT	01-JAN-2004 (first entry)	
XX	DE	Human PRO protein #7.	
XX	KM	human; PRO; cancer; inflammatory bowel disease; ulcerative colitis;	
XX	OS	Crohn's disease.	
XX	PN	Homo sapiens.	
XX	PD	WO2003034984-A2.	
XX	PF	01-MAY-2003.	
XX	PR	15-OCT-2002; 2002WO-US030370.	
XX	PA	19-OCT-2001; 2001US-0340083P.	
XX	PI	(GETH) GENENTECH INC.	
XX		Goddard A, Gurney AL;	

[illegible]

Db	197	ValLeuHISgclmEtrProlLeuHISaSerLeuHISaSerLeuHISaSerLeuHISaSerProlMetAaH	216
QY	38120	TTCAATTCAGAACCAAGCCCTTTCAGGGAATTTAAAGCTCCATGACATGACTCTGAGAGGATTA	38175
Db	217	PheIleGlnProGlyAlaPheLysGluIleArgLeuHISleLysLeuThrLeuArgAaSerAaH	236
QY	38180	TTTAAATGCTCAAAATATATATGAAAACCTTGCCCTTCAAAACCTGGCTGCTTTACACGTCAT	38233
Db	237	PheAspSerLeuHISaValMetLysSThrCysIleGlnGluLysLeuIleGluLysValHIS	256
QY	38240	CGGTTGATCTTGGGAGAATTTAAAGATGAAAGAAACCTGGAAATTTTGAAACCCCTATAC	38299
Db	257	ArgLeuValLeuGlyGluPheArgAaGlnGluLysAsnLeuGluLysPheAspLysSerAla	276
QY	38300	ATGGAAGAGCATATGTGATGTGACCATATGATGATTCAGGTTAAACATATCAATGATTTT	38355
Db	277	LeuIleGluLysLeuCysAsnLeuThrIleGlnGluPheArgLeuAlaLysLeuAspTyrLys	296
QY	38360	TCAGATGATATGTTAAG--TTCCATGCTGTTGGCAATGTTTCGCAATGTCCTCGGCA	38416
Db	297	LeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuVal	316
QY	38417	GGTCAATCTATTAATAATATCTAGAAAGATGTTCCCTAAACATTTGCAAAAGGCAATCCCTATAC	38476
Db	317	SerAlaThrIleGluArgValLysAspPheSerTyrAsnPheIleTyrGlnHISLeuGlu	336
QY	38477	ATCATTTGAATGTCACCACTTAAGCAGTTTCCAACTCTGATCTACCCCTTCTTAAAGTTTG	38536
Db	337	LeuValAsnLysLysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeu	356
QY	38537	ACTTTAACTATGAAACAAAGGGCTTATCAGTTTAAAAAAGTGCCCTTACCAAGTCTCAGC	38596
Db	357	ThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGlu	376
QY	38597	TATCTAATCTTAGTAGAAATGACCTGAGCTTTAAGTGTTGCTGTCTTATTTCTGATTTG	38656
Db	377	PheLeuAspLeuSerIleArgAsnGlyLeuSerPheLysGlyCysSerSerIleAspPhe	396
QY	38657	GGAACAAACAGCCCTGAGACACTTGAACCTCAGCTTCAATAGTGCCCATTTTATGATGGC	38716
Db	397	GlyHISThrSerLeuLysTyrLeuAspLeuSerPheAsnGlyAlaIleHISMetSerSer	416
QY	38717	AATTTCAATGGGCTTAGAAGAGCTGACGACACTTGATTTTCAGACCTCTACTTTAAAGAG	38776
Db	417	AsnHISLeuGlyLeuGlnGluAsnGluHISleuAspPheGlnHISerAsnLeuLysGln	436
QY	38777	GTCACAGAAATTCGAGCGTTCTTATCCCTTGAAAACCTACTTACCTTGACATCTTCTAT	38836
Db	437	MetSerGluPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHIS	456
QY	38837	ACTAAACCAAAATATGACCTCGATGATGATATATTTCTTGCGCTGACGACTCAACACATTA	38896
Db	457	ThrIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeu	476
QY	38897	AAATGCGCTGCAATCTTTCAAGACCAACACCCCTTCAAAATGCTCTTGCAACACACA	38956
Db	477	LysMetIleIleLysMetSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArg	496
QY	38957	AACCTGACATTCCTGGAATCTTTCTTAATATGTCATTTGAAACAATATCTTTGGGGGGTATT	39016
Db	497	AsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnGluLeuSerProThrAlaPhe	516
QY	39017	GACACCCCTCAGACATTCATTAATTAATTAATGACGACACACATTAATGTTTGTGAT	39076
Db	517	AsnSerLeuSerSerLeuGlnValLeuAsnMetSerHISAsnAsnPhePheSerLeuAsp	536
QY	39077	TCATCCCATTAATACAGACTGTATTCCTCTCAGACACTTGATGAGTTTCAATGCGCAT	39136
Db	537	ThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHISle	556
QY	39137	GAGACATCT--AAAGAAATATCTGCAACATTTTCCAAAGAGTCTAGCCCTTCTTCAATCT	39193

```
Dh 557 MetTherSerLysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 576
Qy 39194 ACTPACATTTCTGTTGCTTGTATATGGAACATATGAAATTCCTGCGAGTGGCTCAAGGAA 39253
Dh 577 ThcGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAsp 596
Qy 39254 CAGAAAGATGTTCTTGAGATGTTGAACAATGACATGTCGACACCTGTAAGATGAAT 39313
Dh 597 GlnArgGlnLeuLeuValGlnValGlnArgMetClnCysAlaThrProSerAspLysGln 616
Qy 39314 ACCTCCTAGTGTGATTTTAAATATCTACCTGTATATGTAACAAGACATCATCAGT 39373
Dh 617 GlyMetProValLeuSerLeu---AsnIleThrCysGlnMetAsnLysThrIleLeuGly 635
Qy 39374 GTGTCATGTCGACGTGATTTGTCGATTCACCTGTACCATTTTCTGATATACCACTTGTAT 39433
Dh 636 ValSerValLeuSerValLeuValSerValValAlaValLeuValTyrLysPheTyr 655
Qy 39434 TTTGACCTGATACCTTATTTGCTGCTGTAAAGATGACAGAGGAGAAAGCATCTATGAT 39493
Dh 656 PheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlnArgLysGlnAsnIleTyrAsp 675
Qy 39494 GCATTTGTGATCTACTGAGTCAGATGAGGACTGGGTGAGAAATGAGCTGTAAAGAT 39553
Dh 676 AlaPheValIleTyrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsn 695
Qy 39554 TTGAGAAAGAGAGTCCCGCTTTCACCTGCTTTCATCTACATGACAGACTTTATCCCTGCT 39613
Dh 696 LeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGly 715
Qy 39614 GTAGCCATTTGCTGCGCAACATCATCCAGAGAGGCTTCCCAAGAGCCGGAAGTTATGTTG 39673
Dh 716 ValAlaIleLeuAlaAsnIleIleHisGlnGlnPheHisLysSerAlaGlyLysValIleVal 735
Qy 39674 GTATGTCCTAGACACTTATTCAGAGCCGTTGTATCTTTGAATATGAGATTGCTCAA 39733
Dh 736 ValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGlnIleValIleAlaGln 755
Qy 39734 ACATGGCAGTTTCTGAGCAGCCGCTGCGCATCATCTTTCATTTGCTTGGAGAGTTGAG 39793
Dh 756 ThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGln 775
Qy 39794 AAGTCCCTGTCGAGGACAGAGAGTGAATGTATGACCTTCTTACAGAAACACTTACCTG 39853
Dh 776 LysThrLeuLeuAlaGlnGlnValGlnLeuTyrArgLeuLeuSerAlaGlnThrIleLeu 795
Qy 39854 GAATGGAGAGCAATCCTCTGGAGGAGGACATCTTCTGAGAGACTTAAATATGCCCTTA 39913
Dh 796 GlnTrpGlnAspSerValLeuGlyArgHisIlePheTrpArgLysLeuAlaLeu 815
Qy 39914 TTGGATGGAAGAGCCTGGAATCCTGAGCAACA 39946
Dh 816 LeuAspGlyLysSerTrpAsnProGlnGlyThr 826

RESULT 5
ADD48826
ID ADD48826 standard; protein, 839 AA.
XX
AC ADD48826;
XX
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein AAF05316, SEQ ID NO 14536.
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
FN MO2003016475-A2.
```

```
XX
PD 27-FBB-2003.
XX
XX 14-AUG-2002; 2002MO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
PI Woolf C, D'urso D, Befort K, Coatsigan M,
XX WPI; 2003-268312/26.
XX
DR GENBANK; AAF05316.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
PS
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 839 AA;
XX
XX
XX Alignment Scores:
XX Pred. No.: 2.33e-234 Length: 839
XX Score: 2607.00 Matches: 526
XX Percent Similarity: 73.68% Conservative: 101
XX Best Local Similarity: 61.81% Mismatches: 172
XX Query Match: 3.00% Indels: 52
XX DB: Gaps: 8
XX
XX US-09-396-985B-48 (1-50000) x ADD48826 (1-839)
Qy 37400 TGGAAAAAATGCATTAATTAATGACATACATGACATGCTTTATGTAACCCA 37459
Dh 26 TrpGlnProCysValGlnValAlaProAsnIleThrTyrGln----- 39
Qy 37460 GTATGATCTTGAATGATTTTCTATGATGATTTGCTGCTGACATAGTGATAGTTT 37519
Dh 40 CysMetGlnLeuAsnPheTyrLysIleProAspAsnLeuPro----- 53
Qy 37520 ATCATCTGTAGCAAGTGTGAATAATGACAAATCTGCAGAGTCTCTCTGCTACACC 37579
Dh 54 -----PheSerThrLysAsnLeuAspLysSerPheAsnProLeuArgHis--- 68
```

QY 37580 ATCAACACCTGTTTGTCTCTGACAGTTTCTTTACAAATACATGATATCATCT 37639
 Db 69 -----LeuGlySerTyrSerPhe----- 74
 QY 37640 GTTTGTATCATAGTATGGTAGGAGCTGTATGATCAATTGAAAGGCTTTTTCACGAA 37699
 Db 75 -----PheSerPheProGlu 79
 QY 37700 AAATACATATATGGTATCTTTTGGCCATAGTGTAATTTGAACAAATGAGAGCAAG 37759
 Db 80 LeuGlnValLeuAspLeuSer-----ArgCysGlnIleGlnThrIleGlnAspIly 96
 QY 37760 GCATGCGATGCGCTTACACACCTCTCAACTGTGATCTGACAGAAACCTTACAGAGT 37819
 Db 97 AlaTyrGlnSerLeuSerHisLeuSerThrLeuIleuThrGlyAsnProIleGlnSer 116
 QY 37820 TTTTCCCGAGAGTTTCTCTGAGACTAAACAATTGAGAAATCTGTGGCTGTGGAGCA 37879
 Db 117 LeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIlyLeuValAlaIleGlnThr 136
 QY 37880 AAATGGCTCTCTAGAGAGCTTCCCTATTTGGACAGCTTATTAACCTTAAAGAACTCAAT 37939
 Db 137 AsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuIlyThrLeuIlyGlnLeuAsn 156
 QY 37940 GTGGCTCACAATTTATATCATCTTCCGTAGTATACCTGATATTTTCCAACTGACGAC 37999
 Db 157 ValAlaHisAsnLeuIleGlnSerPheIlySerPheProGluTyrPheSerAsnLeuThrAsn 176
 QY 38000 CTAGACATGATGATCTTTCTTAAATCAATATTCAACTATTACTGTCAACGACTTACAG 38059
 Db 177 LeuGlnHisLeuAspLeuSerSerAsnIlyIleGlnSerIleTyrCysThrAspLeuArg 196
 QY 38060 TTTTACGTGAAATCCACAAGTCAATCTCTTTAGACATGTCTTTGAACCCATTCAC 38119
 Db 197 ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsn 216
 QY 38120 TTCACTCAAGACCAAGCTTTCAGGAGATTAAGCTCCATGACATGACCTAGAGGTAT 38179
 Db 217 PheIleGlnProGlyAlaPheIlyGlnIleArgLeuHisIlySerLeuThrLeuArgAsnAsn 236
 QY 38180 TTTAATAGCTCAATATATATGAAATCTTCCCTTCAAACTGTGGCTGTTTACAGTCCAT 38239
 Db 237 PheAspSerLeuAsnValMetIlyThrCysIleGlnIlyLeuAlaGlyLeuGlnValHis 256
 QY 38240 CCGTTGATCTTGGGAGATTTTAAAGATGAAGGATCTGGAATTTTGAACCTCTATC 38299
 Db 257 ArgLeuValLeuGlyGlnPheArgAsnGlnIlyAsnLeuGlnIlyPheAspIlySerAla 276
 QY 38300 ATGGAAGCATATGATGATGACCATGATGATGATGATGATGATGATGATGATGATGAT 38359
 Db 277 LeuGlnIlyLeuCysAsnLeuThrIleGlnIlyPheArgLeuAlaTyrLeuAspIlyTyr 296
 QY 38360 TCAGATGATATTTGTAAG---TTCCATGCTTGGCGATGTTTGTGCAATGCTCTGCA 38416
 Db 297 LeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuVal 316
 QY 38417 GGTATATCTATTAATATCTGAAGATGCTTCAACATTTCAATGAGCAATCTTATCA 38476
 Db 317 SerAlaThrIleGlnArgValIlyAspSerSerTyrAsnPheGlyTyrGlnHisLeuGln 336
 QY 38477 ATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38536
 Db 337 LeuValAsnCysIlySerPheGlyIlyPheProThrLeuIlySerIlySerLeuIlyArgLeu 356
 QY 38537 ACTTATATGATGACAAAGGCTCTATCATCTTTTAAATAAGGCGCTTACCAAGTCTGAC 38596
 Db 357 ThrPheThrSerAsnIlyGlyAlaAsnAlaPheSerGlyValAspLeuProSerLeuGln 376
 QY 38597 TATCTATGATCTTATGAGAAATGACCTGAGCTTATAGTGTGCTGTTTATCTGATTTG 38656
 Db 377 PheLeuAspLeuSerArgAsnGlyLeuSerPheIlyGlyCysCysSerGlnSerAspPhe 396

QY 38657 GGAACAAACAGCTGAGACATTAATAGACTGATTCATATGGCCATCATTAATAGAGCC 38716
 Db 397 GlyThrThrSerLeuIlyTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSer 416
 QY 38717 AATTTCAATGGCTCTAGAAAGAGCTGCAGACCTTGATTTTCAGCACTCTCATTTTAAAG 38776
 Db 417 AsnPheLeuGlyLeuGlnIlyLeuGlnHisLeuAspPheGlnHisSerAsnLeuIlyGln 436
 QY 38777 GTCAAGAAATCTCAGGCTTCTTATCCCTGAAAAGACTTTTACCTTACATCTCTAT 38836
 Db 437 MetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHis 456
 QY 38837 ACTAACAACAAATGATCTGATGATATTTCTTGGCTTGCACAGTCTCAACATTA 38896
 Db 457 ThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeu 476
 QY 38897 AAAATGGCTGCAATTTCTTTCAAGACAAACCTTTCAATATGCTTTGCAACACACA 38956
 Db 477 LysMetAlaGlyAsnSerPheGlnIlyAsnPheLeuProAspIlePheThrGlnLeuArg 496
 QY 38957 AACTTGCATTTCCGATCTTTCAATGCAATTTGAAACAATATCTTGGGGGTATTT 39016
 Db 497 AsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnIlyLeuSerProThrAlaPhe 516
 QY 39017 GACACCTCCATAGACTTCAATTTATTAATAGATGACAAACAATCTATTGTTTGGAT 39076
 Db 517 AsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeuAsp 536
 QY 39077 TCATCCATATTAACACAGCTGATATCCCTGACACCTGTGATGACAGTTTCAATGCA 39136
 Db 537 ThrPheProTyrIlyCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIle 556
 QY 39137 GAGACATCT---AAGAAATATCTGCACATTTTCCAAAGTCTTACGCTTCTTCACTT 39193
 Db 557 MetThrSerIlyIlyGlnIlyLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 576
 QY 39194 ACTAACAATCTGTTGGCTGTGATATGATGACATGACAAATCTCGACGTGGTCAAGGAA 39253
 Db 577 ThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnIlyPheIlyAsp 596
 QY 39254 CAGAGACAGTTCTTGTGAAATGTTGAACAATGACATGTCGACACCTGTAGAGATGAT 39313
 Db 597 GlnArgIlyLeuLeuValGlnValGlnArgMetCylCysAlaThrProSerAspIlyGln 616
 QY 39314 ACCCTCTTATGTTGATTTTAAATTTCACTGCTTATATGTCACAGACATATCATAGT 39373
 Db 617 GlyMetProValLeuSerLeu---AsnIleThrCysGlnMetAsnIlyThrIleIleGly 635
 QY 39374 GTGTCAGTGGTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 39433
 Db 636 ValSerValLeuSerValLeuValSerValValAlaValLeuValIlyIlyPheTyr 655
 QY 39434 TTTCACTGATCTTATTTGCTGTGCTGTAATAAGTACAGACAGAGAGAAAGCTATGAT 39493
 Db 656 PheHisLeuMetLeuLeuAlaGlyCysIleIlySerIlyIlyArgIlyGlnAsnIleTyrAsp 675
 QY 39494 GCATTTGTATCTACTGAGTACAGATGAGAGCTGGGTGAGAAATGAGCTGTGTAAGAT 39553
 Db 676 AlaPheValIleTyrSerSerGlnAspIlyAspIlyValArgAsnGlyLeuValIlyAsn 695
 QY 39554 TTAGAAGAGAGAGGCGCGCTTACCTGACCTGACCTGACATGACAGAGCTTATCCGGT 39613
 Db 696 LeuGlnIlyGlyValProProPheGlnLeuCysLeuHisTyrTrpAspPheIleProGly 715
 QY 39614 GTAGCATTGCTGCAACATCATCTCAGAGAGGCTTCCACAAGAGCCGGAAGGTTATG 39673
 Db 716 ValAlaIleAlaIleAsnIleIleHisGlnIlyPheHisIlySerAspIlyValIleVal 735
 QY 39674 GTAGTCTTACACATTTATCTACAGCGCTTGTGTATCTTTGAATATGATGTTCTCA 39733
 Db 736 ValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlnIlyTyrGlnIleAlaGln 755
 QY 39734 ACATGGAGTTTCTGAGCACCGCTGCGATCATCTTCAATGCTTGAAGGTTGAG 39793

Db 756 ThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIleValGlu 775
QY 39794 AAGCCCTGCTGAGGACGAGGTGGAATTGATGCTTCTTACAGAAACACCTACTG 39853
Db 776 LysThrLeuLeuArgGlnGlnValGlnLeuYrArgLeuLeuSerArgAsnThrTyrLeu 795
QY 39854 GAATGGAGGACAAATCCTCTGGGAGGACACATCTTCTGAGAAAGACTTAAATGCCCTA 39913
Db 796 GluTrpGlnAspSerValLeuGlyArgHisIlePheThrPArgLeuArgIleValLeu 815
QY 39914 TTGGATGAAAAGCCTCGAATCTGAGCAACA 39946
Db 816 LeuAspGlyLysSerTyrAsnProGluGlyThr 826
RESULT 6
AAW86361
ID AAW86361 standard; protein; 837 AA.
AC AAW86361;
XX
XX 15-MAR-1999 (first entry)
DT
XX
XX Human DNAX toll-1ike receptor DTLR4.
DE
XX DNAX toll-1ike receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KM interleukin 1 receptor; phosphate metabolism; innate immunity response;
KM modulate inflammatory function; morphological effect;
KW immunological disorder.
XX
XX Homo sapiens.
OS
XX W09850547-A2.
PN
XX 12-NOV-1998.
PD
XX
XX 07-MAY-1998; 98W0-US008979.
PF
XX
XX 07-MAY-1997; 97US-0044293P.
PR 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX
XX (SCHE) SCHERING CORP.
PA
XX
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
XX
XX WPI; 1999-059670/05.
DR N-PSDB; AAV80675.
XX
XX Human DNAX toll-1ike receptors, DTLR 2-10 - used to, e.g., alter phosphate
PT metabolism, modulate inflammatory function or innate immunity responses.
XX
XX Claim 3; Page 147-149; 171pp; English.
XX
XX The present invention specifically describes human DNAX toll-1ike
CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC in the present invention. Also described are: (1) a fusion protein
CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC an antibody or antibody fragment which specifically binds to a DTLR
CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC host cell comprising the vector of (4). The host cell of (5) can be used
CC to produce the DTLR proteins. The DTLR proteins can be used to alter
CC phosphate metabolism, to modulate inflammatory function, innate immunity
CC responses or morphological effects. The DTLR proteins can be used in the
CC treatment of conditions exhibiting abnormal expression of the receptors
CC of their ligands. These abnormalities are typically manifested by
CC immunological disorders
XX
SQ Sequence 837 AA;
Alignment Scores: 9.5e-234 Length: 837
Pred. No.:

Score: 2600.50 Matches: 526
Percent Similarity: 73.68% Conservative: 101
Best Local Similarity: 61.81% Mismatches: 171
Query Match: 2.99% Indels: 53
DB: 2 Gaps: 9
US-09-396-985B-48 (1-5000) x AAW86361 (1-837)
QY 37400 TGGAAAAATGCAATTAATTAATCACTACTACATCACTGCTTATGACCCA 37459
Db 25 TrpGlnProCysValGlu--ValProAsnIleThrTyrGln----- 37
QY 37460 GTTATGATCTTGAATGATTTTCTTAATGATTTCTGCTGACATAGTGATGTTT 37519
Db 38 CysMetGlnLeuAsnPheTyrLysIleProAspAsnLeuPro----- 51
QY 37520 ATCATCACTGTACGAAGTGTGAAAATGACAAATCTGCAGATTCCTCTGCTCACACC 37579
Db 52 -----PheSerThrLysAsnLeuAspLysSerPheAsnProLeuArgHis--- 66
QY 37580 ATCATCACCTGTTTGTCTGTACAGTTTCTCTTACATAACATGATATCATATCT 37639
Db 67 -----LeuGlySerTyrSerPhe----- 72
QY 37640 GTTGTGATCATAGTATGATGAGGACTGTATGTCATTAGAAAGGTTTTTTTTCAGCAA 37699
Db 73 -----PheSerPheProGlu 77
QY 37700 AAATPACATATTGATCTTTTGGCCATAGTGGAATTTGAAACATTTGAAAGCAAG 37759
Db 78 LeuGlnValLeuAspLeuSer-----ArgCysGlnIleGlnThrIleGlnAspGly 94
QY 37760 GCATGGCATGCTTATGACACCACTCTCAAACTTATCTGACAGAAACCTATCCAGAGT 37819
Db 95 AlarTyrIleAsnLeuSerIleAsnSerThrIleuIleuThrIleuAsnProIleGlnSer 114
QY 37820 TTTTCCCGCAGAAATTCTCTGAGCTTACAGATTGAGAAATGTGTGCTGTGAGACA 37879
Db 115 LeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGluThr 134
QY 37880 AAATTGGCTCTCTGAGAAAGCTTCCCTATTTGACAGCTTTAACTTTAAAGAACTCAAT 37939
Db 135 AsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGlnLeuAsn 154
QY 37940 GTGGCTCAGAAATTTTATCACTCTGTAAGTACCTGCATATTTTCCATTCGACGAGAC 37999
Db 155 ValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsn 174
QY 38000 CTATGATCATGTGATCTTTCTTATTAATCTATATTCAAACTATTACTGACGACTTACAG 38059
Db 175 LeuGlnHisLeuAsnLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArg 194
QY 38060 TTTCTACGTGAATAATCCACAGATCAATCTCTTTAGACATGTCTTTGAACCCAAATTGAC 38119
Db 195 ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspSerLeuAsnProMetAsn 214
QY 38120 TTGATTCAGAACCAAGCCTTTCAGGGAATTAATCACTTCATCACTCAAGAGGTAAT 38179
Db 215 PheIleGlnProGlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuAlaGAsnAsn 234
QY 38180 TTTTAATAGCTCAATATTAAGAAAACTGCTTCAAAAAGCTGCTGTTTACAGTTCAT 38239
Db 235 PheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHis 254
QY 38240 CGGTGATCTTGGAGAGATTTAAAGATGAAGAAATCTGGAATTTTGAACCTCTATC 38299
Db 255 ArgLeuValLeuGlyGluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAla 274
QY 38300 ATGGAAGCACTATGTGATGACATTTGATGATGATGATGATTAATCAATTAAGATTTT 38359
Db 275 LeuGlnGlyLeuCysAsnLeuThrIleGlnGlnPheArgLeuAlaTyrLeuAspTyrTyr 294
QY 38360 TCAGATGATATTGTATAG--TTCCATGTGCTTGCGAATGTTTCTGCAATGTCTGCGCA 38416

Db 295 LeuAspAspIleIleAspLeuPheAsnCySLeuThrAsnValSerSerPheSerLeuVal 314
 QY 38417 GGTGTATCTTAATAAATACTTGAAGAAGTGTCTTAAACATTTCCAAATGGCAATCTTATCA 38476
 Db 315 SerValThrIleGluArgValValysAspPheSerTYAsnPheGlyTYrGlnIleGlu 334
 QY 38477 ATCATTTAGATGTCACTTAAGCAGTGTCCAACTCTGGATCTACCTTTCTTAAAGTTTG 38536
 Db 335 LeuValAsnCySylsPheGlyGlnPheProThrLeuTyLeuIysSerLeuValArgLeu 354
 QY 38537 ACCTTACTATGAAACAAGGCGTCTATCAAGTTTAAAAAGTGGCCCTTACCAGTCTCAGC 38596
 Db 355 ThrPheThrSerAsnIysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlu 374
 QY 38597 TATCTAGATCTTAGTAAGAAATGCACTGAGCTTTAGTGTGTCTTATTTCTGATTTTG 38656
 Db 375 PheLeuAspLeuSerAsrArgAsnGlyLeuSerPheIysGlyCYeSylSerGlnSerPhe 394
 QY 38657 GGAACAACAAGCTGAGACACTTAGACCTCAGCTCAATGCTGCATCATTAAGATGCC 38716
 Db 395 GlyThrThrSerLeuIysTYrLeuAspLeuSerPheAsnGlyValIleThrMetSerSer 414
 QY 38717 AATTCAATGGGTCTAGAGAAGCTGCAACACTCCGATTTTCAGACGCTTCTTAAAGG 38776
 Db 415 AsnPheLeuGlyLeuGluGlnLeuGlnIleLeuAspPheGlnIleSerAsnLeuIysGln 434
 QY 38777 GTCCACAATAATTCACAGCGTCTTATCCCTTGAAACACTTATTAACCTTACATCTTAT 38836
 Db 435 MetSerGlnPheSerValPheLeuSerLeuAsrArgAsnLeuIleTYrLeuAspIleSerHis 454
 QY 38837 ACTPAACAACAATTAAGCTTCGATGTATTTCTTGCGCTGACACAGTCTCAACATTA 38896
 Db 455 ThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeu 474
 QY 38897 AAAATGGCTGGCAATTTCTTCAAGACACACCTTTCAAAATGTCTTGGCAACACACA 38956
 Db 475 LysMetAlaGlyAsnSerPheGlnGluAspPheLeuProAspIlePheThrGluLeuArg 494
 QY 38957 AACTTGACATTTCCGCAATCTTTCTTAATGTCATTTGGAACAATAATGGGGGGGATTT 39016
 Db 495 AsnLeuThrPheLeuAspLeuSerGlnCYeGlnLeuGlnIleLeuSerProThrAlaPhe 514
 QY 39017 GACACCTTCACAGACTTCAATTATTAATATGAGTCAACAACATCTATTTGTTTGGAT 39076
 Db 515 AsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAspPhePheSerLeuAsp 534
 QY 39077 TCATCCCATTTATACACAGCTGTATCCCTTGACACTCTTGATTTGACGTTCAATGSCAT 39136
 Db 535 ThrPheProTYrIysCYeValAsnSerLeuGlnValLeuAspTYrSerLeuAsnHisTle 554
 QY 39137 GAGCACTCT---AAAGGAATATGCAACAATTTTCCAAAGAGTGTACCTTTCTTCACTTT 39193
 Db 555 MetThrSerIysIysGlnGlnIleGlnIleAspPheProSerSerLeuAlaPheLeuAsnLeu 574
 QY 39194 ACTPAACAATTCGTGTGCTGTATATATGCAACATCAGAAATTCCTGACGTGGGTCAAGAA 39253
 Db 575 ThrGlnAsnAspPheAlaCYeThrCYeGlnHisGlnSerPheLeuGlnIrrPleuAsp 594
 QY 39254 CAGACAGATTTCTTGGAATGTTTGAACAATAATGACATGTGCACACCTGTAGACATGAT 39313
 Db 595 GlnArgGlnLeuLeuValGlnValGluArgMetGlnCYeValAlaThrProSerAspIysGln 614
 QY 39314 ACCTCCTTAGGTGGATTTTAATTAATTCACCTGTTATATATGAAACAACATTCATCAGT 39373
 Db 615 GlyMetProValLeuSerLeu---AsnIleThrCYeGlnMetAsnIysThrIleIleGly 633
 QY 39374 GTGTCACTGTGACATGATGTATGTGTGATCCACTGTAGACATTTCTGATATACACTTTAT 39433
 Db 634 ValSerValIleLeuSerValLeuValValSerValAlaValLeuValTYrIysPheTYr 653
 QY 39434 TTTCACCTGATCTTATTTGCTGGCTGTAAAAAGTACACAGAGGAGAAACATCTATGAT 39493

Db	651	PheHisIseuMetIeuLeuAlaIglCysIleIleValTyrGlyArgGlyIguAsnIleTyrAsp	673
Qy	39494	GCATTGTGATCTTACTCGAGTCAGATGAGAGACTGGGTGAATAAGCTGGTAAAGAT	3955
Db	674	AlaPheValIleIleTyrSerSerGlnAspGlnAspTrpValAlaArgAsnGlnIleuValIleAsn	693
Qy	39554	TTTGAAGAAGAGTGGCCCGCCCTTCACTCCCTGGCTTCACATACAGAGACTTATTCCTGGT	3961
Db	694	LeuGlnIuGlnIglValProProPheGlnIleuCysIleuHisTyrAlaArgAspPheIleProGly	713
Qy	39614	GTAGCCATTGCTGGCAATCATATCCAGAGAGGCTTCCACAAGAGCCGGAAGGTTATTGTG	3967
Db	714	ValAlaIleAlaIleAlaAsnIleIleHisIglGlnIlePheHisIysSerArgIleValIleVal	733
Qy	39674	GTAAGTGTCTAGACACTTATTCACAGCCGTTGGTGTATCTTTGAATATGAGATTGCTCAA	3973
Db	734	ValValIserGlnHisPheIleGlnIserArgTrpCysIlePheGlnIuTyrGlnIleAlaGln	753
Qy	39734	ACATGGAGATTTCTGAGACACCCGCTCGGATCATCTTCACTTGTCTTGAGAAAGCTTGAG	3979
Db	754	ThrTrpGlnPheIleuSerSerArgAlaGlyIleIlePheIleValIleuGlnIlySvalGln	773
Qy	39794	AAGTCCCTGGCTGAGGCGAGAGGTGAATTGTATCGCCCTTGTAGCAAAACACTACCTG	3985
Db	774	LysThrIleuIeuArgIuGlnIvalGlnIleuTyrArgIleuIeuSerArgAsnThrTyrIleu	793
Qy	39854	GAATGGAGAGCAATCCTCTGGGGAGGACACATCTTCTGAGAAAGACTTAAATAATGCCCTA	3991
Db	794	GlnuTrpIuAspSerValIleuGlnIArgHisIlePheThrTrpArgIleuArgIlySAlaIeu	813
Qy	39914	TTGGATGGAAAAGCCTCGAATCCTGAGCAAAACA	39946
Db	814	LeuAspGlyIysSerTrpAsnProGlnIuGlyThr	824
RESULT 7			
ID	AAE16102	AAE16102 standard; protein; 837 AA.	
XX	AAE16102;		
XX	26-MAR-2002 (first entry)		
DE	Human DNAX Toll like receptor (DTLR) 4 #2.		
XX	Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;		
KW	interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.		
XX	Homo sapiens.		
OS	WO200190151-A2.		
PN	29-NOV-2001.		
PD	23-MAY-2001; 2001MO-US016766.		
PF	25-MAY-2000; 2000US-0207558P.		
XX	(SCHE) SCHERING CORP.		
XX	Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y;		
PI	WPI; 2002-083085/11.		
DR	N-PSDB; AAD26292.		
XX	New DNAX Toll like receptor (DTLR) proteins, useful for treating		
PT	conditions exhibiting abnormal expression of the receptors of their		
PT	ligands, particularly abnormalities manifested by immunological		
PT	disorders.		
XX	Claim 3; Page 41; 29pp; English.		
XX	The invention relates to mammalian receptor proteins, e.g., primate,		
CC	human DNAX Toll like receptor (DTLR) protein and their corresponding		


```

QY 39137 GAGACATCT---AAGAGATACGCAACATTTCCAAAGCTGACCTTCTTCATCTT 39193
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 555 MethtserlyslvglnlgluLeuGlnhisphProserSerleuAlaPheLeuashleu 574
QY 39194 ACTAACATCTGTTGCTTGTATATGTGAACATCAAAATTCCTGACGTGGTCAAGAA 39253
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 575 ThrGlnsnaapPheAlaCysThrCysGlnhisGlnSerPheLeuGlnTrpIleLysasp 594
QY 39254 CAGAGAGAGCTTCTGGAATGTTGAACAAATGACATGTGACACCTGACAGATGTGAT 39313
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 595 GlnrArglnLeuLeuValGlnValGlnrGmetGluCysAlaThrProSerAspLysGln 614
QY 39314 ACCTCTTGAAGTGGATTTTAAATATCTACCTGTTTATGTATCAAGACATCATCAGT 39373
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 615 GlyMetProValLeuSerLeu---AsnIleThrCysGlnMetAlanLysThrIleIleLely 633
QY 39374 GTGTGAGTGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGT 39433
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 634 ValSerValLeuSerValLeuValValSerValValAlaValLeuValLysPheTyr 653
QY 39434 TTTCACCTGATATCTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39493
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 654 PhehisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnIleTyrasp 673
QY 39494 GCATTTGTGATCTACTCGAGTCAGATAGAGACTGGGTGAGAAATGAGCTGTAAAGAT 39553
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 674 AlaPheValIleTyrSerSerGlnAspGlnAspIleAspValAlaGlnGlnLeuValLysAsn 693
QY 39554 TTGAAGAGAGAGTGGCCCGCTTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 39613
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 694 LeuGlnGlnGlyValProProPheGlnLeuGlnCysLeuHisTyrArgAspPheIleProGly 713
QY 39614 GTAGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39673
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 714 ValAlaIleAlaAlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleVal 733
QY 39674 GTAGTGTGTAGACATTTATTCAGAGCCGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39733
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 734 ValValSerGlnHisPheIleGlnSerArgTrpCysIlePheGlnIleValGlnIleVal 753
QY 39734 ACATGGAGTGTGTGAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39793
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 754 ThrTrpGlnPheLeuSerSerArgLysIleIlePheIleValLeuGlnLysValGln 773
QY 39794 AAGTCCCTGCTGAGGACAGCTGGAATGTATGCTTCTTGAAGAAACCTACTGCTG 39853
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 774 LysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrIleu 793
QY 39854 GAATGGAGAGACATCTCTGAGGAGAGACATCTCTGAGAAAGCTTAAATGACCTCTA 39913
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 794 GlnTrpGlnAspSerValLeuGlnLysHisIlePheTrpArgLysLeuArgLysAlaLeu 813
QY 39914 TTGATGAGAAAGACCTCGAATCTCTGAGCAACA 39946
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 814 LeuAspGlyLysSerTrpAsnProGlnGlyThr 824

```

```

XX XX
PN W0200278524-A2.
XX XX
PD 10-OCT-2002.
XX XX
PF 28-MAR-2002; 2002W0-US009671.
XX XX
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 06-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX XX
PA (ZYCO-) ZYCOS INC.
XX XX
PT Chicx RM, Tomlinson MJ, Urban RG;
XX XX
DR WPI; 2003-040607/03.
XX XX
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX XX
PS Example 2; SEQ ID NO 1442; 134pp; English.
XX XX
CC The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pot_sequences
XX XX
SQ Sequence 837 AA;

```

Alignment Scores:

Pred. No.:	9-5e-234	Length:	837
Score:	2600.50	Matches:	526
Percent Similarity:	73.68%	Conservative:	101
Best Local Similarity:	61.81%	Mismatches:	171
Query Match:	2.99%	Indels:	53
DB:	6	Gaps:	9

```

US-09-396-985B-48 (1-50000) x ABU04776 (1-837)
QY 37400 TGGAAAAATGCAATTAATTAATTAAGACTACTGATCAATCACTGCTTTATGTACCCA 37459
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 25 TrpGlnProCysValGlu---ValProAsnIleThrTyrGln----- 37
QY 37460 GTTATGATCTTGAATGATTTTCTAATGATTTGCTGCTGCTGCTGCTGCTGCTGCTG 37519
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 38 CysMetGlnLeuAsnPheTyrLysIleProAspAsnLeuPro----- 51
QY 37520 ATCATCACTGAGCAAGTGAATGACAAATGTGAGAGTTCCTCTGCTACAGACC 37579
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 52 -----PheSerThrLysAsnLeuAspLeuSerPheAsnProLeuArgHis--- 66
QY 37580 ATCATCACTGTTTGTCTGTCGATGATTTCTTTTCAATATACATGATATATCT 37639
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 -----LeuGlySerTyrSerPhe----- 72

```

RESULT 8
ABU04776
ID ABU04776 standard; protein; 837 AA.
AC ABU04776;
XX
XX 29-JAN-2003 (first entry)
XX
XX Human expressed protein tag (EPT) #1442.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX protease; protease inhibitor; transporter; cytoskeletal protein;
XX receptor; transcription factor; cancer; MHC;
XX major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
XX Homo sapiens.

Qy 37640 GTTGTGATCATAGTAGTGGAGCTGTATGTCATTAGAAAGGTTTTTTTTCAGCAA 37699
Db 73 -----PheSerPheProGlu 77
Qy 37700 AAATACATAAATGGTATCTCTTTTCCCATAGGTGTGAAATGGAACAATTTGAAGACAG 37759
Db 78 LeuGlnValLeuSerLeuSer-----ArgCysGlnIleGlnThrIleGlnAspGly 94
Qy 37760 GCATGAGCATGGCTTACACCAACCTCTCAACCTGTATCTGACAGGAACCCATCTCAGAGT 37819
Db 95 AlaIyrGlnSerLeuSerHisLeuSerThrLeuIleuThrGlnAsnProIleGlnSer 114
Qy 37820 TTTTCCCGAGGAAGTTTCTCTGACACTAACAGTTTAGAGATCTGTGCTGTGAGACA 37879
Db 115 LeuAlaLeuGlnAlaPheSerGlyLeuSerSerLeuGlnIlySerLeuValAlaValGlnThr 134
Qy 37880 AAATGGCCCTCTTCAAGAAAGCTTCCATTTAGACAGCTTTATACCTTTAAAGAACTCAAT 37939
Db 135 AsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuIlySerThrLeuIlySerGlnLeuAsn 154
Qy 37940 GTGGCTCAACAATTTTATACATCTCTGTAAAGTTACTGTCATTTTTCATCTGACAGAAC 37999
Db 155 ValAlaHisAsnLeuIleGlnSerPheIlySerProGluIyrPheSerAsnLeuThrAsn 174
Qy 38000 CTAGTACATGTCAGATCTTTCTTATACATATATTCATAACTATCTGCAACGACTTACAG 38059
Db 175 LeuGlnHisLeuAsnLeuSerSerAsnIlySerIleGlnSerIleIyrCysThrAspLeuArg 194
Qy 38060 TTTTTCAGTGAAATTCACAGATCAATCTCTCTTTAGACATGTCTTTGAACCCCAATTGAC 38119
Db 195 ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAsnPheSerLeuAsnPrimeAsn 214
Qy 38120 TTCAATCAAGACCAAGGCTTTTCAAGGAATTAAGCTTCAAGCACTGACTTAAAGGTAT 38179
Db 215 PheIleGlnProGlyAlaPheIlySerGlnIleArgLeuHisIlySerThrLeuArgAsnAsn 234
Qy 38180 TTTATAGCTCAAAATATATATGAAATCTTCCCTCAAAACCTGGCTGTTTACAGTCCAT 38239
Db 235 PheAspSerLeuAsnValIleMetIyThrCysIleGlnIlyLeuAlaGlyLeuGlnValHis 254
Qy 38240 CGGTGATCTTTGGAGAAATTTAAAGATGAAGAATCTGGAATTTTGAACCTCTATC 38299
Db 255 ArgLeuValLeuGlyGlnPheArgAsnGlnIlyAsnLeuGlnIlyPheAspIlySerAla 274
Qy 38300 ATGGAAGCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38359
Db 275 LeuGlnIlyLeuCysAsnLeuThrIleGlnIlyPheArgLeuAlaIlyrLeuAspIlyTyr 294
Qy 38360 TCAGATGATATGTTAAG---TTCCATTTGCTGGCGAATGTTTCTGCAATGCTCTGGCA 38416
Db 295 LeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuVal 314
Qy 38417 GGTGTATCTATAAATATCTAGAAAGATGCTCTAAACATTTCAAAATGCGAATCCTTATCA 38476
Db 315 SerValThrIleGlnArgValIlyAspSerSerIyrAsnPheGlyTyrGlnHisLeuGln 334
Qy 38477 ATCATTTAGATTCGCACTTAACGATTTGCACTCTGATCTACCTTTCTTAAAGTTTG 38536
Db 335 LeuValAsnCysIlySerPheGlyGlnPheProThrLeuIlySerLeuIlyArgLeu 354
Qy 38537 ACTTTAATCTATGAACAAGGCTCTATCAGTTTAAAGAGTGGCCCTTCAAGTCTCAGC 38596
Db 355 ThrPheThrSerAsnIlyGlyGlyAsnAlaPheSerGlyValAspLeuProSerLeuGln 374
Qy 38597 TATCTAGATCTTATAGAAATGCACTGACTTTAGTGTGCTGTCTTATTTCTGATTTG 38656
Db 375 PheLeuAspLeuSerArgAsnGlyLeuSerPheIlySerCysCysSerGlnSerAspPhe 394
Qy 38667 GGAACAACACGCTGAGACACTTGAAGCTTCACTGATTCATGTCGATCATTAATGAGGCC 38716
Db 395 GlyThrThrSerLeuIlySerIlyLeuAsnLeuSerPheAsnGlyValIleThrMetSerSer 414
Qy 38717 AATTTCATGGGTCTAGAAAGACTGACGACCTGATTTTTCAGCACTTACTTTAAAGAG 38776

Db 415 AsnPheLeuGlyLeuGlnIleuGlnIleuGlnHisLeuAspPheGlnHisSerAsnLeuIlyGln 434
Qy 38777 GTCAAGAAATTCCTCAGCGTTCTTATCCCTTGAAGAAAGCTATCCCTTGCATCTCTAT 38836
Db 435 MetSerGlnPheSerValPheLeuSerLeuAspAsnLeuIleIyrLeuAspIleSerHis 454
Qy 38837 ACTAACACCAAAATATGACTTCGATGATATTTCTTGGCTTGAACGATCTCAACATTA 38896
Db 455 ThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeu 474
Qy 38897 AAAATGGCTGGCAATTTCTTCAAGACACACCTTTCAATGTCTTTGCAAAACACACA 38956
Db 475 LysMetAlaGlyAsnSerPheGlnIlyAsnPheProAspIlePheThrGlnLeuArg 494
Qy 38957 AACTTGACATCTCTGATCTTTTAAATGTCATTTGGAACAATATCTTGGGGGTATTT 39016
Db 495 AsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnIlyLeuSerProThrAlaPhe 514
Qy 39017 GACACCCCTCATGACTTCAATATTAATTAATGATGACACAAACAATCTATTTGTTGAT 39076
Db 515 AsnSerLeuSerSerLeuGlnIlyValLeuAsnMetSerHisAsnAsnThrPheSerLeuAsp 534
Qy 39077 TCATCCCATTAATACCACTGATTCCTTCAGACCTTTGATTCAGTTTCAATCCGATA 39136
Db 535 ThrPheProIlyrCysLeuAsnSerLeuGlnValLeuAspIlyrSerLeuAsnHisIle 554
Qy 39137 GACACATCT---AAAGGAATACGCAACATTTTCCAAAGCTGTAGCCTTCAATCTT 39193
Db 555 MetThrSerIlySerIlyGlnIlyLeuGlnHisPheProSerSerLeuAlaPheLeuLeu 574
Qy 39194 ACTAACATTTCTGTCTGTATATATGATGACATCAGAAATTCCTGCAAGTGGTCAAGAA 39253
Db 575 ThrGlnAsnAspPheHisCysThrCysGlnHisGlnSerPheLeuGlnIlyrIleIlyAsp 594
Qy 39254 CAGAGCATTTCTTGGTGAATGTTGAACAATGACATGTGCAACACCTGTAGAGATGAAT 39313
Db 595 GlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspIlyGln 614
Qy 39314 ACCCTCTACTGATGATTTTAAATTTTCAACCGTATATGTAACAAGACATCATCAGT 39373
Db 615 GlyMetProAlaLeuSerLeu---AsnIleThrCysGlnMetAsnIlySerThrIleGly 633
Qy 39374 GTGTCAGTGTCTAGTGTATGTGTATGTCACATGTAGCATTTCTGATATACCACTTCTAT 39433
Db 634 ValSerValLeuSerValIleValSerValAlaValAlaLeuValIlyrIlySerPheTyr 653
Qy 39434 TTTCACTGATCTTATTTGCTGTGCTGTAAGATGACAGCAGAGAGAACATCTATGAT 39493
Db 654 PheHisLeuMetLeuLeuAlaGlyCysIleIyTyrGlyArgGlyGlnAsnIleIyAsp 673
Qy 39494 GCATTTGTGATCTTACTGCAATGCAAGATGAGACCTGGTGAAGATGAGCTGTAAAGAT 39553
Db 674 AlaPheValIleIyrSerSerGlnAspGlnAspIlyrAlaArgAsnGlnLeuValIlyAsn 693
Qy 39554 TTAGAGAAGAGAGCGCCGCTTCACTGCTGCTTCACTACAGAGACTTATTTCTGCT 39613
Db 694 LeuGlnIlyGlyValProPheGlnLeuCysLeuHisIlyrArgAspPheIleProGly 713
Qy 39614 GTAGCAATTCCTGCAACATCATTCAGAAAGGCTTCCACAAAGAGCCGGAAGTTATTTG 39673
Db 714 ValAlaIleAlaAlaAsnIleIleHisGlnIlyPheHisIlySerArgIlyValIleVal 733
Qy 39674 GTAGTCTGAGACATTTATTTAGAGCGGTGGTGTATCTTTGAATGATGATTTGCTCAA 39733
Db 734 ValValSerGlnHisPheIleGlnSerArgIlyrCysIlePheGlnIlyrGlnIleAlaGln 753
Qy 39734 ACATGCAATTTCTGACACAGCCGCTGTGCATCATCTTCAATGCTTGAAGAGTTGAG 39793
Db 754 ThrIyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIlyValGln 773
Qy 39794 AAGTCCCTGTGAGACAGAGTGAATGTATGCTTTTGAACAAACACTTACTTG 39853

Db 774 LysThrLeuLeuArgGlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyrLeu 793
 QY 39854 GAATGGAGAGCAATCTCTGGGAGAGCAATCTCTGAGAGAGCTTAATAAATGCCCTA 39913
 Db 794 GluTrpGluAspSerValLeuGlyArgGhiSilePheTrpArgArgLeuArgValLeu 813
 QY 39914 TTGGATGGAAAAAGCCTCGAATCTCTGAGCAACA 39946
 Db 814 LeuAspGlyLysSerTrpAsnProGluGlnGlyThr 824

RESULT 9
 ADOS7791
 ID ADOS7791 standard; protein; 795 AA.
 XX
 AC ADOS7791;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Rhesus monkey toll-like receptor 4 SEQ ID NO:12.
 XX
 KM toll-like receptor 4; TLR4; old world monkey; antibacterial;
 KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
 KM sepsis; severe sepsis; septic shock; asthma; rhesus monkey.
 XX
 OS Macaca mulatta.
 XX
 FH Key location/Qualifiers
 FT Misc-difference 635
 FT /label= Lys, Asn
 XX
 XX MO2004042365-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 03-NOV-2003; 2003WO-US036247.
 XX
 PR 01-NOV-2002; 2002US-0423113P.
 XX
 PA (EVOL-) EVOLUTIONARY GENOMICS LLC.
 XX
 PI Messier W;
 XX
 DR WPI; 2004-400726/37.
 DR N-PSDB; ADOS7789, ADOS7790.
 XX
 PT Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
 PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
 PT sequence of the Old World monkey with that of a human.
 XX
 PS Disclosure; SEQ ID NO 12; 111pp; English.
 XX
 CC The invention relates to a novel method for identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an old world monkey
 CC comprising comparing the TLR4 polynucleotide sequence of the Old World
 CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
 CC method of the invention has antibacterial, immunosuppressive, and
 CC antiasthmatic activity. The method is useful in identifying a nucleotide
 CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
 CC change may be associated with reduced sensitivity to Gram-negative
 CC bacterial infection. The methods, agents and composition are useful in
 CC treating sepsis, severe sepsis or septic shock and asthma. The present
 CC sequence represents rhesus monkey TLR4.
 XX
 SO Sequence 795 AA;

Alignment Scores:
 Pred. No.: 1,28e-233 Length: 795
 Score: 2599.00 Matches: 524
 Percent Similarity: 74.26% Conservative: 99
 Best Local Similarity: 62.46% Mismatches: 164
 Query Match: 2.99% Indels: 52
 DB: 8 Gaps: 8

US-09-396-985B-48 (1-50000) x ADOS7791 (1-795)
 QY 37433 ACATATCAACGCTTTATATGACCCCATATGATCTGATGATTTTCTATATGAT 37492
 Db 6 ThrTyrGln-----CysMetGluLeuAsnPheTyrLysIleProasp 19
 QY 37493 TTGGCGCTGCAATAGTGATGATGATTTATCATCACTGAGCAAGTGAAATGCAAAAT 37552
 Db 20 AsnLeuPro-----PheSerThrLysAsnLeuasp 29
 QY 37553 CTGCAGAGTTCCTCTCTGCTGACACATCATCACTGTTTGGCTGTGACATGTTTCTC 37612
 Db 30 LeuSerPheAsnProLeuArgHis-----LeuGlySerTyrSerPhe--- 43
 QY 37613 TTTACATATACATGATATCATATCTGTTGATCATAGTAGTAGACTGTATAGT 37672
 Db 43 ----- 43
 QY 37673 CATTAGAAAGGTTTTTTTTTTCAGCAAAAATACATAATGGTATCTTTTGGCCATAGG 37732
 Db 44 -----PheSerPheProGluLeuGlnValLeuAspLeuSer-----Arg 56
 QY 37733 TGTGAAATTTGAAACAAATTTGAAAGACAGCATGCGATGCTTTACACCACTCTCAAACTTG 37792
 Db 57 CysGluIleGlnThrIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeu 76
 QY 37793 ATACTGACAGAAACCTATCCAGATGTTTCCCGAGAAATTTCTCTGACATCAAGT 37852
 Db 77 IleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSer 96
 QY 37853 TTAGAGATCTGCGTGTGAGAGACAAATTTGCGCTCTGAGAAAGCTTCCATTGGA 37912
 Db 97 LeuGlnLysLeuValAlaValGluThrAsnLeuAlaSerLeuGluAsnPheProIleGly 116
 QY 37913 CAGCTTATTAACCTTAAAGAAATCAATGTGCGCTGACAAATTTATATCAATCTGTATGTTA 37972
 Db 117 HisLeuThrLeuLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeu 136
 QY 37973 CCTGCATATTTTCCATCTGACGACACTAGTATGATCTTTCTTATATCAATAT 38032
 Db 137 ProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIle 156
 QY 38033 CAAACTATTAAGTGTGCAAGCTTCTACGTGAAATTCACAAAGTCAATCTCTCT 38092
 Db 157 GlnAsnIleTyrCysLysAspLeuGlnValLeuHisGlnMetProLeuSerAsnLeuSer 176
 QY 38093 TTAGACATGCTTTGAAACCAATGACTTCAATTCAGACCAAGCCTTTCAGGAAATTAAG 38152
 Db 177 LeuAspLeuSerLeuAsnProIleAsnPheIleGlnProGlyAlaPheLysGluIleArg 196
 QY 38153 CTGCATGAAGTACTTGAAGAGTATTTATATAGCTCAAAATATATGAATGAACTTGCCTT 38212
 Db 197 LeuHisLysLeuThrLeuArgSerAsnAspAsnLeuAsnValMetLysThrCysIle 216
 QY 38213 CAAACCTGCGTGTGTTACAGCTGATCGGTGATCTTGGAGAAATTTAAAGATGAAG 38272
 Db 217 GlnIleLeuAlaGlyLeuGluValHisArgLeuValLeuGlyGluPheAsnGlnIleArg 236
 QY 38273 AATCTGAAATTTTGAACCCCTATCATGAGAAAGACTATGATGATGACCATTTATGAG 38332
 Db 237 AsnLeuGluGlnPheAspLysSerSerLeuGlnIleCysAsnLeuThrIleGluGln 256
 QY 38333 TTGAGTTACATATACAAATGATTTTTCAGATGATTTGTAAG---TTCATGTGCTTG 38389
 Db 257 PheArgLeuThrTyrLeuAspTyrTyrLeuAspAsnIleIleAspLeuPheAsnCysLeu 276
 QY 38390 GCGAATTTCTGCAATGCTCTGCGAGGTATCTATAAATATCTAGAAAGATGTTCTCT 38449
 Db 277 AlaAsnValSerSerPheSerLeuValSerValSerIleLysArgValGluAspPheSer 296
 QY 38450 AAACATTTCAATGCAATCTTATCAATCATATGATGTCACATTAAGCAATTTCAACT 38509
 Db 297 TyrAsnPheArgTrpGlnHisLeuGluLeuValAsnCysLysPheGlnGlnPheProThr 316

```

QY 38510 CTGGATCTACCCCTTTCTTAAAGTTTGACTTATGAAACAAGGCTCATAGCTTT 38569
DB 317 LeuDIleuGlnSerLeuValArgLeuThrPheThrAlaAsnValGlyValAsnAlaPhe 336
QY 38570 AAAAAGTGGCCCTTACCAAGCTTCAGCTATCTAGATCTTAGTAAATGCACTGAGCTTT 38629
DB 337 SerGluValAspLeuProSerLeuGlnPheLeuAspLeuSerAlaGlnGlyLeuSerPhe 356
QY 38630 AGTGGTTCCTGTTTCTTATTTGATTTGGGAAACAACGCTGAGACACTTAAGCTTACG 38689
DB 357 LysGluCysCysSerGlnSerAspPheGlyThrThrSerLeuValGlyLeuAspLeuSer 376
QY 38690 TTCAATGAGTGCACATTTATGAGGCCAATTTGAGGCTTAGAAGAGCTGACACACTG 38749
DB 377 PheAsnAspValIleThrMetSerAlaPheLeuGlnGlyLeuGlnGlyLeu 396
QY 38750 GATTTTCAGCACTCTACTTTTAAAAAGGATCAACAATTTTCAGGCTTATCCCTTGA 38809
DB 397 AspPheGlnIleSerAlaPheLeuGlnMetSerGlnPheSerValPheLeuSerLeuArg 416
QY 38810 AAGTCTATTACCTTGAATCTTATATCTTACCAACAATTTGATGCTGATGATTTT 38869
DB 417 AsnLeuIleTyrLeuAspPheIleSerAlaThrAlaGlyAlaPheAsnGlyIlePhe 436
QY 38870 CTTCGCTTACCACTCTCAACAACAATTTAAATGCTGCAATTTCTTCAAAACAACACC 38929
DB 437 AspGlyLeuLeuSerLeuValLeuValMetAlaGlyAsnSerPheGlnGlnAspPhe 456
QY 38930 CTTCCAATGCTCTTTCGAAACAACAACAACTTGAATCTTCTGATCTTTCTTAAATGTC 38989
DB 457 LeuProAspPheIlePheThrAlaPheLeuValAsnLeuThrPheLeuAspLeuSerGlnCysGln 476
QY 38990 TTGGAACAATATATCTTGGGGGGGTATTGACACCTCCATGACACTTCAATTTAAATATG 39049
DB 477 LeuIleGlnLeuSerProThrAlaPheAspThrLeuAsnValGlnValLeuAsnMet 496
QY 39050 AGTCACAACATCTAATGTTTGTGATTCATCCCATATACACAGCTGATTTCCCTCAGC 39109
DB 497 SerIleAsnAspPhePheSerLeuAspThrPheProTyrCysLeuProSerLeuGln 516
QY 39110 ACTCTGATTTGCACTTTCATGCAATGCAATGACATCTTAAAGAA--ATACTGCAACATTT 39166
DB 517 ValLeuAspTyrSerLeuAsnAlaIleMetThrSerAlaAsnGlnIleGlnIlePhe 536
QY 39167 CCAAGAGCTAGGCTTTCTTCAATCTTATACAAATCTGTGCTGTATATGGAACAT 39226
DB 537 ProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHis 556
QY 39227 CAGAAATTCCTGCAAGGCTGCAAGAACAGAAAGGTTCTTGATGAAATGTTGAACAATG 39286
DB 557 GlnSerPheLeuGlnThrPheIleValAspGlnMetGlnValGlnAlaGlnMet 576
QY 39287 ACATGTGCACACCTTAGAGATGAATACCTCTTAGTGTGATTTTAAATATCTTACC 39346
DB 577 GluCysAlaThrProSerAspPheGlnGlyMetProValLeuSerLeu--AsnIleThr 595
QY 39347 TGTATATGTACAGACATATATCAGTGTGCTGAGTGCATGATTTGATTCACACT 39406
DB 596 CysGlnMetAsnLysThrIleLeuGlyValSerValPheSerValLeuValValSerVal 615
QY 39407 GTACATTTCTGATATACCACTCTATTTTCACTGAACTTATTTAGGCTGTAAGAAAG 39466
DB 616 ValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeuLeuAlaGlyCysIle*** 635
QY 39467 TACAGCAGAGGAGAAAGCATCTATGATGATCTTGTGATCTTCTGAGTCAAGATGAGAGAC 39526
DB 636 TyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAsp 655
QY 39527 TGGGTGAGAAATGAGCTGTGTAAGAAATTTAAGAGAGAGTGGCCCGCTTTCACCTCTGC 39586
DB 656 TyrValArgAsnGlnLeuValLysAsnLeuGlnGlyValProProPheGlnLeuCys 675

```

```

QY 39587 CTTCACATACAGACCTTTATTCCTGGTGTAGCCATTCGTGCCAATCATCATCAGAAAGC 39646
DB 676 LeuHisTyrArgAspPheIleProGlyValAlaIleAlaAlaAsnIleIleHisGlnGly 695
QY 39647 TTCCACAAGAGCCGGAAGGTTATTTGTGTAGTGTCTAGACACTTTATTCAGACCCGTTGG 39706
DB 696 PheIleLysSerArgLysValIleValAlaValSerGlnHisPheIleGlnSerArgTyr 715
QY 39707 TGTATCTTGAATATATGATGCTGCAACAATGGCACTTTCTGAGCAGCCGCTTGGCATC 39766
DB 716 CysIlePheGlnTyrGlnIleAlaGlnThrPheGlnPheLeuSerSerArgAlaGlyIle 735
QY 39767 ATCTTCATTTCTCTTGAAGAGTTTGAAGATCCCTGCTGAGCAGCAGGTGTAATGTAT 39826
DB 736 IlePheIleValLeuGlnLysValGlyLysThrLeuLeuArgGlnGlnIleLeuTyr 755
QY 39827 CGCCTTTTTCAGAAACACTTACCTGGAATGGAGAGACAATCTTGGGAGGCAACATC 39886
DB 756 ArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGlnAspSerValLeuGlnGlnIle 775
QY 39887 TTCTGAGAAAGACTTTAAAAATGCCCTATTTGAGATGAGAAAGCCCTGAAATCCTGAGCA 39943
DB 776 PheTyrArgArgLeuArgLysAlaLeuLeuAspGlyArgSerTyrAsnProGlnGln 794

RESULT 10
ID AD057803 standard; protein; 808 AA.
AC AD057803;
XX 12-AUG-2004 (first entry)
DT 12-AUG-2004 (first entry)
DE Chimpanzee toll-like receptor 4 SEQ ID NO:24.
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX Pan troglodytes.
XX WO2004042365-A2.
XX 21-MAY-2004.
XX 03-NOV-2003; 2003MO-US036247.
XX 01-NOV-2002; 2002US-0423113P.
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX Messier W;
XX WPI; 2004-400726/37.
XX N-PSDB; AD057801, AD057802.
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX sequence of the Old World monkey with that of a human.
XX Disclosure; SEQ ID NO 24; 11pp; English.
XX The invention relates to a novel method for identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey
XX comprising comparing the TLR4 polynucleotide sequence of the Old World
XX monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX method of the invention has antibacterial, immunosuppressive, and
XX anaesthetic activity. The method is useful in identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey where the
XX change may be associated with reduced sensitivity to Gram-negative
XX bacterial infection. The methods, agents and composition are useful in
XX treating sepsis, severe sepsis or septic shock and asthma. The present
XX sequence represents chimpanzee TLR4.

```

SQ Sequence 808 AA;
 Alignment Scores:
 Pred. No.: 2.47e-233 Length: 808
 Score: 2596.00 Matches: 524
 Percent Similarity: 74.29% Conservative: 100
 Best Local Similarity: 62.38% Mismatches: 164
 Query Match: 2.99% Indels: 52
 Gaps: 8
 DB: 8
 US-09-396-985b-48 (1-50000) x ADOS7803 (1-808)

```

QY 37433 ACATATCAACTGCTTTATGATACCCAGTTATGATCTTGAATGATTTTCTAATGAT 37492
D 6 ThyrtyrGln-----CysMetGluLeuAsnPhenylTyrosylLeuProasp 19
QY 37493 TTGTCCTGACATAGTGTGATGATTATCATCATCTAGCAAGTGTGAAAATGACAAAT 37552
D 20 AsnLeuPro-----PheSerThrIleAsnLeuasp 29
QY 37553 CTGCAAGATTCTCTCTGCTCAACACATCATCATCTGTTGCTCTGATAGTTTCTC 37612
D 30 LeuSerPheAsnProLeuaspGhis-----LeuGlySerTyrosPhe--- 43
QY 37613 TTACAAATACATGATATATATATCTGTTGATCATAGTATGATGAGACCTGTTATGT 37672
D .43 ----- 43
QY 37673 CATTAGAAAGGTTTTTTTTTTCAGCAAAAATACATTAATGATCTTTTGGCCCATAG 37732
D 44 -----PheSerPheProGluLeuGlnValLeuAspLeuSer-----Arg 56
QY 37733 TGTGAATGTAACAATTTGAGACAGCAAGCATGAGCTTACACACCTCTCAACTG 37792
D 57 CysGluIleGlnThrIleGluAspGlyAlaTyrosIleSerHisLeuSerThrIleu 76
QY 37793 ATATGACAGAAACCTATCCAGAGTTTTCACAGAGATTTCTCTGACTAACAAGT 37852
D 77 IleuThrIleGlnAsnProIleGlnSerIleuAlaLeuGlyAlaPheSerGlyLeuSerSer 96
QY 37853 TTGAAGATCTGCTGCTGTGAGACAAATTTGCTCTTGAAGAGCTTCTTATTTGA 37912
D 97 LeuGlnIleuValAlaValGluThrAsnLeuAlaSerLeuGluAsnPheProIleGly 116
QY 37913 CAGCTTATACCTTAAAGAACTCAATGCTGCTCACAATTTTATATCATCTCTGTAAGTTA 37972
D 117 HisIleuYstrIleuLysGluLeuAsnValAlaHisIleuIleGlnSerPheLysIleu 136
QY 37973 CCTGCATATTTTCCAACTGACGAACTTAGACATGATGATCTTTCTTATATCATATTT 38032
D 137 ProGluTyrosPheSerAsnIleuThrAsnIleuGlnIleuAspLeuSerSerHisIle 156
QY 38033 CAAACTATTTACTGTCAACGACTTACAGTTTCTAGCTGGAATAATCCACAGTCAATCTCT 38092
D 157 GlnSerIleTyrosThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSer 176
QY 38093 TTAGACATGCTTTTGAACCCCAATGACTTCAATCAAGCAAGCTTTGAGGAATTTAG 38152
D 177 LeuAspLeuSerIleuAsnProMetAsnPheIleGlnProGlyAlaPheLysGluIleArg 196
QY 38153 CTCATGATGAGCTCTTAAAGGTAATTTTAAATGCTCAATATATAAAGAACTTGCTT 38212
D 197 LeuHisIleuSerIleuThrIleuArgAsnAsnPheAspSerIleuAsnValIleuLysThrCysIle 216
QY 38213 CAAAACTGCTGCTTTTACACGCTCATGCTTGAATCTTTGAGAGAAATTTAAAGAAAG 38272
D 217 GlnGlyLeuAlaGlyLeuGluValHisArgLeuValIleuGlyIleuPheArgAsnGluIle 236
QY 38273 AATCTGGAATTTTGAACCTCTATCATGAGAGACATATGATGATGACATTTGATGAG 38332
D 237 AsnIleuGlnLysPheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnIleu 256
QY 38333 TTCAGTTATACATATACAAATGATTTTTCAGATGATATGTTAAG--TTCATTTGCTTG 38389
  
```

```

D 257 PheArgLeuAlaTyrosLeuAspTyrosTyrosLeuAspPheIleIleAspLeuPheAsnCysLeu 276
QY 38390 GCGAATTTTCTGCAATGCTCTGCGCAGGTGATCTTAAATAATCTAGAAAGATTTCT 38449
D 277 ThrAsnValSerSerPheSerLeuValSerValThrIleLysSerValLysAspPheSer 296
QY 38450 AATCATTTCAATAGCAATCTTATCATCATGATGATGATGATGATGATGATGATGATGAT 38509
D 297 TyrAsnPheGlyTyrosIleuGlnIleuValIleuValIleuValIleuValIleuValIleu 316
QY 38510 CTGATCTACCTCTTTTAAAGTTTGAATTTTAACTTAACTTAACTTAACTTAACTTAACTT 38569
D 317 LeuLysLeuLysSerLeuLysArgLeuThrPheThrSerAsnLysGlyIleuValIleu 336
QY 38570 AAAAAAGTCCCTTCAACAGTCTGATATCTGATATCTTATGATGATGATGATGATGATGAT 38629
D 337 SerGluValAspLeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPhe 356
QY 38630 AGTGTGCTGCTTCTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 38689
D 357 LysGlyCysCysSerGlnSerAspPheGlyThrThrSerLeuLysTyrosLeuAspLeuSer 376
QY 38690 TTCAATGCTGATCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38749
D 377 PheAsnGlyValIleuThrMetSerSerAsnPheLeuGlyLeuGlnIleuGlnIleu 396
QY 38750 GATTTTCAACATCTTATTTAAAGGCTCACAGAAATTTCTGAGGTTCTTATCCCTTGA 38809
D 397 AspPheGlnHisSerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuArg 416
QY 38810 AAGCTACTTATCTTGAATCTCTTATATACCAACCAAAATTTGATCTGATGATATTT 38869
D 417 AsnLeuIleTyrosAspIleSerHisThrHisArgValAlaPheAsnGlyIlePhe 436
QY 38870 CTGCTTGAACAGTCTCAACATTTAAATGCTGCAATTTCTTCAAGACACACC 38929
D 437 AsnGlyLeuSerSerLeuGluValLeuLysMetValIleGlyAsnSerPheGlnIleuAsnPhe 456
QY 38930 CTTTCAATGCTTTTGAACACACAACTTGAATCTCTGATCTTTTCAATTTGCA 38989
D 457 LeuProAspIlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGln 476
QY 38990 TTGGAACAAATATCTTGGGGGATTTTGAACACCTCATGATGATCTTCAATTTAAATG 39049
D 477 LeuGluIleuSerProThrAlaPheAsnSerLeuSerLeuGlnValLeuAsnMet 496
QY 39050 AGTCACAACATCATTTGTTTGGATTTCAATCCATTTAACAACGCTGTATTTCCCTGAGC 39109
D 497 SerHisAsnAsnPheSerSerLeuAspThrPheProTyrosCysLeuAsnSerLeuGln 516
QY 39110 ACTTTGATTTGACTTCAATGCGATAGACATCT--AAAGAAATCTGCAACATTTT 39166
D 517 ValLeuAspTyrosSerLeuAsnHisIleMetThrSerLysGlnIleuGlnIlePhe 536
QY 39167 CCAAGAGCTAGGCTTTCAATCTTATCAATCAATCTGTTGTTGATTTATGATGAT 39226
D 537 ProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHis 556
QY 39227 CAGAAATTTCTGCAAGTGGTCAAGGACAGAGCAAGTCTTTGAGATGTTGAAACAATG 39286
D 557 GlnSerPheLeuGlnThrIleLysAspGlnArgGlnIleuLeuValIleuValIleuValIleu 576
QY 39287 ACATGCAACACTGATGAGATGATATCTCTTATGTTGATTTTAAATTTTCAAC 39346
D 577 GluLysAlaThrProSerArgLysGlnGlyMetProValIleuSerLeu--AsnIleThr 595
QY 39347 TGTATATGTAACAAGAAATCATCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39406
D 596 CysGlnMetAsnLysThrIleIleGlyValSerValLeuSerValLeuValIleuValIleu 615
QY 39407 GTAGCATTTTGTATATACCACTTATTTTCACTGATGATTTTATGCTGCTGCTGCTGCTGCTGCT 39466
  
```

```
Db      616 ValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeuAlaGlyCysIleLys 635
Qy      39467 TACAGCAGAGGAAAGATCATATGATGATTTGATTCATCTAGCTGAGTCAAGAAAGAGAC 39526
Db      636 TyrIcYArgGlyGluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAsp 655
Qy      39527 TGGGTGAGAAATGAGCTGTTAAAGAAATTTAGAAAGAGAGTGCCTCCCTTCACCTTCG 39586
Db      656 TrpAlaArgAsnGluLeuValTyrAsnLeuGluGlyValProPheGlnLeuCys 675
Qy      39587 CTTTACCTACAGACATTTATTCCTGCTGAGTCCATTTGCTGCACATCATTCACAGAAAGC 39646
Db      676 LeuHisTyrArgAspPheIleProGlyValAlaIleAlaAsnIleIleHisGly 695
Qy      39647 TTCCACAGAGCCGGAAGGTATTTGTTAGTGTCTGACACTTATTCAGAGCGCTTG 39706
Db      696 PheHisLysSerAspGlyValIleValValSerGlnHisPheIleGlnSerArgTyr 715
Qy      39707 TGTATCTTGTAAATATGAGATTTGCTCAACATGAGAGTTCCTGACAGCCGCTTGACATC 39766
Db      716 CysIlePheGluTyrGluIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIle 735
Qy      39767 ATCTTCATGTCTCTGAGAGAGCTTGAAGATCCTGCTGAGGACAGCAGTTGAAATTGTAT 39826
Db      736 IlePheIleValIleGlnLysValGluLysThrLeuLeuArgGlnValGluLeuTyr 755
Qy      39827 CGCCTTCTTACAGAAACACCTACCTGGAATGGAGGACATCCTCTGGGGAGGACATC 39886
Db      756 ArgLeuLeuSerAspGlnThrTyrLeuGluTyrGluLysSerValLeuGlyArgHisIle 775
Qy      39887 TTCTGAGAGAGACTTAAATAATGACCTTATTTGATGAGAAAGCCTGAACTCTGAGCAAA 39946
Db      776 PheTrpArgGlyLeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGluGlyThr 795

RESULT 11
AD057797 standard; protein; 801 AA.
AC      AD057797;
XX      12-AUG-2004 (first entry)
XX      Squirrel monkey toll-like receptor 4 SEQ ID NO:18.
XX      DE
XX      KM toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX      KM immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX      KM sepsis; severe sepsis; septic shock; asthma; squirrel monkey.
XX      OS
XX      Saimiri sciureus.
XX      FH
XX      FT Key location/Qualifiers
XX      FT Misc-difference 14
XX      FT /label= Leu, Phe
XX      PN
XX      MO2004042365-A2.
XX      PD
XX      21-MAY-2004.
XX      PF
XX      03-NOV-2003; 2003WO-US036247.
XX      PR
XX      01-NOV-2002; 2002US-0423113P.
XX      PA
XX      (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX      PI
XX      Messier W;
XX      WI; 2004-400726/37.
XX      DR
XX      N-PSDB; AD057795, AD057796.
XX      PT
XX      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX      PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX      PT sequence of the Old World monkey with that of a human.
```

```
PS      Disclosure; SEQ ID NO 18; 11pp; English.
XX
XX      The invention relates to a novel method for identifying a nucleotide
CC      CC change in a TLR4 polynucleotide sequence of an old world monkey
CC      CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC      CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC      CC method of the invention has antibacterial, immunosuppressive, and
CC      CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC      CC change in a TLR4 polynucleotide sequence of an old World monkey where the
CC      CC change may be associated with reduced sensitivity to Gram-negative
CC      CC bacterial infection. The methods, agents and composition are useful in
CC      CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC      CC sequence represents squirrel monkey TLR4.
XX
XX      SQ Sequence 801 AA:
XX
XX      Alignment Scores:
XX      Pred. No.: 3,79e-233 Length: 801
XX      Score: 2594.00 Matches: 509
XX      Percent Similarity: 78.84% Conservative: 87
XX      Best Local Similarity: 67.33% Mismatches: 154
XX      Query Match: 2.99% Indels: 6
XX      DB: 8 Gaps: 4
XX
XX      US-09-396-985B-48 (1-50000) x AD057797 (1-801)
Qy      37685 TTTTTCAGCAAAATATCATATTTGATCTTTTCCCATAGTGTGAAATTTGA 37744
Db      44 PheAsnProGluLeuGlnValIleAspLeuSer-----ArgCysAspIleGln 60
Qy      37745 ACAATTGAGACAGAGGATGAGTGCATTAACACACCTCTCAAACTTGATATGACAGGA 37804
Db      61 ThrIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGly 80
Qy      37805 AACCTATCCAGAGTTTTCCTCCAGAGAGTTTCTCTGAGACTAACAGTTTGAAGATCTG 37864
Db      81 AsnProIleGlnAsnLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnLysLeu 100
Qy      37865 GTGGCTGTGAGACAAATATTTGGCTCTCTAGAAAGCTCCCTTATTTGAGACAGTTTATACC 37924
Db      101 ValAlaValGluThrHisLeuLeuSerLeuGlnAsnProIleGlyHisLeuLysThr 120
Qy      37925 TTAAGAACTCATGTGGCTGACAAATTTATATCATTTCTGTAAATTAAGTTACCTGATATTTT 37984
Db      121 LeuLysAspLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGlyTyrPhe 140
Qy      37985 TCCAAATTTGACGAACCTTAGTACATGTGGATCTTTCTTATACATATATTTCAACTATTA 38044
Db      141 SerAsnLeuThrAsnLeuGluHisLeuAspLeuSerSerAsnAsnIleGlnAsnIleTyr 160
Qy      38045 GTCAAGCACTTACAGTTTCTACGAGAAATCCCAAGTCAATCTCTCTTATAGCATGTCT 38104
Db      161 CysLysAspLeuGlnValIleHisIleGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
Qy      38105 TTGAACCCCAATGATTCATTTCAAGACCAAGCTTTCAAGGAAATTAAGTCCATGAATCTG 38164
Db      181 LeuAsnProIleAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisLysLeu 200
Qy      38165 ACTCTAAGAGTAAATTTTAAATAGCTCAAAATATATGAATACTTGCCCTTCAAAACCTGGCT 38224
Db      201 ThrLeuArgAsnAsnPheAspSerLeuAsnAlaMetCysThrCysIleGlnGlyLeuAla 220
Qy      38225 GGTTCACAGCTTCATCGGTGATCTTGAGGAAATTTAAAGATGAAGAAATTCGAAATTT 38284
Db      221 GlyLeuGluValHisArgLeuValLeuGlyGluPheArgAsnGluHisArgAsnIleGlnAsp 240
Qy      38285 TTGGAACCTCTATCATGAGGAGAGCATATGATGTGACATTAATGATCAAGTTTCAAGTTTACA 38344
Db      241 PheAspLysSerAspAlaLeuGluGlyLeuCysAsnLeuThrIleAsnGluPheArgLeuAla 260
Qy      38345 TATTCAAATGATTTTTCAGATGATATTTGTTAAG---TTCCATTTGCTTGGGGAATGTTCT 38401
Db      261 TyrLeuAspAspPheLeuAspAspIleIleAspLeuPheAsnCysLeuAlaAsnValSer 280
```

QY 38402 GCAATGCTCTGGCAGGTGTATCTTAATAATCTAGAAGATGTTCTTAACATTTGCAA 38461
 Db 281 SerPheSerLeuValAsnValHisIleLeuArgValGluAspPheSerTyrAsnPheArg 300
 QY 38462 TGGCAATCTTATCAATCAATTAAGATGCACTTAAGACAGTTTCAACTCTGGATCTACCC 38521
 Db 301 TrpGlnIleuGluLeuValAsnCyValPheGlnGlnPheProPheLeuIleuValLeu 320
 QY 38522 TTTCTTAAGTTGACTTAACTTAATGAACAAAGGCTCTACAGTTTAAAAAGTGGCC 38581
 Db 321 SerLeuValArgLeuThrPheThrAlaAsnLysGlyArgAsnHisPheSerGluValAsp 340
 QY 38582 CTACCAAGCTCAGGTATCTAGATCTTGTAGAAATGCACTGAGCTTAAAGTGGTCTGT 38641
 Db 341 LeuProSerLeuGluPheLeuAspLeuSerTrpGlnGlyLeuSerPheLysGlyCysCys 360
 QY 38642 TCTTAATTTGATTTGGGAACAACAGCCTGAGACACTTAAGACCTCAGCTTCAATGGTCC 38701
 Db 361 SerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSerPheAsnAspVal 380
 QY 38702 ATCATTAATGAGTGCATTTTATGAGTGTATGAAGAGCTGCAGACACTTGTATTTTCAGAC 38761
 Db 381 IleThrMetGlySerAsnPheLeuGlyLeuGlnGlnIleuAspPheGlnHis 400
 QY 38762 TCTACTTTAAAAAGGTCACAGAAATCTCAGCGTCTTATCCCTTGAAAGCTACTTAC 38821
 Db 401 SerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerLeuAspAsnLeuIleLys 420
 QY 38822 CTGACATCTGTATTAATCAACCAAAATGACTTGATGATATTTCTTGCTTGACC 38881
 Db 421 LeuAspIleSerHisIleThrHisIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuPhe 440
 QY 38882 AGTCTCAACACATTAATAAAGTGTGCAATCTTTCAAAGCAACACCCCTTTCAAATGTC 38941
 Db 441 SerLeuLysValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuGluAspIle 460
 QY 38942 TTTGCAAAACACAAACAACTTACACTCTGGATCTTTTAATGTCATTTGAAACAATA 39001
 Db 461 PheThrAspLeuAsnAsnLeuIlePheLeuAspLeuSerGluCysGlnGlnGlnIleu 480
 QY 39002 TCTTGGGGGGTATTTGACACCCCTCATGACTTCAATTAATTAATGAGTCAACACAT 39061
 Db 481 SerProThrAlaPheAspSerLeuProArgLeuArgIleLeuAsnMetSerHisAsnAsn 500
 QY 39062 CTATGTTTGGATCATCCCATTAATACAGAGCTGATTTCCCTCAGACACTTGTATTC 39121
 Db 501 PhePheAlaLeuAspThrPheProLysTyrHisIleuLysSerLeuGlnValLeuAspTyr 520
 QY 39122 AGTTTCATGCGATAGACATCTTAAGGA--ATACGGAACATTTTCCAAAGAGCTA 39178
 Db 521 SerLeuAsnHisIleGlyThrSerLysAsnGlnGlnLeuGlnHisPheProSerSerLeu 540
 QY 39179 GCCTTCTTCATCTTACTTAACATTTCTGTGCTGTATATGTAAGACATCAGAAATTCCTG 39238
 Db 541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
 QY 39239 CAGTGGGTCAAGAAACAGACAGCTTCTTGATGATTTGAACAATGACATGGCAACA 39298
 Db 561 GlnTrpIleLysAspGlnArgLeuValGluValGluGlnMetGluCysAlaThr 580
 QY 39299 CCTGTAGAGATGATACCTCTTAGTGTGATTTTAATAATCTTACCTGTTATATATGAC 39358
 Db 581 ProLeuAsnArgLysGlyIleProValLeuSerLeu--AsnIleThrCysGlnMetSer 599
 QY 39359 AAGCAATCATCAGTGTGTCAAGTGTCAAGTGTGATGATGATGATGATGATGATGATGAT 39418
 Db 600 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaValLeu 619
 QY 39419 ATATACACCTTCTATTTTACCTGATATTGCTGGCTGTAAAAAGTACAGACAGAGA 39478
 Db 620 ValTyrLysPheTyrPheHisIleuMetLeuValGlyCysIleLysTyrGlyArgGly 639

QY 39479 GAAGACATCTATGATGATTTTGATCTACTCGAGTCAAGATGAGACTGGGTGAGAAAT 39538
 Db 640 GluSerThrTyrAspAlaPheValIleTyrSerSerGlnAspGluAspTrpValArgAsn 659
 QY 39539 GAGCTGGTAAAGATTTTGAAGAAGAGATGCCCCGCTTCACTCTGCTTCACTACAGA 39598
 Db 660 GluLeuValLysAsnLeuGlnGluGlyValProProPheGlnLeuCyLeuHisTyrArg 679
 QY 39599 GACTTATTCCTGGTGTAGACATGTGTCGCAACATCAATCCAGAGAGCTTCCACAGAGC 39658
 Db 680 AspPheIleProGlyValAlaIleAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSer 699
 QY 39659 CGAAGGTTATTTGATGATGTCATGACACTTATTAAGACCCCTGATGATCTTTGAA 39718
 Db 700 ArgLysValIleValValSerGlnHisPheIleGlnSerAlaGlyTrpCysIlePheGln 719
 QY 39719 TATGAGATTTGCTCAACATGAGCAGTTTCTGAGACAGCCGCTGAGCATCATCTTATGTC 39778
 Db 720 TyrGluIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 739
 QY 39779 CTGAGAGAGTTTGAAGATGCTCCTGTCAGACAGAGTGGAAATGATTCGCTTACG 39838
 Db 740 LeuGlnLysValGlnLysSerLeuLeuArgGlnGlnValGluLeuTyrArgLeuLeuSer 759
 QY 39839 AGAAACACCTTACCTGGAATGGAAGACATCTCTGGGAGGACATCTTCTGAGAGA 39898
 Db 760 ArgAsnThrTyrLeuGlnTrpGluAspSerValLeuLysArgHisIlePheThrArgArg 779
 QY 39899 CTTAAAAATGCTTATTTGATGAGAAAACCTCGAATCTGAGCAACA 39946
 Db 780 LeuArgLysAlaLeuLeuAspGlyArgProTrpAsnProGlnGlyThr 795
 RESULT 12
 ID AAE16116 standard; protein; 837 AA.
 AC AAE16116;
 XX 26-MAR-2002 (first entry)
 DT
 XX Human DNAX Toll like receptor (DTLR) 4 #2, alternative version.
 DE
 XX Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
 KW Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 211
 FT /label= "Unknown
 FT /note= "Encoded by AAY"
 PN WO200190151-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 23-MAY-2001; 2001WO-US016766.
 XX
 PR 25-MAY-2000; 2000US-0207558P.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Hardman GT, Rock FL, Bazan JF, Kastelein RA, Ho SMK, Liu Y;
 XX
 DR WPI; 2002-063085/11.
 DR N-PSDB; AAD26306.
 XX
 PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 XX
 PS Claim 3; Page 240-243; 297pp; English.

XX The invention relates to mammalian receptor proteins, e.g., primate, CC human DNAX Toll like receptor (TLR) protein and their corresponding CC nucleic acids. The TLR is useful for treating conditions exhibiting CC abnormal expression of the receptors of their ligands. Such abnormality CC is manifested by immunological disorders. In particular, the TLR is CC useful for treating various disease or disorders associated with abnormal CC expression or abnormal triggering of response to a ligand. The TLR is CC also useful as an immunogen for the production of antisera or antibodies CC specific, e.g., capable of distinguishing between other interleukin (IL)-1 CC receptor family members, for the TLR or its various fragments. The CC purified TLR can be used to screen monoclonal antibodies or antigen- CC binding fragments. The antibodies are useful for screening expression CC libraries for particular expression products. These are useful for CC detecting or diagnosing various immunological conditions related to CC expression of TLR or cells that express it. The present sequence is CC human DLR4 protein, alternative version. The DLR4 gene is located on CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to CC be similar to the sequence shown in page 41 (AAE16102). However these CC sequences differ at several locations

XX Sequence 837 AA:

Alignment Scores:

	Pred. No.:	4.32e-233	Length:	837
Score:		2593.50	Matches:	525
Percent Similarity:		73.56%	Conservative:	101
Best Local Similarity:		61.69%	Mismatches:	172
Query Match:		2.98%	Indels:	53
DB:		5	Gaps:	9

US-09-396-985B-48 (1-50000) x AAE16116 (1-837)

QY 37400 TGGAAAAATGCATAAATTAATCTAAGACCTACATACACTGCTTTATGACCCCA 37459
Db 25 TgplubProCyValGlu---ValProAmileThrYrGln----- 37
QY 37460 GTTATGATCTTGATGATGATTTTTCATAGATTTGCGCTGACATAGTGTGATGTTT 37519
Db 38 CysheTgIuLeuAaPhetYrLysIleProAspAaLeuPro----- 51
QY 37520 ATCATCACTGTAGAGAGTGTGAATAATGCATAATCTGCAGATCTCTCTGCACACC 37579
Db 52 -----PheSerThrLysAaAaLeuAaPheSerPheAaProLeuAaGHis--- 66
QY 37580 ATCATCACTGTTTGTCTGTCTGTGATTTCTCTTACAAATACATGATATATCT 37639
Db 67 -----LeuGlySerTyrSerPhe----- 72
QY 37640 GTTTGTATCATAGTATGAGTGTAGGACTGTATGTATAGAAAGGTTTTTTTTCAGCA 37699
Db 73 -----PheSerPheProGlu 77
QY 37700 AAATACATATTTGGTATCTTTTGGCCATAGTGTGAATAATGAACAATGAAGACAAAG 37759
Db 78 LeuGlnValLeuAaPheLeuSer-----ArgCysGlnIleGlnThrIleGlnAspGly 94
QY 37760 GCATGGCATGGCTTACACCACTCTCAAACTTGATCTGACAGGAAACCTATCCAGAGT 37819
Db 95 AAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGlyAaProIleGlnSer 114
QY 37820 TTTTCCCAAGAGATTTCTGTGAGCTATACAGTTGTAGAGATCTGTGGCTGTGAGACA 37879
Db 115 LeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIlybLeuValAlaValGlnThr 134
QY 37880 AAATGGCTCTCTAGAGAGCTCCCTATGTGACAGCTTATACCTTAAGAAATCTCAAT 37939
Db 135 AaAaLeuAlaSerLeuGlnAaAaPheProIleGlnHisLeuYrThrLeuIlybGlyLeuAaAa 154
QY 37940 GTGGCTCACAATTTTATACATCTCTGTAGAGTTTACCTGCATATTTTTCATCTGACGAA 37999
Db 155 ValAlaHisAaAaLeuIleGlnSerPheYrLeuProGlyYrPheSerAaAaLeuThrAaAa 174

QY 38000 CTAGTACATGGATGATCTTTCTTATTAATCTATTAATCAACTATTACTGTCAACGACTTACAG 38059
Db 175 LeuGlnHisLeuAaPheLeuSerSerAaAaIlybIleGlnSerIleYrCysThrAaPheAaG 194
QY 38060 TTTTCAGTGAATAATCCACAAAGTCAATCTCTTTAGACATGCTTTGAACCAATGAC 38119
Db 195 ValLeuHisIleGlnMetProLeuLeuAaAaLeuSerLeuAaPheLeuSerLeuAaAa 214
QY 38120 TTTATTCAGAACCAACCTTTTCAGGAAATTAATTAACCTCAATGAACTGATCTTAAGAGTAA 38179
Db 215 PheIleGlnProGlyAlaPheYrGlnIleAaGlyLeuHisLeuThrLeuAaAaAaAa 234
QY 38180 TTTTAATAGCTCAATTAATTAATGAATACTGCTCAAAACCTGGCTGATTTACAGCTCAT 38239
Db 235 PheAaPheSerLeuAa 254
QY 38240 CCGTGTATCTTGGAGAAATTTAAAGATGAAGAAATCTGGAATTTTGAACCTCTATC 38299
Db 255 ArgLeuValLeuGlyIlybPheAaGlnGlyAaAaLeuGlnIlybPheAaPheYrSerAla 274
QY 38300 ATGGAAGATATATGTATGTATGTACCATTTGATGATCTCAGGTTACATTAACAAATGATTT 38359
Db 275 LeuGlnIlybLeuCyAaAaLeuThrIleGlnIlybPheAaAaAaAaAaAaAaAaAaAaAa 294
QY 38360 TCAGATGATATGTAG--TTCCATGTGCTGGCAATGTTTCTGCAATGTCTGTGCA 38416
Db 295 LeuAaPhePheIleAaPheLeuPheAaCyAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 314
QY 38417 GGTGTATCTTAATTAATTAATCTAGAAAGTGTCTTAACATTTGAATGGCAATCTTATCA 38476
Db 315 SerValThrIleGlnAaGlyAa 334
QY 38477 ATCATTAAGATCAACTTAAGAGTTTCCAACTGTGATTAACCTTTCTTAAGAGTTT 38536
Db 335 LeuValAa 354
QY 38537 ACTTAATCTAATGAACAAAGGCTATCATCACTTTTAAATAAGTGGCCCTACCAAGTCTCAGC 38596
Db 355 ThrPheThrSerAa 374
QY 38597 TATCTAGATCTTATAGTAAATGACCTGAGCTTTATAGTGTGCTGTCTTATTTGATTTG 38656
Db 375 PheLeuAaPheLeuSerAa 394
QY 38657 GGAACAAACAGCTGTAGACACCTTAAGCTTCAATGATGATCAATTAAGAGTCC 38716
Db 395 GlyThrThrSerLeuYrIlybAaPheLeuSerPheAaAaAaAaAaAaAaAaAaAaAaAaAa 414
QY 38717 AATTTCATGGGTCTAGAAAGCTGACAGCACTGTGATTTGACAGCTTATTAAGAG 38776
Db 415 AaAaPheLeuGlyLeuGlnIlybLeuGlnHisIlybAaPheGlnHisSerAaAaAaAaAaAa 434
QY 38777 GTCAAGAAATTTCTCAGGTTCTTATCCCTTGAAGCTTATCTTATCAATCTTAT 38836
Db 435 MetSerGlnPheSerValPheLeuSerLeuAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 454
QY 38837 ACTTAACCAAAATGACTTGTGATGATTTCTTGGCTTGAACAGTCTCAACACATTA 38896
Db 455 ThrHisThrIlybValAlaPheAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 474
QY 38897 AAATGGCTGGCAATTTCTTCAAAAGACACCACTTCAATGCTTTGAAACACACACA 38956
Db 475 LysMetAlaGlyAa 494
QY 38957 AACTTGACATTTCTGATCTTTTCAATATGTCATTTGGAACAAATATCTGGGGGATTT 39016
Db 495 Aa 514
QY 39017 GACACCTTCATAGACTTCAATTAATTAATGATGACACAAATCATTAATGTTTGGAT 39076
Db 515 Aa 534
QY 39077 TCATCCATTAATAACAGCTGTATTCCTCAGACCTGTGATTCATTAATCGCATA 39136

```

Db      535  ThrProTyrLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIle 554
QY      39137  GAGCATCT---AAAGAAATCTGCACATCTTCCAAAGAGCTAGACCTTCTCAATCTT 39193
Db      555  MetThrSerLysLysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 574
QY      39194  ACTACACATTCCTGCTTGTATATGTGACATGAGAAATCTCGAGTGGGTCAAGGAA 39253
Db      575  ThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrrPLeuAsp 594
QY      39254  CAGAAAGCATCTTGTGGTGAATGTGACAAATGACATGTGACACCTGTGAGATGAT 39313
Db      595  GlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAlaIrrProSerAspLysGln 614
QY      39314  ACCCTCTTGAATGTTAATTAATCTACCTGTTATATGTCACAGACATCACTAGT 39373
Db      615  GlyMetProValLeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleLeuGly 633
QY      39374  GTGTCAAGTGTCAAGTGTATGTGGTATCCACTGATGATTCGATATACACTTCTAT 39433
Db      634  ValSerValLeuSerValLeuValSerValValAlaValLeuValTyrLysPheTyr 653
QY      39434  TTTCACCTGATATCTTATTTGCTGGCTGTAAAGTACAGACAGAGAAAGCATCTATGAT 39493
Db      654  PheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGlyGlnAsnIleTyrAsp 673
QY      39494  GCATTGTGATCTACTCGAGTCAGATGAGATGAGACTGGGTGAGAAATGAGCTGTAAAGAT 39553
Db      674  AlaPheValIleTyrSerSerGlnAspGlnAspIrrValArgAsnGlnLeuValLysAsn 693
QY      39554  TTAGAAGAAGAGAGGCCCGCTTCACTGCTGCTCACTCACTGAGACTTATTCCTGCT 39613
Db      694  LeuGlnGlnGlyValProProPheGlnLeuGlySleuHisTyrArgAspPheIleProGly 713
QY      39614  GTAGCCATTTGCTGCCCAATCATCATCCAGAGAGCTTCCACAAAGCCGAGAGCTTATTTG 39673
Db      714  ValAlaIleAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleVal 733
QY      39674  GTAGTGTCTAGACACTTATTCAGAGCCGTGGTGTATCTTGTGAATATGAGATGCTCA 39733
Db      734  ValValSerGlnHisPheIleGlnSerTyrTyrCysIlePheGlnTyrGlnIleAlaGln 753
QY      39734  ACATGAGAGTTCTGAGCAGCCGCTCGATCATCTTCACTGCTGCTGAGAGAGTTGAG 39793
Db      754  ThrTrrPheLeuSerSerArgAlaIleIlePheIleValLeuGlnLysValGln 773
QY      39794  AAGTCCCTGCTGAGCAGCAGAGTGAATGTATGCGCTTCTTACAGAAACCTTACCTG 39853
Db      774  LysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeu 793
QY      39854  GAATGGAGAGGCAATCCTCTGGGAGGAGCAGCATCTTCTGAGAAAGCTTAAAGCCCTA 39913
Db      794  GlnTrrPheLysPheSerValLeuGlnLysIlePheTrrPArgLysArgLysAlaLeu 813
QY      39914  TTGATGGAAGAAAGCCTGATCCTGAGCAACA 39946
Db      814  LeuAspGlyLysSerTrrPAsnProGlnGlyThr 824

RESULT 13
AD057782
ID      AD057782 standard; protein, 808 AA.
XX
AC      AD057782;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Chimpanzee toll-like receptor 4 SEQ ID NO:3.
XX
KW      toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW      immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW      sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX

```

```

OS      Pan troglodytes.
XX
FN      WO2004042365-A2.
XX
PD      21-MAY-2004.
XX
PE      03-NOV-2003; 2003WO-US036247.
XX
PR      01-NOV-2002; 2002US-0423113P.
XX
PA      (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
PI      Messier W;
XX
DR      WPI; 2004-400726/37.
XX
N-PSDB; AD057780, AD057781.
XX
PT      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT      sequence of the Old World monkey with that of a human.
XX
PS      Example 1; SEQ ID NO 3; 11pp; English.
XX
CC      The invention relates to a novel method for identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an old world monkey
CC      comprising comparing the TLR4 polynucleotide sequence of the Old World
CC      monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC      method of the invention has antibacterial, immunosuppressive, and
CC      antiasthmatic activity. The method is useful in identifying a nucleotide
CC      change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC      change may be associated with reduced sensitivity to Gram-negative
CC      bacterial infection. The methods, agents and composition are useful in
CC      treating sepsis, severe sepsis or septic shock and asthma. The present
CC      sequence represents chimpanzee TLR4.
XX
SQ      Sequence 808 AA;
XX
Alignment Scores:
Pred. No.:      5,87e-233      Length:      808
Score:          2592.00      Matches:      524
Percent Similarity: 74.17%      Conservative: 99
Best Local Similarity: 62.38%      Mismatches: 165
Query Match:    2.98%      Indels:      52
DB:             8      Gaps:      8
US-09-396-985b-48 (1-50000) x AD057782 (1-808)
QY      37433  ACATATCAACTGCTTATATGATACCCAGTTATGATCTGAATGATTTTCTAATGAT 37492
Db      6  ThrTyrGln-----CysMetGlnLeuAsnPheTyrLysIleProAsp 19
QY      37493  TTGTGCTGCTGACATAGTGTGATGATTATATCATCTAGTGAAGATGCAAAATGACAAAT 37552
Db      20  AsnLeuPro-----PheSerTrpLysAsnLeuAsp 29
QY      37553  CTGCAAGATTCCTCTCGTGTGCTACACCATCATCACTGTTTGTCTGTACAGTTTCTC 37612
Db      30  LeuSerPheAsnProLeuArgHis-----LeuGlySerTyrSerPhe--- 43
QY      37613  TTACAAATACATGATATATCATATCTGTTGTATCATAGTATGATGAGGACTGTATGT 37672
Db      43  ----- 43
QY      37673  CATTAGAAAGGCTTTTTCACGAAATAATATGATGATCTTTTGCCCATNGG 37732
Db      44  -----PheSerPheProGlnLeuGlnValLeuAspLeuSer-----Arg 56
QY      37733  TGTGAATGTGAAGAAATGTGAAGAACAGATGGCTTACACCACTCTCAAACTTG 37792
Db      57  CysGlnIleGlnTrpIleGlnAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeu 76
QY      37793  ATATGACAGAGAAACCTATTCAGAGTGTTCCTCCAGAGAACTTCTGTGACTAACAAGT 37852

```


Dh 77 IleuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSer 96
Qy 37853 TTAGAGATGCTGGGGCTGGGAGACAAATGCGCTCTAGAAACCTCCCATTTGA 37912
Dh 97 LeuGlnLeuSerLeuValAlaValGluThrAsnLeuAlaSerLeuGluAsnProIleGly 116
Qy 37913 CAGCTTAACCTTAAGAAACATGATGGCTCACAAATTTTATACATCTTCCGTAAGTTA 37972
Dh 117 HisLeuLeuSerThrLeuLeuValGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLeu 136
Qy 37973 CTGCATATATTTTTCAAATGACCAACCTAGATGATGATCTTTCTTATATATAT 38032
Dh 137 ProGluTyPheSerAsnLeuThrAsnLeuGlnHisLeuAsnLeuSerSerAsnIle 156
Qy 38033 CAACACTTACTGCAACGATTAACATTTCTACGTAAATCCACAAGTCATCTCT 38092
Dh 157 GlnSerIleTyCysThrAsnLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSer 176
Qy 38093 TTAGACATGCTTTGAAACCAATGATGATTCACAACCAAGCTTTCAGGAAATTAAG 38152
Dh 177 LeuAsnLeuSerLeuAsnProMetAsnPheIleGlnProGlyAlaPheLeuValLeuArg 196
Qy 38153 CTCCATGACTGACTTGAAGAGTAATTTTATAGTCAATATATATGAAAATCTGCCT 38212
Dh 197 LeuHisLeuThrLeuArgAsnAsnPheAsnSerLeuAsnValMetLeuSerCysIle 216
Qy 38213 CAACACCTGGCTGGTTTACACGTCATCGGTGATCTTGGAGAAATTAAGATGAAG 38272
Dh 217 GlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeuGlyGluPheArgAsnGly 236
Qy 38273 AATCTGAAATTTTGAACCTCTATCATGGAAGAGACTATGATGATGACATTTGATAG 38332
Dh 237 AsnLeuGluLeuPheAsnLeuSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGlu 256
Qy 38333 TTCAAGTTAACATATACAAATGATTTTTCAGATGATTTGTTAAG--TTCCATGCTTG 38389
Dh 257 PheArgLeuAlaTyLeuAsnArgTyTyLeuAsnArgPheIleIleAsnLeuPheAsnCysLeu 276
Qy 38390 GCGAATTTCTGCATGCTCGGACGAGTGTATCTTAATAATCTAGAAAGATGCTCT 38449
Dh 277 ThrAsnAlaSerSerPheSerLeuValSerAlaThrIleLeuSerValValAsnPheSer 296
Qy 38450 AAACATGCAATGCAATCCTTATCATCATGATTAAGATCAATTAAGACTTCCAACT 38509
Dh 297 TyAsnPheGlyTyPheGlnHisLeuGluLeuValAsnValSerPheGlyGlnPheProThr 316
Qy 38510 CTGGATTTACCTTTCTTAAAGTTTGACTTAACTATGAACAAAGGATCTATCAATTT 38569
Dh 317 LeuLeuLeuLeuSerLeuLeuArgLeuThrPheThrSerAsnValGlyGlyAlaPhe 336
Qy 38570 AAAAAGTGGCCCAAGCTCAGCTATCTAGATCTTATGAATGACATGAGCTTT 38629
Dh 337 SerGluValAsnLeuProSerLeuGluPheLeuAsnLeuSerAlaArgAsnGlyLeuSerPhe 356
Qy 38630 AGTGGTGTCTGTCTTATGATTTGGAAACAAACAGCTGAGCACTTGAAGCTCAGC 38689
Dh 357 TyGlyLeuSerCysSerGlnSerAsnArgPheGlyThrThrSerLeuSerTyLeuAsnLeuSer 376
Qy 38690 TTCAATGGTGCATATTAAGTGCATATTAAGGATGATGAAGAGCTGACAGCTTG 38749
Dh 377 PheAsnIleValIleThrMetSerSerAsnPheLeuGlnGluGlnGlnHisLeu 396
Qy 38750 GATTTGAGACCTACTTAAAGAGGTACAGATTTCTCAGGTTCTTATCCCTTGA 38809
Dh 397 AspPheGlnHisSerAsnLeuValGlnMetSerGluPheSerValPheLeuSerLeuArg 416
Qy 38810 AAGCTTATACCTTGAATCTTATATACAAACAAATGATGATCTGATGATATTT 38869
Dh 417 AsnLeuLeuTyLeuAsnArgIleSerHisThrHisThrArgValAlaPheAsnGlyIlePhe 436
Qy 38870 CTGGCTTGAACAGCTGTCAACATTAATAAGCTGGCAATTTCTTCAAGACACACC 38929
Dh 437 AsnGlyLeuSerSerLeuGluValLeuLeuSerAlaGlyAsnSerPheGlnGluAsnPhe 456

Qy 38930 CTTTCAATGCTTTTGCAAAACACACAACTTGACATTTCTGAGATCTTTCTAATGCA 38989
Dh 457 LeuProAsnIlePheThrGluLeuArgAsnLeuThrPheLeuAsnLeuSerGlnCysGln 476
Qy 38990 TTGAAACAATATCTTGGGGGATTTTGAACACCTCCATAGACTTCAATTAATATATG 39049
Dh 477 LeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMet 496
Qy 39050 AGTCACAACATTTATTTGTTTGGATTCATCCATTAATACCAAGCTGTATTCCTCAGC 39109
Dh 497 SerHisAsnAsnPhePheSerLeuAsnThrPheProTyIleCysLeuAsnSerLeuGln 516
Qy 39110 ACTCTGATGCTGCAATCCGATAGACATCT--AAAGAAATCTGCAACATTTT 39166
Dh 517 ValLeuAsnTySerLeuAsnHisIleMetThrSerLeuValGlnLeuGlnHisPhe 536
Qy 39167 CCAAGAGCTAGCTTCTTCAATCTTATCTAACATTTCTGTTCTGTATATATGAACT 39226
Dh 537 ProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsnPheAlaCysThrCysGlnHis 556
Qy 39227 CAGAAATCTCGCAGTGGGCTCAGAGAACAGACAGCTTCTGGTGAATGTTGAACAAATG 39286
Dh 557 GlnSerPheLeuGlnTyPheLeuAsnArgLeuValGluValGluArgMet 576
Qy 39287 ACATGGCAACACCTGTAGAGATGAATACCTCTTATGTTGATTTTAATATTTAC 39346
Dh 577 GluCysAlaThrProSerAsnArgPheGlnGlyMetProValLeuSerLeu--AsnIleThr 595
Qy 39347 TGTATATGTACAAACATCATCACTAGTGTGTCAGTGTGATGATTTGTATCCACT 39406
Dh 596 CysGlnMetAsnLeuSerThrIleIleGlyValSerValLeuSerValLeuValIleVal 615
Qy 39407 GTAGCATTTGTGATATACCTCTTATTTTCACTGATATCTTATGCTGGCTGTAAAG 39466
Dh 616 ValAlaValLeuValTyTyPheTyPheHisLeuMetLeuLeuAlaGlyCysIleLeu 635
Qy 39467 TACAGCAGAGAGAAACATCTATGATGATTTGTGATCTGATCTGAGTCAAGATGAGAC 39526
Dh 636 TyGlyArgGlyGluAsnIleTyAsnAlaPheValIleTySerSerGlnAsnArgLeuAsp 655
Qy 39527 TGGGTGAATAGCTGTGAAGAAATTAAGAAAGAGTGGCCGCTTTCACCTTGC 39586
Dh 656 TrpValArgAsnGluLeuValValAsnLeuGlnGlyValProPheGlnLeuCys 675
Qy 39587 CTTCATCTACAGACCTTATTTCTGCTGATGACATTTGCTGCAACATCATCAGAAAGC 39646
Dh 676 LeuHisTyArgAsnPheIleProGlyValAlaIleAlaAsnIleIleHisGlnGly 695
Qy 39647 TTCCACAAGCCGGAAGGTTATTTGTGTAGTGTCTAGACCTTTATTCAGAGCCGTTG 39706
Dh 696 PheHisLeuSerArgLeuValIleValValValSerGlnHisPheIleGlnSerAsnArgTrp 715
Qy 39707 TGTATCTTGAATATAGATTTGCTCAACATGSCAGTTTCTGACAGCCGCTGAGATC 39766
Dh 716 CysIlePheGlnTyTyGlnIleAlaGlnThrTrpGlnPheLeuSerSerAlaGlyIle 735
Qy 39767 ATCTTCAATTTCTTGAAGAGTTTGAAGATCCCTGCTGAGCAGCAGGTGGAATTTAT 39826
Dh 736 IlePheIleValLeuGlnValGlnTySerThrLeuLeuArgTrpGlnValGluLeuTy 755
Qy 39827 CGCCTTGTAGCAAAACACTACCTGGAATGGAGAGCACTTCTGGGAGGACATC 39886
Dh 756 ArgLeuLeuSerArgAsnThrTyLeuGlnTrpGlnAsnSerValLeuGlyArgHisIle 775
Qy 39887 TTCTGAGAAAGCTTAATAAATGCCCTAATTTGATGAGAAACCTCGAATCTTGACAAACA 39946
Dh 776 PheTrpArgTrpLeuArgTyValAlaLeuLeuAspGlyLeuSerTrpAsnProGlnGlyThr 795

RESULT 14
AAW86352
ID AAW86352 standard; protein; 799 AA.
XX


```

AC AA086352;
XX
DT 15-MAR-1999 (first entry)
DE Human DMAX toll-like receptor DTLR4.
KW DMAX toll-like receptor; DTLR; Drosophila toll receptor; Il-1 receptor; interleukin-1 receptor; phosphate metabolism; innate immunity response; modulate inflammatory function; morphological effect; immunological disorder.
XX
OS Homo sapiens.
PN WO9805047-A2.
PD 12-NOV-1998.
XX
PF 07-MAY-1998; 98WO-US008979.
PR 07-MAY-1997; 97US-0044293P.
PR 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
XX
PA (SCHE ) SCHERING CORP.
PI Hardiman GT, Rock FL, Bazan JF, Kastelein RA; WPI; 1999-059670/05.
DR N-PSDB; AAV80666.
PT Human DMAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate metabolism, modulate inflammatory function or innate immunity responses.
XX
PS Example; Page 115-117; 171pp; English.
CC The present invention specifically describes human DMAX toll-like receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given in the present invention. Also described are: (1) a fusion protein comprising a DTLR protein or peptide; (2) a binding compound, preferably an antibody or antibody fragment which specifically binds to a DTLR protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide; (4) an expression vector comprising the nucleic acid of (3); and (5) a host cell comprising the vector of (4). The host cell of (5) can be used to produce the DTLR proteins. The DTLR proteins can be used to alter phosphate metabolism, to modulate inflammatory function, innate immunity responses or morphological effects. The DTLR proteins can be used in the treatment of conditions exhibiting abnormal expression of the receptors of their ligands. These abnormalities are typically manifested by immunological disorders
CC XX
SQ Sequence 799 AA;
Alignment Scores:
Pred. No.:          7.24e-233      Length:          799
Score:              2591.00       Matches:           508
Percent Similarity: 79.76%        Conservative:     95
Best Local Similarity: 67.20%    Mismatches:      147
Query Match:         2.98%        Indels:           6
                               Gaps:             4
US-09-396-985B-48 (1-50000) x AA086352 (1-799)
OY 37685 TTTTTCGACGAATAATCATTAATTGGATCTTTTTGCCAGTAGTGCGAATTTGAA 37744
   ||| ||| :: :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db PheSerHeProGluLeuGlnValIleuAspLeuSer-----ArgCysGluIleGln 51
OY 37745 ACAATTGAAGCAAGGCATGGCATGGCTTACACACCCTGTCAAATTGATATGACAAGA 37804
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db ThrIleGluAspGlyAlaIleuArgIleSerLeuSerHisIleuSerThrIleuLeuThrGly 71
OY 37805 AACCTTTCAGAGATTTTCCCACGAGAAGTTCTCTCGAATAACAAGTTTAAAGATCTCG 37864
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db AsnProIleGlnSerIleuAlaIleuGlyAlaPheSerCtyIleuSerIleuSerIleuGlnIleu 91

```

[illegible]

```
QY 38942 TTGGCAACACAACTGACATTCCTGATCTTTCTAATGTCATTTGCAACAATA 39001
Db 452 PhehtrgluleuarganleuhtnrPheleuaspseuSerGlnGlnleuGlnleu 471
QY 39002 TCTTGGGGGATTTGACACCCCTCCATAGACTTCAATATTAATATAGATCAACAAT 39061
Db 472 SerProthralaPheAensSerleuSerSerleuGlnValleuAenMetSerHlaAen 491
QY 39062 CTATGTTGTTGGATTCATCCATTAATACAGCTGATTCCTCAGACACTTTGATTC 39121
Db 492 PhePheSerleuAptlrPheProtyrLysCysleuAenSerleuGlnValleuAptLyr 511
QY 39122 AGTTTCAATCGCATAGACATCT--AAAGAAATATCGCAACATTTCCAAAGACTA 39178
Db 512 SerleuAenHlaIleMetHnSerLysGlnleuGlnleuGlnHlaPheProSerleu 531
QY 39179 GCCTTCTTCACTTACTTAACAATTCGTGCTGTATGATATGTAACATCAAGAAATTC 39238
Db 532 AlaPheleuAenleuThnGlnAenAapPheAlaCysHnSerGlnHlaGlnSerPheleu 551
QY 39239 CAGTGGGTCAAGAACAGACAGCTTTGGTGAATGTTGAACAATGACATGTGCACA 39298
Db 552 GlntrPleleuAapGlnArgGlnleuValGlnValGlnArgMetGlnCysAlaThr 571
QY 39299 CCTGTAGAGATGATACCTCTTAGTGTGATTTTAATATCTACTGTTATATGTAC 39358
Db 572 ProSerAptLysGlnGlnMetProValleuSerleu--AenIleHnSerGlnMetAen 590
QY 39359 AAGACATCATCAGTGTGTGTCAGTGTGTCAGTGTGATGTCAGTGTGATTCG 39418
Db 591 LysHnIleleuGlnValSerValleuSerValleuValSerValleuValleu 610
QY 39419 ATATACCATCTTCTATTTTCACTGATCTTATTCCTGCTGCTGTAATAAGTACAGACAG 39478
Db 611 ValLysLysPheLysPheHnIleMetleuAenLysGlnLysLysGlnLysGln 630
QY 39479 GAAACATCATATGATGATTTGATGATCTACTGATGATGATGATGATGATGATGAT 39538
Db 631 GlnAenIleLysAapAlaPheValleuValleuValleuValleuValleuValleu 650
QY 39539 GAGCTGTGAAGATTTGAAGAAGAGAGTCCCGCTTTCACCTGCTGCTTCACTACAGA 39598
Db 651 GlnleuValLysAenleuGlnGlnGlnValProProPheGlnleuGlnLysArg 670
QY 39599 GACTTTATCTGCTGTGATGACCATGCTGCGCAACATCATCCAGAGAGCTTCAACAAGC 39658
Db 671 AspPheIleProGlnValAlaIleAlaAenIleIleHnIleGlnGlnPheHnLysSer 690
QY 39659 CGAAGGTATTTGGTATGATGTACACTTATTCAGAGCGCTGATGATCTTTGAA 39718
Db 691 ArgLysValIleValIleValIleValSerGlnHnIlePheIleGlnSerArgTrpCysIlePheGln 710
QY 39719 TATGAGATTGCTCAACATGAGCATTTCTGACAGCGCTGTCATCATCTTCAATGTC 39778
Db 711 TyrGlnIleAlaGlnHntrPglHnPheleuSerSerArgAlaGlnIleIlePheIleVal 730
QY 39779 CTTGAGAAAGTTGAGAGACTCCCTGCTGAGGACAGAGGTGGAATGTATCGCTTTCAGC 39838
Db 731 LeuGlnLysValGlnLysThreleuAargGlnGlnValGlnleuLysArgleuLysSer 750
QY 39839 AGAAACACCTACCTCGGAATGAGAGAGCAATCTCTCGGGGAGAGCACTTTTGAGAGA 39898
Db 751 ArgAenHntrLysleuGlntrPglLysSerValleuGlnLysArgHnIlePheTrpArgArg 770
QY 39899 CTTAAAAATGCCCTATTGATGATGAAAAAGCTCGAATCCTGAGCAACA 39946
Db 771 LeuArgLysAlaLeuLeuAapGlnLysSerTrpAenProGlnGlnLysThr 786
RESULT 15
AAE16093
ID AAE16093 standard; protein; 799 AA.
XX
AC AAE16093;
```

```
XX
DT 26-MAR-2002 (first entry)
XX
DE Human DNAX Toll like receptor (DTLR) 4 #1.
XX
KW Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
KM Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX
OS Homo sapiens.
XX
PN WO200190151-A2.
XX
PD 29-NOV-2001.
XX
PF 23-MAY-2001; 2001WO-US016766.
XX
PR 25-MAY-2000; 2000US-0207558P.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Hardiman GT, Rock FL, Bazan JF, Kaetzelin RA, Ho SMK, Liu Y;
XX
XX WPI; 2002-083085/11.
XX
DR N-PSDB; AAD26283.
XX
PT New DNAX Toll like receptor (DTLR) proteins, useful for treating
PT conditions exhibiting abnormal expression of the receptors of their
PT ligands, particularly abnormalities manifested by immunological
PT disorders.
XX
PS Claim 1; Page 35; 297pp; English.
XX
CC The invention relates to mammalian receptor proteins, e.g., primate,
CC human DNAX Toll like receptor (DTLR) protein and their corresponding
CC nucleic acids. The DTLR is useful for treating conditions exhibiting
CC abnormal expression of the receptors of their ligands. Such abnormality
CC is manifested by immunological disorders. In particular, the DTLR is
CC useful for treating various disease or disorders associated with abnormal
CC expression or abnormal triggering of response to a ligand. The DTLR is
CC also useful as an immunogen for the production of antisera or antibodies
CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
CC receptor family members, for the DTLR or its various fragments. The
CC purified DTLR can be used to screen monoclonal antibodies or antigen-
CC binding fragments. The antibodies are useful for screening expression
CC libraries for particular expression products. These are useful for
CC detecting or diagnosing various immunological conditions related to
CC expression of DTLR or cells that express it. The present sequence is
CC human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33
XX
SQ Sequence 799 AA.
XX
Alignment Scores:
Pred. No.: 7.24e-233 Length: 799
Score: 2591.00 Matches: 508
Percent Similarity: 79.76% Conservative: 95
Best Local Similarity: 67.20% Mismatches: 147
Query Match: 2.98% Indels: 6
DB: Gaps: 4
US-09-396-985B-48 (1-5000) x AAE16093 (1-799)
QY 37685 TTTTTCATGAGAAAATACATTAATGATCTTTTGCATAGGATGTAATGAA 37744
Db 35 PheSerPheProGlnleuGlnValleuAapLysSer-----ArgCysGlnIleGln 51
QY 37745 ACAATTGAAGACAGAGCATGAGCTTACACCACTCTCAACTGATAGTACAGAGA 37804
Db 52 ThrIleGlnAapGlnAlaLysArgGlnSerLysSerHisLysSerHnIleuLysThrGly 71
QY 37805 AACCTTACAGAGTTTTCCTCCAGAGAGTTTCTGTGACTTCAACAGTTAGAGATCTG 37864
Db 72 AsnProIleGlnSerleuAlaLeuGlnAlaPheSerGlnLysSerSerleuGlnLysLeu 91
```

QY 37865 GTGGCTGTGAGACAAATGGGCTCTTAGAAGCTTCCCTATTGACAACTTAAACC 37924
 Db ValAlaValAlaGluThrAsnLeuValSerLeuGluAsnProIleGluHisLeuLysThr 111
 QY 37925 TTTAAGAACTCAATGTGGCTCAACAATTTTATCACTTCTGTAAAGTTACCTGCATATTTT 37984
 Db LeuLysGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysProGluTyrPhe 131
 QY 37985 TCCAACTGACGAACCTAGTACATGTGGATCTTTCTTATCACTTATATCAAACTTAAT 38044
 Db SerAsnLeuThrAsnLeuGlnHisLeuAsnProIleGlnSerAsnLysIleGlnSerIleTyr 151
 QY 38045 GTCAACGACCTTACAGTTTCTACGTGAATTCACAAAGTCAATCTCTCTTATGACATGCT 38104
 Db CysThrAsnProIleValLeuHisGlnMetProLeuAsnLeuSerLeuAsnProIle 171
 QY 38105 TTGAACCAATTCATCTTATCAACAAGACCTTTCAGGGAATTAAGCTCAATGAACCTG 38164
 Db LeuAsnProIleAsnProIleGlnProGluAlaPheLysGluIleArgLeuHisLysLeu 191
 QY 38165 ACTGTAAGAGGTAATTTTATAGCTCAAAATTAATGAAGAACTTGCTCAAAACCTGGCT 38224
 Db ThrLeuThrAsnAsnProIleAsnProIleGlnSerLeuAsnValMetLysThrCysIleGlnGlyLeuAla 211
 QY 38225 GGTTTACACGTCATCGGTTGATCTTGGAGAAATTTAAAGATGAAGGAATCTGGAAT 38284
 Db GlyLeuGluValHisArgLeuValLeuGluGluThrPheAsnGlnGluGluAsnLeuGlnLys 231
 QY 38285 TTGACACCTCTATCATGAAGAACTATGATGATGACCAATGATGATGATGATGATGAT 38344
 Db PheAsnProIleAlaLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 251
 QY 38345 TATCAAAATGATTTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 38401
 Db TyrLeuAsnProIleGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 271
 QY 38402 GCAATGCTCTGAGAGGTTGATCTATGAATATCTAGAAAGATGTTCTTAACCTTGAAC 38461
 Db SerPheSerLeuValSerValThrIleGluArgValLysAsnProIleTyrAsnProIle 291
 QY 38462 TGGCAATCTTATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38521
 Db TrpIleHisLeuGluLeuValAsnCysLeuPheGlnPheProIleLeuLysLeuLys 311
 QY 38522 TTTTCTTAAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38581
 Db SerLeuLysAsnLeuThrPheThrSerAsnLysGluGluGluGluGluGluGluGluGlu 331
 QY 38582 CTACCAAGTCTACGATCTGATCTTATGATGATGATGATGATGATGATGATGATGATGAT 38641
 Db LeuProSerLeuGluThrPheLeuAsnProIleGlnSerLeuGlnSerLeuGlnSerLeu 351
 QY 38642 TCTTATTTCTGATTTTGGAGAAACAGCTGAGCACTTGAACCTGACCTTCAATGATGCT 38701
 Db SerGlnSerAsnProIleGlnSerLeuLysLeuLysLeuLysLeuLysLeuLysLeuLys 371
 QY 38702 ATCATTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38761
 Db IleThrMetSerSerAsnProIleGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 391
 QY 38762 TCTACTTTAAAGGATGACGAATCTGACGTTTCTTATCTTAAAGGATGATGATGATGAT 38821
 Db SerLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuAsnGlnMetLysLeu 411
 QY 38822 CTTGACATCTTCTTATCAACAACAAATGATGATGATGATGATGATGATGATGATGATGAT 38881
 Db LeuAsnProIleSerHisThrHisThrArgValAlaPheAsnGlnIlePheAsnGlnLysSer 431
 QY 38882 AGTGTCAACACATTTAAATGGCTGGCAATCTTCTTCAAAAGCAACACCTTCAAAATGTC 38941
 Db SerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnGlnGlnGlnGlnGlnGln 451
 QY 38942 TTTGCAAAACAAACAACTTGAATCTTCTTCAAAATGATGATGATGATGATGATGATGAT 39001

Db 452 PheThrGluLeuArgAsnLeuThrPheLeuAsnProIleGlnSerLeuGlnGlnGlnGln 471
 QY 39002 TCTTGGGGGATTTTGGACACCTCCATGACCTTCAATATTAATGATGATGATGATGAT 39061
 Db SerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsn 491
 QY 39062 CTATGTTTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39121
 Db PhePheSerLeuAsnProIlePheProTyrLysCysLeuAsnSerLeuGlnValLeuAsnPro 511
 QY 39122 AGTTTCAATGCAATGACATCT--AAAGAAATCTGCAACATTTTCCAAAGCTTA 39178
 Db SerLeuAsnHisIleMetThrSerLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 531
 QY 39179 GCCTTCTTCAATCTTATCAACAATTCGTGCTTGTATGATGATGATGATGATGATGAT 39238
 Db AlaPheLeuAsnLeuThrGlnAsnAsnProIleCysThrCysGlnHisGlnSerPheLeu 551
 QY 39239 CAGTGGGTCAAGGACAAAGACAGTTCTGTGAATGATGATGATGATGATGATGATGATGAT 39298
 Db GlnThrPheLysAsnGlnMetGlnLeuValGluValGluArgMetGluCysAlaThr 571
 QY 39299 CTTGTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39358
 Db ProSerAsnProIleGlnGlnMetProValLeuSerLeu--AsnIleThrCysGlnMetAsn 590
 QY 39359 AAGACATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39418
 Db LysThrIleIleGluValSerValLeuSerValLeuValSerValAlaAlaValLeu 610
 QY 39419 ATATACCATCTTATTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 39478
 Db ValTyrLysPheThrPheHisLeuMetLeuValAlaCysIleLysTyrGluArgGly 630
 QY 39479 GAAACATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39538
 Db GluAsnIleThrAsnAlaPheValIleTyrSerSerGlnAsnProIlePheValArgAsn 650
 QY 39539 GAGCTGGTAAAGAAATTTGAAGAAAGAGTCCCGCTTCACTGCTGCTTCACTGATGAT 39598
 Db GlnLeuValLysAsnLeuGlnGlnGluGluValProProPheGlnLeuGlnCysLeuHisTyrArg 670
 QY 39599 GACTTATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39658
 Db AspPheIleProGluValAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 690
 QY 39659 CGGAAAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39718
 Db ArgLysValIleValValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGln 710
 QY 39719 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39778
 Db TyrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 730
 QY 39779 CTTGAGAGGTTGAGAAAGTCCGCTGAGGACAGGTTGAATGATGATGATGATGATGATGAT 39838
 Db LeuGlnLysValGlnLysThrLeuLeuArgGlnGlnAlaGlnLeuLysTyrArgLeuSer 750
 QY 39839 AGAAACACCTACCTGGAATGAGAGACAACTCTGGGAGAGACATCTTCTGAGAGAGA 39898
 Db ArgAsnThrTyrLeuGlnTrpGlnLysSerValLeuGlnLysArgHisIlePheThrPheArg 770
 QY 39899 CTTAAAAATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39946
 Db LeuArgLysAlaLeuLeuAsnProIleGlnSerTyrAsnProIleGlnGlnGlnGlnGln 786

Search completed: March 30, 2005, 02:13:46
 Job time : 4273.5 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 14:31:58 / Search time 447 Seconds
(without alignments)
16700.014 Million cell updates/sec

Title: US-09-396-985B-48
Perfect score: 86900
Sequence: 1 ttccatcatcatgtagtc.....catttagtatttcaga 50000

Scoring table:
BIOSIM62
Xgapop 10.0, Ygapext 0.5
Xgapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 2054180

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p model -DEV=xlh
-O=/cg2_1/USF10.spool/US09396985/rnat_28032005_155744_21170/app_query.faeta_1.85098
-DB=Issued_Patents_AA -OPMT=faetan -SUFFIX=rai -MINMATCH=0.1 -LOPCL=0
-LIST=45 -DOCALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=Pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09396985 @CGN 1.1 732 @rnat_28032005_155744_21170 -NCPUR=6 -ICPU=3
-NO_MMAP -LARGEOUTRY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA.*

1: /cg2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cg2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cg2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cg2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cg2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cg2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2592	3.0	844	4	US-09-949-016-9438
2	502.5	0.6	661	1	US-08-514-014-4
3	502.5	0.6	661	2	US-08-833-823-4
4	464	0.5	784	4	US-09-982-308B-23
5	402.5	0.5	775	4	US-09-949-016-8799
6	365.5	0.4	129	4	US-09-513-999C-7214
7	269.5	0.3	1059	4	US-09-907-794A-290
8	269.5	0.3	1059	4	US-09-905-125A-290
9	269.5	0.3	1059	4	US-09-902-775A-290
10	269.5	0.3	1059	4	US-09-906-700A-290
11	269.5	0.3	1059	4	US-09-903-603A-290
12	269.5	0.3	1059	4	US-09-904-920A-290

13	269.5	0.3	1059	4	US-09-909-064-290	Sequence 290, App
14	269.5	0.3	1059	4	US-09-905-381A-290	Sequence 290, App
15	269.5	0.3	1059	4	US-09-906-618-290	Sequence 290, App
16	269.5	0.3	1119	4	US-09-907-794A-294	Sequence 294, App
17	269.5	0.3	1119	4	US-09-905-125A-294	Sequence 294, App
18	269.5	0.3	1119	4	US-09-902-775A-294	Sequence 294, App
19	269.5	0.3	1119	4	US-09-906-700-294	Sequence 294, App
20	269.5	0.3	1119	4	US-09-903-603A-294	Sequence 294, App
21	269.5	0.3	1119	4	US-09-904-920A-294	Sequence 294, App
22	269.5	0.3	1119	4	US-09-909-064-294	Sequence 294, App
23	269.5	0.3	1119	4	US-09-905-381A-294	Sequence 294, App
24	269.5	0.3	1119	4	US-09-906-618-294	Sequence 294, App
25	266.5	0.3	1053	4	US-09-513-505-6	Sequence 6, Appli
26	266.5	0.3	1053	4	US-09-513-505-8	Sequence 8, Appli
27	264.5	0.3	605	3	US-09-063-950-5	Sequence 5, Appli
28	261.5	0.3	102	4	US-09-513-999C-8144	Sequence 8144, Ap
29	254.5	0.3	1112	3	US-09-353-585-2	Sequence 2, Appli
30	249.5	0.3	1112	3	US-09-353-585-3	Sequence 3, Appli
31	247	0.3	84	3	US-09-420-592A-9	Sequence 9, Appli
32	247	0.3	84	4	US-09-985-442-9	Sequence 9, Appli
33	247	0.3	84	4	US-09-983-580-9	Sequence 9, Appli
34	241	0.3	84	3	US-09-420-592A-11	Sequence 11, Appli
35	241	0.3	84	4	US-09-985-442-11	Sequence 11, Appli
36	241	0.3	84	4	US-09-983-580-11	Sequence 11, Appli
37	241	0.3	160	4	US-09-543-681A-8310	Sequence 8310, Ap
38	239	0.3	112	4	US-09-543-681A-8319	Sequence 8319, Ap
39	238.5	0.3	605	1	US-08-190-802A-49	Sequence 49, Appli
40	238.5	0.3	605	3	US-08-477-346-49	Sequence 49, Appli
41	238.5	0.3	605	3	US-08-473-089-49	Sequence 49, Appli
42	238.5	0.3	605	4	US-08-487-072A-49	Sequence 49, Appli
43	238.5	0.3	605	4	US-09-538-092-1087	Sequence 1087, Ap
44	238.5	0.3	623	4	US-09-949-016-10995	Sequence 10995, A
45	237.5	0.3	603	1	US-08-190-802A-50	Sequence 50, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-9438
Sequence 9438, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTUR, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9438
LENGTH: 844
TYPE: PRT
ORGANISM: Human
US-09-949-016-9438

Alignment Scores:
Pred. No.: 3.04e-237
Score: 2592.00
Percent Similarity: 74.17%
Best Local Similarity: 62.38%
Query Match: 2.98%
DB: 4
Gaps: 8

US-09-396-985B-48 (1-50000) x US-09-949-016-9438 (1-844)
37433 ACATATCACTGCTTATATGATCCAGTATGATCTTGAAATGATTTTCTAATGAT 37492

Db 42 ThrTyrGln-----CysMetGluLeuAsnPheTyrLysIleProAsp 55
Qy 37493 TTGGCTGCTGACATAGTGTAGTATTATCATCTAGTACAGTGTGAAATAACAAAT 37552
Db 56 AsnLeuPro-----PheSerThrLysAsnLeuAsp 65
Qy 37553 CTGCAGAGTTCCTCTCGTGCATACACCATCATCACTGTTTGGCTGTGACAGTTTCTC 37612
Db 66 LeuSerPheAsnProLeuArgHis-----LeuGlySerTyrSerPhe--- 79
Qy 37613 TTACAAATAACATGATATCATATCTGTTGATCATAGTATGATGAGGACGTGTATGT 37672
Db 79 ----- 79
Qy 37673 CATTAGAAAGGTTTTTTTTTTCAGCAAAATAACATAATGTGATCTCTTTGGCCATAGC 37732
Db 80 -----PheSerPheProGluLeuGlnValLeuAspLeuSer-----Arg 92
Qy 37733 TTGTAAATTGAAACAATTGAAAGACAGGACATGAGCTTTACACCACTCTCAACTG 37792
Db 93 CysGluLysGlnTrpLysIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeu 112
Qy 37793 ATACTGACAGGAAACCTATCCAGAGTTCCTCCAGGAAAGTTTCTCTGACATAACAGT 37852
Db 113 IleLeuThrGlyAsnProLysGlnSerLeuHisLeuGlyAlaPheSerGlyLeuSerSer 132
Qy 37853 TTAGAGAACTGCGTGGCTGTGAGACAAATTGGCTCTCTGACAAAGCTTCCATTGGA 37912
Db 133 LeuGlnLysLeuValAlaValGluThrAsnLeuHisLeuGlnLysLeuAsnProLysGly 152
Qy 37913 CAGCTTAATACCTTAAGAAACTCAATGTGCTGACATTTTATACATTCCTGTAAAGTA 37972
Db 153 HisLeuLysThrLeuLysGlnLeuAsnValAlaHisAsnLeuLysGlnSerPheLysLeu 172
Qy 37973 CCTGCATATTTTTCCAATCTGACAGCACTAGTACATGATGATCTTTTATATATAT 38032
Db 173 ProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIle 192
Qy 38033 CAACATTTACTGTCAAGCATTTACAGTTTACGTGTAATAATCCACAGTCAATCTCT 38092
Db 193 GlnSerLysLeuTyrCysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSer 212
Qy 38093 TTACAGATGCTTGAACCCCAATGACTTCATTCAGACCAAGCCCTTCAAGGAATTAG 38152
Db 213 LeuAspLeuSerLeuAsnProMetCysAsnPheLysGlnProGlyAlaPheLysGlnLys 232
Qy 38153 CTCATGAAGTACTGTAGAAGTAAATTTTAAAGTCAATATATATGAAAACTTGCCT 38212
Db 233 LeuHisLysLeuThrIleLeuArgAsnAsnPheAsnSerLeuAsnValMetLysThrCysIle 252
Qy 38213 CAAAACCTGGCTGTTTACAGCTGATGCTGATCTTTGGAGAAATTTAAAGATGAAG 38272
Db 253 GlnLysLeuLysArgLysLeuGlnValHisArgLeuValLeuGlnGlyLysPheArgAsnGly 272
Qy 38273 AATGTGAAATTTTGAACCTCTATATCATGAGAGACTATGATGAGACCATGAGAG 38332
Db 273 AsnLeuGlnLysPheAspLysSerAlaLeuGlnGlnLysCysAsnLeuThrIleGlnGln 292
Qy 38333 TTCAAGTTAATATACATATGATATTTTTCAGATATTTGTAAG--TTCCATTTGCTTG 38389
Db 293 PheArgLeuAlaTyrLysLeuAspLysTyrLysLeuAspArgLysIleLeuAspLeuPheAsnCysLeu 312
Qy 38390 GCGAATGTTTTCGAATGCTCTGCGACAGGTATCTATAAATTTCTAGAAAGATGTTCT 38449
Db 313 ThrAsnValSerSerPheSerLeuValSerValThrIleGlnValGlyAspPheSer 332
Qy 38450 AAAATTTCAAAATGAGCAATCTTATTCATCATTTAGTGAAGTGAACCTTACACT 38509
Db 333 TyrAsnPheGlyTyrGlnHisLeuGlnLeuValAsnCysLysPheGlyGlnPheProHis 352
Qy 38510 CTGATCTACCCCTTTCTTAAAGTTTGACTTTAACTATGAACAAGGCTTATGAGTTT 38569
Db 352 ----- 352

Db 353 LeuLysLeuSerSerLeuLysArgLeuThrPheThrSerAsnLysGlyGlnAlaPhe 372
Qy 38570 AAAAAGTGCCCTTACCAAGCTTCACAGTATCTATGATCTTATGTAAGTGAAGCTT 38629
Db 373 SerGlnValAspLeuProSerLeuGlnPheLeuAspLeuSerLysArgAsnGlyLeuSerPhe 392
Qy 38630 AGTGTGTGCTGTTCTTATTTCTGATTTTGGAAACAAAGCCCTGAGACATTTAGACTCAGC 38689
Db 393 LysGlyCysCysSerGlnSerAspPheGlyThrThrSerLeuLysTyrLeuAspLeuSer 412
Qy 38690 TTCAATGGTCCATCATTTATGATGCCAATTTATGAGGCTTACAAAGCTGACAGCTTG 38749
Db 413 PheAsnGlyValIleThrMetSerSerAsnPheLeuGlnLysLeuGlnLysLeu 432
Qy 38750 GATTTTCAGACCTCTTAAAGAGGTCAAGAAATTCACAGCTTATCCCTTGA 38809
Db 433 AspPheGlnHisSerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArg 452
Qy 38810 AAGCTACTTTCACCTTACATCTCTTATATACACCAAAATTTGATTCGATGATATTT 38869
Db 453 AsnLeuLysTyrLeuAspLysSerHisThrHisThrArgValAlaPheAsnGlyLysPhe 472
Qy 38870 CTGGCTTGAACAGTTCACACATTTAAATAGGCTGGCAATTTCTTCAAGACACACC 38929
Db 473 AsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnAspPhe 492
Qy 38930 CTTTCAAAATGCTTTTGAACACACAAACTTGAACATTCCTGATCTTCTTAATGCA 38989
Db 493 LeuProAspLysLeuThrGlnLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGln 512
Qy 38990 TTGAAACAATATCTTGGGGGATTTTGAACACCTCCATGACTTCAATTTAAATATG 39049
Db 513 LeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMet 532
Qy 39050 AGTCACAACTTATTTGTTTGGATTCATCCCATTTATACCAAGCTGTATCCCTCAGC 39109
Db 533 SerHisAsnAsnPhePheSerLeuAspThrPheProGlyLysCysLeuAsnSerLeuGln 552
Qy 39110 ACTCTGATTTGCAAGTTTCATTCGATAGAGACATCT--AAAGAAATACGCAACATTT 39166
Db 553 ValLeuAspLysTyrSerLeuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPhe 572
Qy 39167 CSAAAGATCTAGCCCTTTCATCTTATCAATCAATTTCTGCTGCTGATATGTAACAT 39226
Db 573 ProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHis 592
Qy 39227 CAGAAATCTCGAGTGGTCAAGAAACAGACAGAGTCTTGGTGAATGTTGAACAAATG 39286
Db 593 GlnSerPheLeuGlnTrpLysIleLysAspGlnArgGlnLeuValGlnValArgMet 612
Qy 39287 ACATGGCAACACCTGTAGAGATGAAATACCTCTGTGTGTGATTTTATATTTCTAC 39346
Db 613 GluCysValThrProSerAspLysGlnLysMetProValLeuSerLeu--AsnIleThr 631
Qy 39347 TGTATATGTACAACAATCATCAGTGTGCTAGTGTGCTGATGTTGTTGATCCACT 39406
Db 632 CysGlnMetCysLysThrIleIleGlyValSerValLeuSerValLeuValSerVal 651
Qy 39407 GTAGCATTTGTGATATACCACTTATTTTCACTGATCACTTATGCTGCTGTTAAAG 39466
Db 652 ValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeuLeuHisGlyCysIleLys 671
Qy 39467 TACAGCAGAGAAACATCTATGATGATGATTTGTATGATCACTGAGTGAAGAGAG 39526
Db 672 TyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAsp 691
Qy 39527 TGGGTGAGATAGCTGCTGAAGAAATTTAGAAAGAGAGTGGCCCTTCACTTGC 39586
Db 692 TrpValArgAsnGlnLeuValLysAsnLeuGlnGlnLysAlaProPheProGlnLeuCys 711
Qy 39587 CTTTCACTACAGACTTATTTCTGCTGATGCAATTTGCTGCAACATCTCAAGAAAGC 39646
Db 712 LeuHisTyrArgAspPheIleProGlyValAlaIleAlaAlaAsnIleIleHisGlnGly 731

```

QY      39647  TTCACAAAGCCCGAAGGTATATGGTAGTGTCTAGACACTTTATTCAGAGCCGTTGG      39706
Db      732   PheHisLysSerArgLysValIleValValSerGlnHisPheIleGlnSerArgTirp      751
QY      39707  TGTATCTTTGAATATATGAGATTGGCTCAAAACATGCGACGTTTCTGAGACCGCGCTCTGGCATC      39766
Db      752   CysIlePheGlnIuYrGluIleIaGlnThrTrpGlnPheLysSerSerArgHisIaGlyIle      771
QY      39767  ATCTCATTTGTCTCTTGAAAGGTTTGAGAACTCCCTGCTGAGCGACAGAGGTGGAATTGTT      39826
Db      772   IlePheIleValLeuGlnLysValIaGluYrThrLeuLeuArgGlnGlnValGlnLeuYr      791
QY      39827  CGCGCTTTCTTGACAAACACCTTACTCGGAATGGAGAGACACATCTCTGGGAGGACATC      39886
Db      792   ArgLeuLeuSerLysArgHisThrIYrLeuGlnITrpgIlnuSpSerValLeuIaYrHisIle      811
QY      39887  TTCTGAGAAAGACTTAATAAAATGCCCTATTTGGATGAGAAAGCCCTCGAATCTTGAGCAACA      39946
Db      812   PheTrpArgTrgArgLeuArgLysValIaLeuLeuAspGlyLysSerTrpAsnProGlnGluYrThr      831

RESULT 2
US-08-514-014-4
: Sequence 4, Application US/08514014
: Patent No. 5707829
: GENERAL INFORMATION:
: APPLICANT: Jacobs, Kenneth
: APPLICANT: McCoy, John
: APPLICANT: Kelleher, Kerry
: APPLICANT: Carlin, McKeough
: TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
: TITLE OF INVENTION: ENCODED THEREBY
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
: STREET: 87 Cambridgepark Drive
: CITY: Cambridge
: STATE: Massachusetts
: COUNTRY: USA
: ZIP: 02140
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/514,014
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Brown, Scott A.
: REGISTRATION NUMBER: 32,724
: REFERENCE/DOCKET NUMBER: GI6000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 498-8224
: TELEFAX: (617) 876-5851
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 661 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-514-014-4

Alignment Scores:
Pred. No.:
Score: 66-38
Percent Similarity: 502.50
Best Local Similarity: 46.31%
Query Match: 27.52%
DB: 0.58%
      1
      18

```

QY	37730	AGGAGGAAATGA	AAACCTTA	GTAAAGCAAGG	ATGGCAATG	GGCTTACACCACTTCAAC	378789						
Db	86	ArgcysglnI	IeasntP	IlehtsgI	uapThr	pheGlnSer	IhIbGlnuSerThr 105						
QY	37790	TTATATCTG	CAGAAACCTTA	TCCAGATTTT	TTCGCCGAGAA	GTTCCTGTGACATA	CA 37849						
Db	106	LeuValIeu	thrcI	uysnPro	IeuleI	ePheMeT	laGlnThrSerIeudsnI	uProl	ys 125				
QY	37850	AGTTAGAGA	ATCTG	TGCTG	AGACAA	AAATGG	CTCTGA	AAAGCTTCC	TAT 37909				
Db	126	SerIeu	yehI	SerPhe	IeuI	IegIn	thrcI	ylIeSer	AsnIeuGlnPheI	leProva 145			
QY	37910	GGACAGT	TTAACCTTA	AAAGAA	CTCATG	GGCTCA	CAATTTAT	TACATTC	CTGTAG 37965				
Db	146	HisAsn	IeuGln	uasnIeu	SerIeu	ylIeuGln	ylSer	AsnIhI	IeSer	IeuIeys 165			
QY	37970	TTACCTG	CATATTTT	TCCATCTG	ACGACCTAG	CAATGATG	ATCTTTCTTA	TAACTAT 38029					
Db	166	PhePro	lyAspPhe	Pro--	--Ala	AsnIeu	lyS	ValIeu	AspPheGln	snIhIa 184			
QY	38030	ATTCAAC	TATTA	CTGTCA	ACGACTTA	CGATTCTA	CGTAAC	TAATCC	AACTCAATCTC 38089				
Db	185	Ile	hI	Sty	ylIe	Ser	ArgI	uAspMet	ArgSerIeuGln	-----AlaIe	snIeu 202		
QY	38090	TCTTTAG	ACATG	CTTTGA	ACCAATG	CACTTCAT	TCAAG	ACCAAG	CTTTAG	GAAT 38149			
Db	203	SerIeu	Asn	Phe	AsnI	ylAsn	snVal	ylGlnI	IeGln	ylAlaPhe	AspSerThr 222		
QY	38150	AACTCC	ATGA	TGACT	CTAAGAG	GTATTTTA	TAGCTCA	AAATTA	TGAAAC	CTTGC 38209			
Db	223	ValPhe	Gln	SerIeu	snPhe	Gln	ylGln	ThrPro	AsnSer	ValIlePhe	snIy--- 241		
QY	38210	CTTCAAA	ACCTG	CTGTTT	TACACG	CCATCG	GTGATCTT	GGAGAA	TTTAA	ATGA 38269			
Db	242	LeuGln	Asn	SerThr	-----Thr	Gln	SerIeu	ThrPhe	Gln	ylThrPhe	Gln	AspIle 258	
QY	38270	AGCAAT	CTGGA	ATTTTGA	ACCCTG	CTATCA	TGAA	GAGCTAT	GTGATG	TGACCA	TTGAT 38329		
Db	259	Asp	Asp	Gln	uAspIle	---Ser	serI	Am	etIeu	ylGln	ylIeu	CysGlnMetSer	ValGln 277
QY	38330	GAGTT	CAGG	TTAACAT	ATACAT	ATATTTT	TGAGT--						


```

Dd 278 Serleuansleu--GlnGlnHisargPheSerapIleSerSerThrPheGlnCys 296
Qy 38387 TTGGGCAATGTTTTCGACATGTCTGCGACAGTGATCTAATAATATCTAGAAAGATGTT 38446
Dd 297 PheThrGlnleuGlnleuAspLeuThrIleAlaThr-----HisleuLysGlyLeu 313
Qy 38447 CCTAAACATTTTCAATGCGAATCTTATCAATCATTTAGA----- 38485
Dd 314 ProSerGlyMetLys-----GlyleuAsnleuLysLysleuValleuSerValAsn 331
Qy 38486 -----TGTCAACTTAAG-----CAGTTTCCCACTCTGAGATCTACCTTT 38524
Dd 332 HisPheargGlnleuCysGlnIleSerAlaIleAsnPheProSerLeuThrHisleuGly 351
Qy 38525 CTAAAGATTGACTTTTAAGTATGACAAAGAGGCTATCATGCTTTTAAAAAGTGCGCCCTA 38584
Dd 352 IleargGlyAsnValLysLysleuHisleuGlyValGlyCysleuGlnLys-----Leu 369
Qy 38585 CCAAGTCTCAGCTATCTAGATCTTATGAGAAATGACATGAGCTTTAGTGTGCTGTTCT 38644
Dd 370 GlyAsnleuGlnThrleuAspLeuSerHisAsnAspIleGluAlaSerAspCysSer 389
Qy 38645 TATTTGATTTGGGCAACAAACAGCTGAGACATTTAGACCTTCAAGTTTATGTCGCATC 38704
Dd 390 LeuGlnleuLysAsnleuSerHisleuGlnThrleuAsnleuSerHisAsnGlnProleu 409
Qy 38705 ---ATTATGAGTGGCAATTTTCATGGGCTTAGAAGAGCTGAGACCTTGATTTTCAGAC 38761
Dd 410 GlyleuGlnSerGlnIleAspLysGlyCysProGlnleuGlnleuAspLeuAlaPhe 429
Qy 38762 TCTACTTAAAAAGGGTCACAGAAATTTCTCAGCTTTTATCCCTTGAAGACTTTTAC 38821
Dd 430 ThrArgleuHisIleAsnAlaProGlnSerProPheGlnAsnleuHisPheleuGlnVal 449
Qy 38822 CTTGACATCTCTTATCTAACAACAAATTTGACTTCGATATTTCTTGCTTGACC 38881
Dd 450 LeuAsnleuThrLysCysPheleuAspThrSerAsnGlnHisleuLeuAlaGlyleuPro 469
Qy 38882 AGTCTCAACACATTTAAAAATGCTGCGCAATCTTTCAAGACACACACCTT-----TCA 38935
Dd 470 ValleuArgHisleuAsnleuLysGlyAsnHisPheGlnAspGlyThrIleThrLysThr 489
Qy 38936 AATGCTTTTGCAACACAAACAACTTGACATCTCTGATCTTTTGAATGTCAATTGGA 38995
Dd 490 AsnleuGlnThrValGlySerleuGlnValleuIleuSerSerCysGlyleuLeu 509
Qy 38996 CAATATCTTGGGGGGATTTTGACACCTTCATGACTTCAATTAATTAATAGATGAC 39055
Dd 510 SerleuAspGlnIleAlaPheHisSerleuGlyLysMetSerHisValAspLeuSerHis 529
Qy 39056 AACATCTAATG-----TTTTTGATTTCA---TCCCATTTAACAAGCTGATTTCCCTC 39106
Dd 530 AsnSerleuThrCysAspSerIleAspSerleuSerHisleuLysGlyIleLys----- 547
Qy 39107 AGCATCTGATTTGACATTTCAATGACATGACATGACATTTAAGAAATATGCAACATTTT 39166
Dd 548 -----LeuAsnleuAlaIleAsnSerIleAsnIleIleSerProAspGlyleuProIle 565
Qy 39167 CCAAGAGTCTAGCTTCTTCAATCTTATCTAACAATTTGTTGCTTGTATATGTAACAT 39226
Dd 566 LeuSerGlnleuSerThrIleAsnleuSerHisAsnProleuAspCysThrCysSerAsn 585
Qy 39227 CAGAAATCTCGACAGTGGGTCAAGAAACAGAGATTTCTTGAGAAATGTTGAACAATG 39286
Dd 586 IleHisPheleuThrTrpLysGlnAsnleuHisLysleuGlnGlySerGlnGlnThr 605
Qy 39287 ACATGTCACACCTGTAGAGATGAAT-----ACCTTCCTTAGTGTGATTTT 39334
Dd 606 ThrCysAlaAsnProProSerleuArgGlyValLysleuSerAspValLysleuSerCys 625
Qy 39335 AATAATCTACCTGTATATGATCAACACATCATCATGCTGTGACAGTGTGATTT 39394
Dd 626 GlyIleThrIleGlyIlePhePheleuIleValPheleuLeuLeuAlaIleLeu 645

```

```

Qy 39395 GTGGATCCACTGATGACATTTCTGATATACCACTTCAATTTCAAGCTG 39442
Dd 646 LeuPhePheAlaValLysTrpLeuLeuArgTrpLysTrpGlnHisIle 661

RESULT 4
US-09-982-308B-23
; Sequence 23, Application US/09982308B
; Patent No. 6531290
; GENERAL INFORMATION:
; APPLICANT: Dalle, Barbara
; APPLICANT: Fan, Xuedong
; APPLICANT: Lundell, Daniel
; APPLICANT: Lunn, Charles A.
; APPLICANT: Tann, Jimmy C.
; APPLICANT: Zavadny, Paul J.
; TITLE OF INVENTION: Mammalian TNF-alpha Convertases
; FILE REFERENCE: JB0601QC
; CURRENT APPLICATION NUMBER: US/09/982,308B
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/156,163
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 08/889,909
; PRIOR FILING DATE: 1997-07-10
; PRIOR APPLICATION NUMBER: 60/021,710
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-308B-23

Alignment Scores:
Pred. No.: 3,13e-34 Length: 784
Score: 464.00 Matches: 207
Percent Similarity: 41.96% Conservative: 122
Best local Similarity: 26.40% Mismatches: 305
Query Match: 0.53% Indels: 150
DB: Gaps: 32

US-09-396-985B-48 (1-50000) x US-09-982-308B-23 (1-784)
Qy 37778 CACCTTCGAACCTTGATATGACAGAAACCTTCCAGAGTTTTCACGAAAGTTTC 37837
Dd 77 AsnleuGlnAlaLeuValleuThrSerAsnGlyLeuAsnThrIleGlnGluAspSerPhe 96
Qy 37838 TCTGGACTAACAAGTTTAGAAGATCTGTGGCTGTGAGACAAAAATTTGGCCTCTGAA 37897
Dd 97 SerSerleuGlySerleuGlnHisleuAspLeuSerTyraAsnTrpLysleuSerAsnleuSer 116
Qy 37898 AGCTTCCTTATGACAGCTTATTAACCTTAAGAACTCAATGTGCTCAATTTTATA 37957
Dd 117 SerSerTrpPheLysProLeuSerSerleuThrPheleuAsnleuLysGlyAsnProLys 136
Qy 37958 CATTCCTGTAACTTCTGCAATTTTCCAAATTTGACGAACCTTAGACATGTGATCTT 38017
Dd 137 LysThrleuGlyGlnThrSerleuPheSerHisleuThrLysSerleuGlnIleLeuArgVal 156
Qy 38018 -----TCTTAATCTAATTAATTAACAATTTACTGTCAACGACTTAGAGTTTCTA 38065
Dd 157 GlyAsnMetAspThrPheThrLysIleGlnArgLysAspPheAlaGlyleuThrPheleu 176
Qy 38066 CGTGAAGATCCACAACTCAATCTCTCTTGAACATGCTTTGAACCAATTTGACTTCA 38125
Dd 177 GlnGlu-----LeuGlnIleAspAlaSerAspLeuGlnSerLys 189
Qy 38126 CAAGACCAAGCTTTGAGGAATTT-----AGCTC 38155
Dd 190 GlnProLysSerleuLysSerIleGlnAsnValSerHisleuIleuHisMetLysGln 209
Qy 38156 CATGAACGACTTAAGAGGTAATTTTAATAGCTCAAAATTAATGAAGAACTTGCTTCA 38215

```

Db 210 HistLeuLeuLeuLeuGluIlePheValAlaPheValThrSerSerValGlu---CysLeuGlu 228
Qy 38216 -----AACCTGGCTGTTTACAGCTCCATCGGTTGATCTTGGAGAAATTTAAA 38263
Db 229 LeuArgAspThrAspLeuAspThrPheHisPheSerGluLeuSerThrGlyGluThrAsn 248
Qy 38264 GAT-----GAAAGGAATCTGGAAATTTTGTGAACCTCTATCATCGAA 38305
Db 249 SerLeuIleuValysPheThrPheArgAsnValIleThrAspGluSerLeuPheGln 268
Qy 38306 -----GACTATGATGATGACCATTTGATGATTCAGG 38338
Db 269 ValMetLysLeuLeuAsnGlnIleSerGlyLeuLeuGluLeuPheAspArgCysThr 288
Qy 38339 TTAAACATATACAAATGATTTT-----TCAGATGATATTTGTAAGTTCCATTCCTGGCG 38392
Db 289 LeuAsnGlyValGlyAsnPheArgAlaSerAspAsn----- 300
Qy 38393 AATGTTCTGCAATGCTCTGGCAGGATGATCTATAAATATCTAGAAGATGTTCTTAA 38452
Db 301 -----AspArgValIleAsp 305
Qy 38453 CATTTCAATGGCAATCTTATCATCATGATGCACTTAAGCAAGTTCCAACTCTG 38512
Db 306 ProGlyLysValGluThrLeuThrIleArgArgLeuHisIleProArgPheThrLeuPhe 325
Qy 38513 ---GATCTACCTTTCTTAAAAAGTTTGACTTTAACTATGAACAAAGGCTCATAGCTTTT 38569
Db 326 TyrAspLeuSerThrLeuTyrSerLeuThrGluArgIleHisValGluAsn 345
Qy 38570 AAAAAAGG-----GCCCTACCAAGCTTCAGCTATCTA 38602
Db 346 SerLysValPheLeuValProCysLeuLeuSerGlnHisLeuLysSerLeuGluTyrLeu 365
Qy 38603 GATCTTGTAGTAAATGCA-----CTGAGCTTTAGTGGTGC---TGTTCT 38644
Db 366 AspLeuSerGluAsnLeuMetValGluGluTyrLeuLysAsnSerAlaCysGluAspAla 385
Qy 38645 TATTCTGATTTGGGACAAACAGCCTGAGA-----CACTTA---GACCTCAGCTTCAT 38695
Db 386 TyrProSerLeuGlnThrLeuIleLeuArgGluAsnHisIleuAlaSerLeuGluLysThr 405
Qy 38696 GGTCGCACTATTAGAGGCCAATTTATGCGTCTAGAGAGCGTCGAGCACTGGATTTT 38755
Db 406 GlyIuThrLeuLeuThr-----LeuLysAsnLeuThrAsnIleAspIle 420
Qy 38756 CAGCACTCTACTTTAAAAAGGTCACAGAAATTCAGCGTTCTTATCCCTTGAAGCTA 38815
Db 421 SerLysAsnSerPheHisSerMetProGluThrCysGlnTrp-----ProGluLysMet 438
Qy 38816 CTTTACCTGACATCTCTTATCTAACACCAAAATGACCTTCGATGATATTTCTTGGC 38875
Db 439 LysTyrLeuAsnLeuSerSerThr----- 446
Qy 38876 TTGACACAGTCCACACACTTAATAATGCTGGCAATCTTCAAGAACAACCCCTTCA 38935
Db 447 -----ArgIleHisSerValThr 452
Qy 38936 AATGCTTTTGCAACACAACTTGACATTCCTGATCTTTTAAATGTCATTTGAA 38995
Db 453 GlyCysIleProLysThr-----LeuGluIleLeuAspValSerAsnAsnLeuAsn 470
Qy 38996 CAATATCTTGGGGGGATTTTGAACCCCTGCATGACTTCATATTAATATAGTCAC 39055
Db 471 LeuPheSerLeu-----AsnLeuProGlnLeuLysGluLeuTyrIleSerArg 486
Qy 39056 AACCAATCATGTTTGGATTATCCATATATAACGCGTGTATCCCTCAGACACTT 39115
Db 487 AsnLysLeuMetThrLeuProAspAla-----SerLeuLeuProMetLeuLeuValLeu 504
Qy 39116 GATTGCAAGTTTCAATCGCATAGAGACA---TCTAAGGAAATATGCAACATTTTCCAAG 39172

Db 505 LysIleSerArgAsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe---His 523
Qy 39173 AGCTAGACCTTTCTTCAATCTTACTAATCAATTCCTGTTGCTTGTATATGTAACATGAGAA 39232
Db 524 ThrLeuLysThrLeuGluAlaGlyGlyAsnAsnPheIleCysSerCysGlu----- 540
Qy 39233 TTCCTCAGTGGTGCACAGAAAGCAAGATTCCTTGGTGAATGTT----- 39277
Db 541 PheLeuSerPheThrGlnGlnGluin---GlnAlaLeuAlaLysValLeuIleAspTrpPro 559
Qy 39278 GAACAAAATGACATGTCGAACACCTGTAGAGATGAATACCTCTTACTGTTGCAT----- 39331
Db 560 AlaAsnTyrLeuLysAspSerProSerHisLeuValArgGlyGlnGlnValGlnAspValArg 579
Qy 39332 TTTAATATATCTACCTGTTATATATGTAACAGACATCATCAGTGTGTCAGTGCAGTGTG 39391
Db 580 LeuSerValSerLysCysHisArgIleAlaLeuValSerLysCysValAlaLeuPhe 599
Qy 39392 ATTGTGGTATCCACTGTAGCACTTCTGATATACCACTTC-----TATTTTCAC 39439
Db 600 LeuLeuIleLeuLeuThrGlyValLeuCysHisArgPheHisGlyLeuTyrTrpMetLys 619
Qy 39440 CTGATA-----CTTATGCTGCTGTAAAGATGACGACGAGAGAAAGC----- 39484
Db 620 MetMetTrpAlaThrLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIle 639
Qy 39485 ATCTATGATGCAATTTGTGATCTCTGAGTCAGACAAATAGAGACTGGGTGAGAAATGAGCTG 39544
Db 640 CysTyrAspAlaPheValSerTyrSerGluArgAspAlaTyrTrpValGluAsnLeuMet 659
Qy 39545 GTAAGATTTTGAAGAAGAGAGTGCCTGCTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 39604
Db 660 ValGlnGluLeuLysAsnPheAsnProProPheLysLeuCysLeuHisIleLysArgAspPhe 679
Qy 39605 ATTCCTGCTGTAGCCATTCCTGTCACCATCATCATCAGAGAGCTTCCACAAAGCCGAGAG 39664
Db 680 IleProGlyLysTrpIleIleAspAsnIleIle---AspSerIleGluLysSerHisLys 698
Qy 39665 GTTATGCTGATGCTGTAGACACTTATTCACAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 39724
Db 699 ThrValPheValLeuSerGluAsnPheValLysSerGluTyrCysLysTyrGluLeuAsp 718
Qy 39725 ATTGCTCAAAATGAGGAGGAGTTCTGAGACGCGCTGTCATCTTCACTTATGCTGCTGCTGAG 39784
Db 719 PheSerHisPheArgLeuPheAspGluAsnAsnAspAlaIleLeuIleLeuLeuGlu 738
Qy 39785 AAGGTGAGAGTCCCTGCTGAGGACAGCAG---GTGAAATGTATGCGCTTTCAGACA 39841
Db 739 ProIleGluLysLysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThr 758
Qy 39842 AACACCTACTGGAATGGGAGGACAAATCCCTGGGGAGGACATCTTCTGAGAGAGCTT 39901
Db 759 LysThrTyrLeuGluTyrProMetAspGluAlaGlnArgGluGlyPheTrpValAsnLeu 778
Qy 39902 AAAAATGCCTTA 39913
Db 779 ArgAlaAlaIle 782

RESULT 5
US-09-949-016-8799
Sequence 8799, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03

```

; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8799
; LENGTH: 775
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8799

Alignment Scores:
Pred. No.: 2,296-28      Length: 775
Score: 402.50           Matches: 196
Percent Similarity: 40.08% Conservative: 107
Best Local Similarity: 25.93% Mismatch: 276
Query Match: 0.46%      Indels: 177
DB: 4                   Gaps: 31

US-09-396-985b-48 (1-50000) x US-09-949-016-8799 (1-775)

QY 37778 CACCTCTCAAACTTGATCTGACAGAGAAACCTATCCAGAGTTTCCCGAGAGTTTC 37837
DB 112 AsnLeuGlnAlaLeuValLeuThrSerAsnGlyIleAsnThrIleGluGlnAspSerPhe 131
QY 37838 TCTGACTAACAAGTTTAGAGATCTGGTGGCTGAGACAGAAATGGCGCTCTAGAA 37897
DB 132 SerSerLeuGlySerLeuGlnHisLeuAspLeuSerTyraSerTyLeuSerAsnLeuSer 151
QY 37898 AGCTTCCTATTGACAGACTTATTAACCTTAAAGAACTCAATGAGTGGCTCACAATTTTATA 37957
DB 152 SerSerTyPheLeuProLeuSerSerLeuThrPheLeuAsnLeuGlnGlyAsnProTy 171
QY 37958 CATTCCTGTAAGTAACTGCGATATTTTCCATCTGACAGAACTTGACATGAGATCTT 38017
DB 172 LysThrLeuGlyGluThrSerLeuPheSerHisLeuThrLysLeuGlnIleLeuArgVal 191
QY 38018 TCTTATTAACATATTCACAACTATTAAGTCTGACAGACTTACAGTTTCTA 38065
DB 192 GlyAsnMetAspThrPheThrLysIleGlnArgLysAspPheAlaGlyLeuThrPheLeu 211
QY 38066 CGTGAAAATCCACAGAGCAATCTCTTTAGACATGCTTTGAAACCAATTGACTTCATT 38125
DB 212 GluGlu-----LeuGlnIleAspAlaSerAspLeuGlnSerTy 224
QY 38126 CAAGCAAGCCTTTCAGAGAAAT-----AAGCTC 38155
DB 225 GluProLysSerLeuLysSerIleGlnAsnValSerHisLeuIleLeuHisMetLysGln 244
QY 38156 CATGACACTGACTCTAAGAGTAAATTTTAAAGCTCAAAATATATGAAAACTTGACCTTCA 38215
DB 245 HisIleLeuLeuLeuGlnIlePheValAspValThrSerSerValGlu---CysLeuGln 263
QY 38216 -----ACCTGCGCTGGTTTACACGTCATCGGTTGATCTGGAGAAATTTTAA 38263
DB 264 LeuArgAspThrAspLeuAspThrPheHisPheSerGluLeuSerThrGlyGlnThrAsn 283
QY 38264 GAT-----GAAAGAACTCGGAAATTTTGAACCTCTATCATGGAA 38305
DB 284 SerLeuIleLysLysPheThrPheArgAsnValLysIleThrAspGluSerLeuPheGln 303
QY 38306 -----GACATGATGTAGTGACCATGATGATGATGAGTTCAGG 38338
DB 304 ValMetLysLeuLeuAsnGlnIleSerGlyLeuLeuGlnLeuGluPheAspSerPheThr 323
QY 38339 TTAACATATACAAATGATTTT-----TCAGATGATTTGTTAAGTTCCATTTGCTTGGCG 38392
DB 324 LeuAsnGlyValGlyAsnPheArgLysSerAspAsn----- 335
QY 38393 AATGTTTCTGCAATGCTCTGCGAGGTGATATATAAATATCTAGAAGATGTTCTTAA 38452
DB 336 -----AspArgValIleAsp 340
QY 38453 CATTTCAATGAGCAATCTTATTCATCATATAGATGTCAATTAGACAGTTTCAACTCTG 38512

```

```

DB 341 ProGlyLysValGluThrLeuThrIleArgArgLeuHisIleProArgPheTyLeuPhe 360
QY 38513 ---GATCTACCTTTCTTAAAGTTTGACTTAACTATGAACAAGGCTCTATCAGTTT 38569
DB 361 TyrAspLeuSerThrLeuTySerLeuThrGluArgValLysArgIleThrValGlnAsn 380
QY 38570 AAAAAAGT-----GCCCTACCAAGCTCAGCTATCTA 38602
DB 381 SerLysValPheLeuValProCysLeuLeuSerGlnHisLeuLysSerLeuGlnTyLeu 400
QY 38603 GATCTTAGTACAAATGCA-----CTGAGCTTTAGTGTTC---TGTTCT 38644
DB 401 AspLeuSerGluAsnLeuMetValGluGluTyLeuLysAsnSerAlaCysGlnAspAla 420
QY 38645 TATTCTGATTTGGGACAAACAGCTGAGA-----CACTTA---GACCTCAGCTTCAAT 38695
DB 421 TrpProSerLeuGlnThrLeuIleLeuArgGlnAsnHisLeuAlaSerLeuGlnLysThr 440
QY 38696 GATGCAATCATTTATGAGGCCAATTTGATGGGCTTAGAAGAGCTGACAGCTGGATTTT 38755
DB 441 GlyGluThrLeuLeuThr-----LeuLysAsnLeuThrAsnIleAspIle 455
QY 38756 CAGCACTCTACTTAAAGGCTCAGCAAAATTCACGGCTTCTTATCCCTGAAAAGCTA 38815
DB 456 SerLysAsnSerPheHisSerMetProGluThrCysGlnTrp-----ProGluLysMet 473
QY 38816 CTTTACCTTGACATCTCTTATATCTTAAACCAAAATTGACCTTGATATTTCTTGCC 38875
DB 474 LysTyLeuAsnLeuSerSerThr----- 481
QY 38876 TTGACAGCTCAACACATTTAAATGCGTGGCAATCTTCAAGAACACACCTTCA 38935
DB 482 -----ArgIleHisSerValThr 487
QY 38936 AATGCTTTTGCAACACACAACTGACATCTCGATCTTGTAAATGTCAATGTGAA 38995
DB 488 GlyCysIleProLysThr-----LeuGlnIleLeuAspValSerAsnAsnAsnLeuAsn 505
QY 38996 CAATATCTTGGGGGATTTTGAACACCTCCATGACTTCATATTTAAATATGAGTCAC 39055
DB 506 LeuPheSerLeu-----AsnLeuProIleLeuLysGluLeuTyLysSerArg 521
QY 39056 AACATCTATTTGTTTGAATTCATCCCATTTATACACGCTGATTCCTCAGACCTCTT 39115
DB 522 AsnLysLeuMetThrLeuProAspAla-----SerLeuLeuProMetLeuLeuValLeu 539
QY 39116 GATTGACGTTTCAATCCATGAGACA---TCTAAGGAAATACCTGCAACATTTTCAAG 39172
DB 540 LysIleSerArgAsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe---His 558
QY 39173 AGCTGACCTTCTTCAATCTTACTTAACAATTTGCTGCTGTATATGAAATCAGAAA 39232
DB 559 ThrLeuLysThrLeuGlnAlaGlyLysAsnHisPheIleCysSerCysGlu----- 575
QY 39233 TTCTGAGAGGGGTCAAGAAACAGACAGCATCTTGGTGAATTT----- 39277
DB 576 PheLeuSerPheThrGlnGlnGlu---GlnAlaLeuAlaLysValLeuIleAspTrpPro 594
QY 39278 GAACAAATGACATGTGACACACCTGTAGAGATGAATCCTCTTATGTTGATTTTAAAT 39337
DB 595 AlaAsnTyLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArg 614
QY 39338 AATTTACCTGTTATATGATACAGACAAATCATCATCAGTGTGACGTGATGATGTG 39397
DB 615 LeuSerValSerGluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeu--- 633
QY 39398 GTATCACTGAGATTTTGATATATACCATCTTATTTTACCTCGATATCTTATGCTGGC 39457
DB 634 -----PheLeuLeuIleLeuLeuThrGly 641
QY 39458 ---TGTAAGAGTAC----- 39469

```

Db	642	ValLeuCyhriIaRgrhnehiIsgIyleuTrpYrMeLyMeMeMetrPaIaTrpIeuIn	661
Qy	39470	-----ACGAGAGAGAAAGCAATCATGATGATTCGTTGGT	39502
Db	662	AlaIyArgrLySPRoArgrLySaIaProSerArg-AsnIleCyetrYrAepIaIaPheVal	680
Qy	39503	ATCTACTCGAGTCAAGAAATGAGACTGGGTGAGAAAGAGACTGGTAAGAAATTAAAGAA	39562
Db	681	SerYrIserIuIaRgrAepaIaIaYrTrpIvaGIuAsnIleMetValGIuIuIeuGIuAsn	700
Qy	39563	GGAGTGGCCCGCTTTTCACTGCTGCTTCACTACAGAGACTTTATTCGTGGTAGCCATT	39622
Db	701	PheAsnProIroPheLySleCySleuHIsLyArhAepPheIleProGIuLyStrIle	720
Qy	39623	GCTGCCAACATCATCCAGAGAGCTTCCACAGAGCCGGAAGGTATTTGCTAGTGTCT	39682
Db	721	IleAepIuIeIle--AepSerIleGIuLySerhIeIyetrhValPheValIeuSer	739
Qy	39683	AGACACTTTATTCAGAGCCGTGGTGTATCTTTGAATATGAGATTGCTCAACATGGCAG	39742
Db	740	GIuAsnIheValIySerGIuTrpCySlyrGIuIeAspPheSerhIaPheArgrIeu	759
Qy	39743	TTTTGAGCAGCGGCTCGCATCATCTTCATTCCTTGAGAGGTT	39790
Db	760	PheAepGIuAsnAepaIaIaIeIleuIeIeuGIuProIle	775
RESULT 6			
US-09-513-999C-7214			
; Sequence 7214, Application US/09513999C			
; Patent No. 6783961			
; GENERAL INFORMATION:			
; APPLICANT: Dumas Milne Edwards, J. B.			
; APPLICANT: Duclert, A.			
; APPLICANT: Giordano, J. Y.			
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.			
; Patent No. 6783961			
; FILE REFERENCE: 59.US2.REG			
; CURRENT APPLICATION NUMBER: US/09/513.999C			
; CURRENT FILING DATE: 2000-02-24			
; PRIOR APPLICATION NUMBER: US 60/122,487			
; PRIOR FILING DATE: 1999-02-26			
; NUMBER OF SEQ ID NOS: 36681			
; SOFTWARE: Patent.pm			
; SEQ ID NO 7214			
; LENGTH: 129			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: UNSURE			
; LOCATION: 108			
; OTHER INFORMATION: Xaa=Ala or Asp or Gly			
US-09-513-999C-7214			
Alignment Scores:			
Pred. No.:		2.39e-24	Length: 129
Score:		365.50	Matches: 73
Percent Similarity:		70.54%	Conservative: 18
Best Local Similarity:		56.59%	Mismatches: 37
Query Match:		0.42%	Indels: 2
DB:		4	Gaps: 1
US-09-396-985B-48 (1-50000) x US-09-513-999C-7214 (1-129)			
Qy	36357	CTTAAGAGAAGAAATTCTCAACTGAGAGATCTGATGATGACTGAAGAACTGAACCTAAAAAAATGT	36298
Db	1	MetAepArgrhIaPheSerLySGIuAspIleYrAlaIaLySlyShIShetLySlyCyS	20
Qy	36297	TTAACTACTTATGATCATCAGGGAATCAATCAATCAAAACAACCTGTATATTCACATTTCACA	36238
Db	21	SerSerSerIeuAlaIleArgrGIuMetChnIleYetrhTrhMetArgrYrhiSleuThr	40
Qy	36237	CCAGTCGATGACTTAAGATCAAAAACTCAAGTGACAGCAGATGCTCGCAAG-TCGTAGA	36179

Dd		41	ProValArgMetAlaIleLeuYsbSerGIyAenAmnArgCysTrpArgLysCysGly	60
Oy		36178	GAAGAGAACTCTTCATCGTGGCAAACTGTAACTATAATACACTCTGGAAA ::: :::	36119
Dd		61	GluIleArgThrLeuLeuHisCysTrpTPRAspCysLyLeuValGlnProLeuTrpLys	80
Oy		36118	TGCATTGGTGCTCCCTCGAAAAATTGACACGTACTCTACCGAGAGATCCACCATPACA ::: :::	36059
Oy		36058	CTCCAAAGCAAAATATCCAGATGAT--GCTTCACCTTTGTAATATAGACACATGCTTACT 	36002
Dd		101	LeuLeuGluLysIleTryProLys**TyrrLysSerCysCytylLysAspHrCysThrHis	120
Oy		36001	ATGTTCAATACCACTTTATTATTAATAATA	35975
Dd		121	MetPhelIleAlaIleuPheThrIle	129
RESULT 7				
		US-09-907-794A-290		
/		Sequence 290, Application US/09907794A		
/		Patent No. 6635468		
/		GENERAL INFORMATION:		
/		APPLICANT: Genentech, Inc.		
/		APPLICANT: Ashkenazi, Avi		
/		APPLICANT: Botstein, David		
/		APPLICANT: Desnoyers, Luc		
/		APPLICANT: Eaton, Dan L.		
/		APPLICANT: Ferrara, Napoleone		
/		APPLICANT: Filvaroff, Ellen		
/		APPLICANT: Fong, Sherman		
/		APPLICANT: Gao, Wei-Qiang		
/		APPLICANT: Garber, Hanspeter		
/		APPLICANT: Gerritsen, Mary E.		
/		APPLICANT: Goddard, A.		
/		APPLICANT: Grimaldi, Christopher J.		
/		APPLICANT: Gurney, Austin L.		
/		APPLICANT: Hillan, Kenneth, J.		
/		APPLICANT: Kljavin, Ivar J.		
/		APPLICANT: Mather, Jennie P.		
/		APPLICANT: Pan, James		
/		APPLICANT: Paoni, Nicholas F.		
/		APPLICANT: Roy, Margaret Ann		
/		APPLICANT: Stewart, Timothy A.		
/		APPLICANT: Tumas, Daniel		
/		APPLICANT: Williams, P. Mickey		
/		APPLICANT: Wood, William, I.		
/		TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic		
/		FILE REFERENCE: 10466-14		
/		CURRENT APPLICATION NUMBER: US/09/907,794A		
/		PRIOR APPLICATION NUMBER: PCT/US00/04414		
/		PRIOR FILING DATE: 2000-02-22		
/		PRIOR APPLICATION NUMBER: US 60/143,048		
/		PRIOR FILING DATE: 1999-07-07		
/		PRIOR APPLICATION NUMBER: US 60/145,698		
/		PRIOR FILING DATE: 1999-07-26		
/		PRIOR APPLICATION NUMBER: US 60/146,222		
/		PRIOR FILING DATE: 1999-07-28		
/		PRIOR APPLICATION NUMBER: PCT/US99/20594		
/		PRIOR FILING DATE: 1999-09-08		
/		PRIOR APPLICATION NUMBER: PCT/US99/20944		
/		PRIOR FILING DATE: 1999-09-13		
/		PRIOR APPLICATION NUMBER: PCT/US99/21090		
/		PRIOR FILING DATE: 1999-09-15		
/		PRIOR APPLICATION NUMBER: PCT/US99/21547		
/		PRIOR FILING DATE: 1999-09-15		
/		PRIOR APPLICATION NUMBER: PCT/US99/23089		
/		PRIOR FILING DATE: 1999-10-05		
/		PRIOR APPLICATION NUMBER: PCT/US99/20214		
/		PRIOR FILING DATE: 1999-11-29		


```

; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 290
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-125A-290

Alignment Scores:
Pred. No.:      1,35e-15      Length:      1059
Score:          269.50      Matches:      101
Percent Similarity: 42.78%      Conservative: 56
Best Local Similarity: 27.52%      Mismatches: 135
Query Match:      0.31%      Indels:      75
DB:               4          Gaps:      15

US-09-396-985B-48 (1-50000) x US-09-905-125A-290 (1-1059)

QY      38390 GCGAATGTTTCGCAATGCTCTGCGAGGTGATCTATAAAATATCTAGAAGATGTTCTT 38449
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      61 AlaleuSerLeuSerLeuSerLeuSerLeuSerLeuSerLeuSerLeuSerLeuSerLeu 78
QY      38450 AAAAATTTCAAA---TGCAATCCTTATCAATCAATTCATGATTCACATTTAGACAG----- 38500
      ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      79 GluHisLeuysGluPheGlnSerLeuGluThrLeuSpleuSerSerSerSerSerSerSer 98
QY      38501 -----TTTCCAACTCTGAGTCACTACCCCTTTCTT----- 38527
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      99 GluLeuGlnThrAlaPheProAlaLeuGlnLeuysrTyLeuSpleuSerSerSerSer 118
QY      38528 ----- 38545
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      119 ValThrSerMetGluProGlyTyPheAspAsnLeuAlaSerThrLeuLeuValLeuLys 138
QY      38546 ATGAACAAGGGGTCTATGATTTT-----AAAAAGTGGCCCTTACCAAGTCTCAGC 38596
      ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      139 LeuAsnTrpAsnArgIleSerAlaIleProProIleSerPheLysProGlnLeuGln 158
QY      38597 TATCTAGATCTTAGAGAAATGACCTGAGCTTTAGTGCTGCTGCTGCTTATCTGATTTG 38656
      ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      159 HisLeuGluLeuAsnArgAsnLysIleLysAsnValSerGlyLeuThrPheGlnGlyLeu 178
QY      38657 GGAACAAACAGCCTGAGACACTTGAACCTTCAGCTTCAATGTTGCATC---ATTATGAGT 38713
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

```

Db      179 Gly-----AlaLeuysSerLeuysMetGlnArgAsnGlyValThrLysLeuMetAsp 196
QY      38714 GCCAATTTCATGGCTCTAGAGAGCTGACAGCAGCTGATTTTACAGCATCTTACTTAA 38773
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      197 GlyAlaPheTrpGlyLeuSerAsnMetGluIleLeuGlnLeuAspHisAsnLeuThr 216
QY      38774 AGGGTCACAGAAATTC----- 38788
      ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      217 GluIleThrLysGlyTrpLeuTyrglyLeuLeuMetLeuGlnGluLeuHisLeuSerGln 236
QY      38789 -----TCAGCGTCTTATTCCTTGAAGAACTTACTTTACCTT 38824
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      237 AsnAlaIleAsnArgIleSerProAspAlaTrpGluPheCysGlnLysLeuSerGluLeu 256
QY      38825 GACATCTCTTATCTAAC---ACCAAAATTTGATTTGATGCTTATTTCTTGGCTTGACC 38881
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      257 AspLeuThrPheAsnHisLeuSerArgLeuAsp---AspSerSerPheLeuGlyLeuSer 275
QY      38882 AGTCTCAACACATTAATAATGGCTGGCAATTTCTTCAAGACAAACACCCCTTCAAAATGTC 38941
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      276 LeuLeuAsnThrLeuHisIle---GlyAsnAsnArgValSerTyrlleAlaAspCysAla 294
QY      38942 TTTGCAAAACAAACAACTTGACATTCCTGATCTTTCTTAATGTCATTTGAAACAATA 39001
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      295 PheArgGlyLeuSerSerLeuLysThrLeuAspLeuLysAsn-----AangluIle 311
QY      39002 TCTTTGG-----GGGATTTTGAACACCTCCATAGACTTCAATTTA 39043
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      312 SerTrpThrIleGluAspMetAsnGlyAlaPheSerGlyLeuAspLysLeuArgLeu 331
QY      39044 AATATGAGTCACAAACATCTATTGTTTGGATTCATCCATTAACGATTAACGATTTCC 39103
      ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      332 IleLeuGlnGlyAsnArgIleArgSerIleThrLysAlaIleThrGlyLeuAspAla 351
QY      39104 CTGACACTCTTGATTTGACGTTTCAATTCGATTAAGACATCTAAGAAATCTGCAACAT 39163
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      352 LeuGluHisLeuAspLeuSerAspAsnAlaIleMetSerLeuGlnGlyAsnAlaPheSer 371
QY      39164 TTTCCAAAGGCTGAGCTTCTTCAATCTTACATCAATCTCTGCTGCTATATGAA 39223
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      372 GluMetLysLysLeuGlnGlnLeuHisLeuAsnThrSerSerLeuLysAspCysGln 391
QY      39224 CATCAGAAATTCCTGACAGTGGGTCAAGAACAGAG---CAGTTCTTGGTGAATGTTGAA 39280
      ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      392 LeuLysTrpLeuProGlnTrpValAlaGluAsnAsnPheGlnSerPheValAsnAla--- 410
QY      39281 CAAATGACATGTGCACACCT 39301
      ::|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db      411 -----SerCysAlaHisPro 415

RESULT 9
US-09-902-775A-290
; Sequence 290, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Goddard, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.

```

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 290
LENGTH: 1059
TYPE: PRT
ORGANISM: Homo Sapien
US-09-902-775A-290
Alignment Scores:
Pred. No.: 1,35e-15 Length: 1059
Score: 269.50 Matches: 101
Percent Similarity: 42.78% Conservative: 56
Best Local Similarity: 27.52% Mismatches: 135
Query Match: 0.31% Indels: 75
DB: 4 Gaps: 15
US-09-396-985B-48 (1-50000) x US-09-902-775A-290 (1-1059)
QY 38390 GCCAATTTCTGCAATGCTCTGCGACGTCATCTATAAATATCTAGAAAGATTCTTCT 38449
DB 61 AAlasnllethrleuSerleuAlaGlyAsnArglle-----ValGluileleuPro 78
QY 38450 AAACATTTCAAA--TGCGAATCCTTATCATCATTTAGATGATCAACTTAAGCAG----- 38500
DB 79 GluhlsleuylsglupneglnSerleuGluThrleuAspleuSerSerAsnAsnIleSer 98
QY 38501 -----TTTCCAACTCTGGATCTACCTTTCTT----- 38527

DB 99 GluleuGlnThrAlaPheProAlaLeuGlnleuLysTyrlleuTyrlleuAsnSerAsnArg 118
QY 38528 -----AAAGTTGACTTTAACT 38545
DB 119 ValIleSerMetGluProGlyTyrlPheAspAsnleuAlaAsnThrleuValleuLys 138
QY 38546 ATGAACAAGAGGCTATACATTTT-----AAAAAGTGGCCCTACCAAGTCTCAGC 38596
DB 139 leuAsnArgAsnArglleSerAlaIleProProLysMetPheLysleuProGlnleuGln 158
QY 38597 TATCTAATCTTACTAGAAATGACGTAGCTTTAGTGGTGTCTTCTTATCTGATTTG 38656
DB 159 HisleuGlnleuAsnArgAsnLysIleLysAsnValAspGlyleuThrPheGlnGlyleu 178
QY 38657 GGACAACAAGCCGGAACACTTAGCTTACCTGACCTTACAGTTCAGTGGCATT-----ATTATGAGT 38713
DB 179 Gly-----AlaLeuLysSerleuLysMetGlnArgAsnGlyValThrLysleuMetAsp 196
QY 38714 GCCAATTTTCATGGCTCTAGAAAGAGCTGACGACCTGGATTTTTCAGCACTTACTTTAAA 38773
DB 197 GlyAlaPheThrPglLysleuSerAsnMetGluIleleuGlnleuAspHisAsnleuThr 216
QY 38774 AGGCTCACAGAAATTC----- 38788
DB 217 GluIleThrLysGlyTrpLysTyrlleuLysleuMetleuGlnGluLeuHisleuSerGln 236
QY 38789 -----TCAGCGTCTTATCCCTTGAAGAGTCTTAACTT 38824
DB 237 AsnAlaIleAsnArglleSerProAspAlaIleTrpGluPheCysGlnLysleuSerGluLeu 256
QY 38825 GACATCTCTTAATCTAAC---ACCAAAATTCAGTCTGATGATATTTTCTTGGCTTGAC 38881
DB 257 AspLeuThrPheAsnHisleuSerArgleuAsp---AspSerSerPheleuGlyleuSer 275
QY 38882 AGTCTAACACATTAATAAATGGCTGGCAATTTCTTCAAGACAAACCCCTTCAAAATGTC 38941
DB 276 leuLeuAsnThrleuHisIle---GlyAsnAsnArgValSerTyrlleuAlaAspCysAla 294
QY 38942 TTTCGAACAACAACAATCTGACATTCCTGGATCTTCTTAATGCAATTCGAACAATA 39001
DB 295 PheArgGlyleuSerSerleuLysThrleuAspLeuLysAsn-----AsnGlnIle 311
QY 39002 TCTTTG-----GGGGTATTTTGACACCCCTCCATGACCTTCAATTTATTA 39043
DB 312 SerTrpThrIleGluAspMetAsnGlyAlaPheSerGlyleuAspLysleuArgleu 331
QY 39044 AATATGAGTCACAACAATCTATTTGTTTGGATTCATCCATTTAAACCAAGCTGTATTC 39103
DB 332 IleleuGlnGlyAsnArglleArgSerIleThrLysAlaPheThrGlyleuAspAla 351
QY 39104 CTCAGCACTTTGATTTGACATTTTCATGCGATAGACATCTAAAGAAATTCGCAACAT 39163
DB 352 leuGlnHisleuAspLeuSerAspAsnAlaIleMetSerleuGlnGlyAsnAlaPheSer 371
QY 39164 TTTCGAAGAAGTCTTAGGCTTCTTCAATCTTACTTAACAATCTGTGGCTGTGATTTGGA 39223
DB 372 GlMetLysLysleuGlnGlnleuHisleuAsnThrSerSerleuLysCysAspCysGln 391
QY 39224 CATCAGAAATCTCTGACAGTGGGTCAGAAAGAAAG---CAGTTCTTGGAATGTTGAA 39280
DB 392 leuLysTrpLeuProGlnTrpValAlaGluAsnAsnPheGlnSerPheValAsnAla--- 410
QY 39281 CAATGACATGTGCAACCT 39301
DB 411 -----SerCysAlaHisPro 415
RESULT 10
US-09-906-700-290
Sequence 290 Application US/09906700
Patent No. 6723535
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi

APPLICANT:	Botstein, David
APPLICANT:	Desnovers, Luc
APPLICANT:	Baton, Dan L.
APPLICANT:	Ferrara, Napoleone
APPLICANT:	Filvaroff, Ellen
APPLICANT:	Fong, Sherman
APPLICANT:	Gao, Wei-Qiang
APPLICANT:	Gerber, Hanspeter
APPLICANT:	Gertlisen, Mary E.
APPLICANT:	Goddard, A.
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, Christopher J.
APPLICANT:	Gurney, Austin L.
APPLICANT:	Hillan, Kenneth J.
APPLICANT:	Kijavlin, Ivar U.
APPLICANT:	Mather, Jennie P.
APPLICANT:	Pan, James
APPLICANT:	Paoni, Nicholas F.
APPLICANT:	Roy, Margaret Ann
APPLICANT:	Stewart, Timothy A.
APPLICANT:	Thomas, Daniel
APPLICANT:	Williams, P. Mickey
APPLICANT:	Wood, William, I.
TITLE OF INVENTION:	Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION:	Acids Encoding the Same
FILE REFERENCE:	10466-14
CURRENT APPLICATION NUMBER:	US/09/906,700
CURRENT FILING DATE:	2000-09-18
PRIOR APPLICATION NUMBER:	PCT/US00/04414
PRIOR FILING DATE:	2000-02-22
PRIOR APPLICATION NUMBER:	US 60/143,048
PRIOR FILING DATE:	1999-07-07
PRIOR APPLICATION NUMBER:	US 60/145,698
PRIOR FILING DATE:	1999-07-26
PRIOR APPLICATION NUMBER:	US 60/146,222
PRIOR FILING DATE:	1999-07-28
PRIOR APPLICATION NUMBER:	PCT/US99/20594
PRIOR FILING DATE:	1999-09-08
PRIOR APPLICATION NUMBER:	PCT/US99/20944
PRIOR FILING DATE:	1999-09-13
PRIOR APPLICATION NUMBER:	PCT/US99/21090
PRIOR FILING DATE:	1999-09-15
PRIOR APPLICATION NUMBER:	PCT/US99/21547
PRIOR FILING DATE:	1999-09-15
PRIOR APPLICATION NUMBER:	PCT/US99/23089
PRIOR FILING DATE:	1999-10-05
PRIOR APPLICATION NUMBER:	PCT/US99/28214
PRIOR FILING DATE:	1999-11-29
PRIOR APPLICATION NUMBER:	PCT/US99/28313
PRIOR FILING DATE:	1999-11-30
PRIOR APPLICATION NUMBER:	PCT/US99/28564
PRIOR FILING DATE:	1999-12-02
PRIOR APPLICATION NUMBER:	PCT/US99/28565
PRIOR FILING DATE:	1999-12-02
PRIOR APPLICATION NUMBER:	PCT/US99/30095
PRIOR FILING DATE:	1999-12-16
PRIOR APPLICATION NUMBER:	PCT/US99/30911
PRIOR FILING DATE:	1999-12-20
PRIOR APPLICATION NUMBER:	PCT/US99/30999
PRIOR FILING DATE:	1999-12-20
PRIOR APPLICATION NUMBER:	PCT/US00/00219
PRIOR FILING DATE:	2000-01-05
NUMBER OF SEQ ID NOS:	423
SEQ ID NO 290	
LENGTH:	1059
TYPE:	PRT
ORGANISM:	Homo Sapien
US-09-906-700-290	
Alignment Scores:	
Pred. No.:	1,35e-15
Score:	269.50
Percent Similarity:	42.78%
Length:	1059
Matches:	101
Conservative:	56

Query	DB	Best Local Similarity:	27.52%	Mismatches:	135
Query Match:	DB:	0.31%	Indels:	75	
			Gaps:	15	
US-09-396-985B-48 (1-50000) x US-09-906-700-290 (1-1059)					
QY 38390	GCGAATGTTTCGCAAGTCTCTGGAGGATGATCTATAAATATCTAGAGATGTTCT	384439			
DB 61	AlaAsnIleThrLeuLeuSerLeuAlaGlyAsnArgIle-----ValGluLeuPro	78			
QY 38450	AAACATTTTCAA---TGGCAATCCCTTATCAATCATAGATGATGCACTTAAGCAG-----	385000			
DB 79	GluHisLeuLysGluProGlnSerLeuGluThrLeuAspLeuSerSerAsnHisLeuSer	98			
QY 38501	-----TTTCAACTCTGGATCTAACCTTTCTT-----	385277			
DB 99	GluLeuGlnThrAlaPheProAlaLeuGlnLeuLysTyrLeuLysAsnSerAsnArg	118			
QY 38528	-----	385455			
DB 119	ValThrSerMetGluProGlyTyrPheAspAsnLeuAlaAsnThrLeuLeuValLeuLys	138			
QY 38546	ATGAAACAAGGCTCTAGCTATGCTTT-----AAAAAGTGGCCCTTACCAAGTCTCAGC	385966			
DB 139	LeuAsnArgAsnAlaGlnIleSerAlaIleProProLysMetPheLysLeuProGlnLeuGln	158			
QY 38597	TATCTAGATCTTATAGTAAATGCACTGAGCTTTAGTGTTGCTGTTCTTATTTCTGATTTG	386566			
DB 159	HisLeuGluLeuAsnArgAsnLysIleLysAsnValAspGlyLeuThrPheGlnGlyLeu	178			
QY 38657	GGAACAAACAGCCCTGAGACACTTGAACCTCAGCTTCAATGATGTCCTC--ATTATGACT	387133			
DB 179	Gly-----AlaLeuLysSerLeuLysMetGlnArgAsnGlyValThrLysLeuMetAsp	196			
QY 38714	GCAATTTTCATGGGTCTAGAGAAGAGCTGACAGCACTGATTTTCAGACACTCTCTTTAA	387733			
DB 197	GlyAlaPheThrPglLysLeuSerAsnMetGluIleLeuGlnLeuAspHisAsnLeuThr	216			
QY 38774	AGGGCTCAGCAAGATTTC-----	387888			
DB 217	GluIleThrLysGlyTyrPheLysTyrGlyLeuLeuMetLeuGlnLeuHisLeuSerGln	236			
QY 38789	-----TCAGCTTTTATCCCTTGAAGAAAGCTACTTATACCTT	388248			
DB 237	AsnAlaIleAsnArgLysSerProAspAlaIleTgLuPheCysGlnLysLeuSerGluLeu	256			
QY 38825	GACATCTCTTATATATAC--ACCAAAATGATCTGGATGATATATTTCTGGCTTGACC	388811			
DB 257	AspLeuThrPheAsnHisLeuSerAsnArgLeuAsp--AspSerSerPheLeuGlyLeuSer	275			
QY 38882	AGTCTCAACACTTAAATAAATGCTGGCAATCTTTCAAAAGACAACACCCTTTCAATGTC	389411			
DB 276	LeuLeuAsnHisThrLeuHisIle---GlyAsnAsnArgValSerTyrIleAlaAspCysAla	294			
QY 38942	TTTGCAAAACACAAACTTGACATTCCTGGATCTTTCTTAATGTCAATTGGAACAATA	390011			
DB 295	PheArgGlyLeuSerSerLeuLysThrLeuAspLeuLysAsn-----AsnGluIle	311			
QY 39002	TCTTGG-----GGGGATTTTGACACCCTCATAGACTGATCAATTATTA	390433			
DB 312	SerTyrThrIleGluAspMetAsnGlyAlaPheSerGlyLeuAspLysLeuThrArgLeu	331			
QY 39044	AATATGATGTCACAAACATCTATTGTTTGGATTCTATCCATTAATACAGCGCTGATTC	391030			
DB 332	IleLeuGlnGlyAsnAlaGlnIleArgSerIleThrLysLysAlaPheThrGlyLeuAspAla	351			
QY 39104	CTCAGCACTCTTGAATGTCAGTTCAATCGCATGAGACACTTAAGAAATACGCAACAT	391633			
DB 352	LeuGlnHisLeuAspLeuSerAspAsnAlaIleMetSerLeuGlnGlyAsnAlaPheSer	371			
QY 39164	TTTCCAAAAGAGCTAGCGCTTCTTCATCTTATCAACAATTTCTGCTCTGTATATGTGA	392233			
DB 372	GlnMetLysLysLeuGlnGlnLeuHisIleLeuAsnHisSerSerLeuLeuLysAspCysGln	391			

QY 39224 CATCAAAATTCCTGAGTGGTCAAGAACAGAG---CACTTCTGTGTAATGTGA 39280
Db 392 LeuysrTbPleuPrgIntrYalAlaGluAsnAenPheGlnSerPheValAsnAla--- 410
QY 39281 CAATGACATGTGCAACACT 39301
Db 411 -----SerCyAlaHisPro 415
RESULT 11
US-09-903-603A-290
Sequence 290, Application US/09903603A
Patent No. 6767995
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Grimaldi, Paul J.
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Macher, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: GNE.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A
PRIOR FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 290
LENGTH: 1059
TYPE: PRT
ORGANISM: Homo Sapien
US-09-903-603A-290
Alignment Scores:
Pred. No.: 1,35e-15 Length: 1059
Score: 269.50 Matches: 101
Percent Similarity: 42.78% Conservative: 56
Best Local Similarity: 27.52% Mismatches: 135
Query Match: 0.31% Indels: 75
Gaps: 15
US-09-396-985b-48 (1-50000) x US-09-903-603A-290 (1-1059)
QY 38390 GCGAATGTTTCTGCAATGCTCTGCGAGTGTATCTATAAATATCTAGAAGATGTTCT 38449
Db 61 AlaAsnIleThrLeuLeuSerLeuAlaGlyAsnArgIle-----ValGluIleLeuPro 78
QY 38450 AAACATTTCAAA---TGCGAATCCTTATCAATCATTTGATGTCAACTTAAGCAG----- 38500
Db 79 GluHisLeuysGluPheGlnSerLeuGluThrLeuAspLeuSerSerAsnAsnIleSer 98
QY 38501 -----TTTCCAACTCTGGAATCTACCCCTTTCTT----- 38527
Db 99 GluLeuGlnThrAlaPheProAlaLeuGlnLeuysrTyLeuTyLeuAsnSerAsnArg 118
QY 38528 ----- 38545
Db 119 ValThrSerMetGluProGlyTyThrPheAspAsnLeuAlaSerThrLeuValLeuLys 138
QY 38546 ATGACCAAGAGGCTTATCACTTTT-----AAAAAGTGAGCCCTTACCAAGTCTCAGC 38596
Db 139 LeuAsnArgAsnArgIleSerAlaIleProProLysMetPheLysLeuProGlnLeuGln 158
QY 38597 TATCTAGATCTTATGAAATGACAGCTGAGCTTATGTTGCTTCTTATCTGATTTG 38656
Db 159 HisLeuGluLeuAsnArgAsnLysIleLysAsnValAspGlyLeuThrPheGlnGlyLeu 178
QY 38657 GGAACAAACAGCCTGAGACACTTACAGCTTCAATGAGTGCATC---ATTATGAGT 38713
Db 179 Gly-----AlaLeuysSerLeuLysMetGlnArgAsnGlyValThrLeuMetAsp 196
QY 38714 GCCAATTTCATGGGCTTGAAGAAGCTGACAGCAGCTGATTTTCAGCACTTACTTTAAA 38773
Db 197 GlyAlaPheTrpGlyLeuSerAsnMetGluIleLeuGlnLeuAspHisAsnAsnLeuThr 216
QY 38774 AGGCTCAACAATTC----- 38788
Db 217 GluIleThrLysGlyTybPleuTyGlyLeuLeuMetLeuGlnGluLeuHisLeuSerGln 236
QY 38789 -----TCAGCGTTCTTATCCCTTGAAGAAAGTACTTACTT 38824
Db 237 AsnAlaIleAsnArgIleSerProAspAlaTrpGluPheGlyGlnLysLeuSerGluLeu 256
QY 38825 GACATCTCTTATTAATAAC---ACCAAAATGACTTCAGTGTATATTTCTTGGCTTAC 38881
Db 257 AspLeuThrPheAsnHisLeuSerArgLeuAsp---AspSerSerPheLeuGlyLeuSer 275
QY 38882 AGCTCAACATCTTAAATAAAGCGCTGCAATCTTTTCAAAACAAACACCTTTCAAAATGTC 38941
Db 276 LeuLeuAsnThrLeuHisIle---GlyAsnAsnArgValSerTyrlleAlaAspCyala 294
QY 38942 TTTCGAAACAAACAACTTACATTCCTGAGTCTTCTTCTAATGTCAATGGAACAATA 39001
Db 295 PheArgGlyLeuSerSerLeuysrThrLeuAspLeuLysAsn-----AsnGluIle 311

```
QY 39002 TCTTGG-----GGGGATTGACACCCCTCCATAGACTTATTTA 39043
Db 312 SerThrIrrleGluAspMetAsnGlyAlaPheSerGlyLeuAspGlyLeu 331
QY 39044 AATTAGTACACAACTATTGTTTGGATTCCATCCATTATACACAGCTGTATCC 39103
Db 332 IleuLeuIngluAsnArgIleArgSerIleThrIlyAspAlaPheThrIngluLeuAspAla 351
QY 39104 CTCAGCACTTGTGATTCGAGTTTCAATCGCATAGACACTTAAAGAAATACGCAACAT 39163
Db 352 LeuGluInlIleuAspLeuSerAspAsnAlaIleMetSerLeuIngluAsnAlaPheSer 371
QY 39164 TTTCGCAAGAGTCTAGGCTTCTTAATCTTAACAATCTGTGCTTGATTAATGTGAA 39223
Db 372 GluMetIlyAspLeuIngluInlIleuAsnThrSerSerLeuLeuCyAspGlyIn 391
QY 39224 CATCAGAAATTCCTCGAGTGGTCAAGAACAGAG--CAGTCTTGAGTAATGTGAA 39280
Db 392 LeuIlySerIleuProGlnTrpValAlaGluAsnAsnGlnGlnSerPheValAsnAla--- 410
QY 39281 CAAATGACATGTGCACACCT 39301
Db 411 -----SerCyAlaInlAspPro 415

RESULT 12
US-09-304-920A-290
/ Sequence 290, Application US/09904920A
/ Patent No. 6806352
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi.
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Baton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Mather, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas P.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ TITLE OR INVENTION: Acids Encoding the Same
/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/904, 920A
/ CURRENT FILING DATE: 2001-07-13
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143, 048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145, 698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146, 222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
```

```

/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 290
/ LENGTH: 1059
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-304-920A-290

Alignment Scores:
Pred. No.: 1,35e-15 Length: 1059
Score: 269.50 Matches: 101
Percent Similarity: 42.78% Conservative: 56
Best Local Similarity: 27.52% Mismatches: 135
Query Match: 0.31% Gaps: 75
DB: 4

US-09-396-985B-48 (1-50000) x US-09-304-920A-290 (1-1059)
QY 38390 GCGAATGTTTCTGCAATGTCCTCGCAGCGTGTATCTATAAATCTAGAAGATGTTCTT 38449
Db 61 AlaAsnIleThrLeuLeuSerIleuAlaGlyAsnArgIle-----ValGluIleLeuPro 78
QY 38450 AAACATTTCAA---TGGCAATCCTTATCAATCATTAAGATGTCACCTTAAGCAG----- 38500
Db 79 GluIleuLeuGluLeuGlnSerIleuGlnThrLeuAspLeuSerSerAsnAlaIleSer 98
QY 38501 -----TTTCCAACTGTGATCTACCTTTCTT----- 38527
Db 99 GluLeuGlnThrAlaPheProAlaLeuGlnIleuIlyTyThrLeuAspLeuSerSerAsnArg 118
QY 38528 ----- 38545
Db 119 ValThrSerMetGluProGlyTyThrPheAspAsnLeuAlaAsnThrIleuValLeuIly 138
QY 38546 ATGACAAAGGCTCTACAGTTT-----AAAAAGTGGCCCTTACCAAGTCTCAGC 38596
Db 139 LeuAsnArgAsnArgIleSerAlaIleProProIyMetChelysleuProGlnIleuGln 158
QY 38597 TATCTAGATCTTGTAGAAATGCACTGACGCTTGTAGTGGTTCGTCTTATCTGATTTG 38656
Db 159 HisLeuGlnIleuAsnArgAsnIlyIleTyAsnValAspIlyLeuThrPheGlnIlyLeu 178
QY 38657 GGAACAAACGCTGAGACACTTACAGCTTCAATGAGTGCATC---ATTAGAGT 38713
Db 179 Gly-----AlaLeuIlySerIleuIlyMetGlnArgAsnIlyValThrIlysleuMetAsp 196
QY 38714 GCAATTTCAATGGGTCTAGAAAGAGCTGCAGACCTGATTTTGCACACTTACTTAAAA 38773
Db 197 GlyAlaPheTrpGlyIleuSerAsnMetGluIleuGlnIleuAspHisAsnAlaIleThr 216
QY 38774 AGGCTCAGCAAAATTC----- 38788
Db 217 GluIleThrIlyGlyTrpLeuTyArgIlyLeuLeuMetLeuGlnIleuHisleuSerGln 236
```

```

QY 38789 -----TCAGCTTCTTATCCCTTGAAGACCTTACCTT 38824
Db 237 AsnAlaIleAsnArgIleSerProAspAlaTrpGluPheCysGlnIleSerGlnIleu 256
QY 38825 GACATCTCTTAACTAAC--ACCAAAATGACTCGATGATATTTCTTGCTGACC 38881
Db 257 AspThrPheAsnHisIleuSerArgIleuAsp--AspSerSerPheLeuGlyIleuSer 275
QY 38882 AGTTCACACATTTAAATGGCTGGCAATCTTTCAAAAGACACACCTTTCAAAATGC 38941
Db 276 LeuLeuAsnThrIleuHisIle--GlyAsnAsnArgValSerTyrIleAlaAspCysAla 294
QY 38942 TTTCACAAACACACAAATGACTGACATTCCTGATCTTTCTTAATGTCAATGACAAATA 39001
Db 295 PheArgGlyIleuSerSerIleuIleuSerIleuAspIleuAspIleuAspIleu 311
QY 39002 TCTTGG-----GGGATATTTGACACCCCTCCATAGACTTCAATTAATTA 39043
Db 312 SerTrpThrIleGluAspMetAsnGlyAlaPheSerGlyIleuAspIleuArgIleu 331
QY 39044 AATATGACTCAACATCTATTTGTTTGGATTCATCCCTTATTAACCACTGATATCC 39103
Db 332 IleLeuGlnGlyAsnArgIleArgSerIleThrIleIleAspAlaPheThrGlyIleuAspAla 351
QY 39104 CTCAGCACTCTGATGAGATTTGATGACATGACATGACATGACATGACATGACAT 39163
Db 352 LeuGlnIleIleuAspIleuSerAspAsnAlaIleMetSerIleuGlnGlyAsnAlaPheSer 371
QY 39164 TTTCACAAAGACTGACCTTCTTCAATCTTCAATCTTCAATCTTCTGCTGATATGTA 39223
Db 372 GlnMetIleIleuAspIleuGlnIleuHisIleuAsnThrSerSerIleuLeuCysAspCysGln 391
QY 39224 CATGAGAAATTCCTGCACTGGGTCAAGACAGAG--CAGTCTTGCTGTAATGTTGAA 39280
Db 392 LeuIleIleuIleuProGlnIleuValAlaGlnAsnAsnPheGlnSerPheValAsnAla--- 410
QY 39281 CAATGACATGTGCAACACCT 39301
Db 411 -----SerCysAlaHisPro 415

RESULT 13
US-09-909-064-290
; Sequence 290, Application US/09909064
; Patent NO. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie F.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumes, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

```

```

FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/909, 064
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143, 048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145, 698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146, 222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 280
LENGTH: 1059
TYPE: PRT
ORGANISM: Homo Sapien
US-09-909-064-290

Alignment Scores:
Pred. No.: 1,35e-15 Length: 1059
Score: 269.50 Matches: 101
Percent Similarity: 42.78% Conservative: 56
Best Local Similarity: 27.52% Mismatches: 135
Query Match: 0.31% Indels: 75
DB: 4 Gaps: 15

US-09-396-985b-48 (1-5000) x US-09-909-064-290 (1-1059)
QY 38390 GCGAATGTTCTGCAATGTCTGGCAGGTGATCTATAAATATCTAGAAGATGTTCT 38449
Db 61 AlaAsnIleThrIleuSerIleuAlaGlyAsnArgIle-----ValGlnIleLeuPro 78
QY 38450 AAACATTTCAA--TGCAATCCTTATCAATCATTAAGATGATCACTTAAGCAG----- 38500
Db 79 GlnHisIleuIleuGlnPheGlnSerIleuGlnThrIleuAspIleuSerAsnAlaIleSer 98
QY 38501 -----TTTCCAACTCTGATCTACCTTTCTT----- 38527
Db 99 GlnLeuGlnThrAlaPheProAlaLeuGlnIleuIleuIleuIleuIleuIleuIleu 118
QY 38528 -----AAAATTGACTTTACT 38545
Db 119 ValThrSerMetGluProGlyTyrPheAspAsnLeuAlaAsnThrIleuValIleuIleu 138
QY 38546 ATGACAAAGGCTCTATCACTTT-----AAAAAGTGCCCTTACCAAGTCTCAGC 38596
Db 139 LeuAsnArgAsnArgIleSerAlaIleProProIleuMetPheIleuIleuProGlnIleuGln 158

```

```
QY 38597 TATCTAGATCTTAGTGAAGATGCACTGATTTAGTGTTGCTGTCTTATTTGATTTG 38656
    ::::::::::::::::::::
Db 159 HisteuGlueuAsnArgAsnValArgIleuThrPheGlnGlyLeu 178
QY 38657 GGAACAAACAGCCCTGAGACACTTAGCTCAGCTTCAATGGTGCCATC---ATTAGAGT 38713
    ::::::::::::::::::::
Db 179 Gly-----AlaLeuYSerLeuMetGlnArgAsnGlyValThrIleuMetAsp 196
QY 38714 GCCAATTTCATGGCTTGAAGAGCTGACAGCTTGATTTTCAGACTCTTCACTTTAAA 38773
    ::::::::::::::::::::
Db 197 GlyAlaPheThrGlyLeuSerAsnMetGluIleuGlnLeuAspHisAsnAsnLeuThr 216
QY 38774 AGGCTCACAGATTC-----TCAGCGTTCTTATCCCTGAAAAGCTTATACCTT 38788
    ::::::::::::::::::::
Db 217 GluIleThrIysGlyTyrPleuTyrGlyLeuLeuMetLeuGlnIleuHisLeuSerGln 236
QY 38789 -----TCAGCGTTCTTATCCCTGAAAAGCTTATACCTT 38824
    ::::::::::::::::::::
Db 237 AsnAlaIleAsnArgIleSerProAspAlaTrpGluPheCysGlnIleuSerGlyLeu 256
QY 38825 GACATCTCTTATCTAAC---ACCAAAATTCATTCATGATATATTTCTTGCTTGACC 38881
    ::::::::::::::::::::
Db 257 AspLeuThrPheAsnHisLeuSerArgLeuAsp---AspSerSerPheLeuGlyLeuSer 275
QY 38882 AGTCTCAACACATTAATAATGGCTGGCAGATCTTTCAAAAGACAACACCCCTTCAATGTC 38941
    ::::::::::::::::::::
Db 276 LeuLeuAsnThrIleuHisIle---GlyAsnAsnArgValSerTyrIleAlaAspCysAla 294
QY 38942 TTTCGAAACACACAACTTGACATTCCTGATCTTTCAATGTCAATTGGAACAAATA 39001
    ::::::::::::::::::::
Db 295 PheArgGlyLeuSerSerLeuIleThrLeuAspLeuAsn-----AsnGluIle 311
QY 39002 TCTTGG-----GGGATATTGACACCCCTCAACATTCATTCATTTA 39043
    ::::::::::::::::::::
Db 312 SerThrThrIleGluAspMetAsnGlyAlaPheSerGlyLeuAspIleuArgGlyLeu 331
QY 39044 AATATGAGTCACACAACTTATGTTTGGATTCATCCCATTAACAGCTGATATTC 39103
    ::::::::::::::::::::
Db 332 IleuGlnGlyAsnArgGlyIleArgSerIleThrIysValAlaPheThrGlyLeuAspAla 351
QY 39104 CTCAGACACTTGTGATGTCAGTTTCAATGACATGACATGTAAGAATATCTCAACAT 39163
    ::::::::::::::::::::
Db 352 LeuGluHisLeuAspLeuSerAspAsnAlaIleMetSerIleuGlnGlyAsnAlaPheSer 371
QY 39164 TTTCGAAAGAGCTTAGGCTTTTCAATTTCAATCAATTTGCTGCTGTAATGTGAA 39223
    ::::::::::::::::::::
Db 372 GlnMetIysValLeuGlnGlnLeuHisLeuAsnThrSerSerLeuLeuCysAspCysGln 391
QY 39224 CATCAGAAATTCCTGAGTGGGTCAAGGACAGAGAAG---CAGTTCTTGTAATGTGAA 39280
    ::::::::::::::::::::
Db 392 LeuIysThrLeuProGlnTrpValAlaGluAsnAsnPheGlnSerPheValAsnAla--- 410
QY 39281 CAAATGACATGTGCAACACT 39301
    ::::::::::::::::::::
Db 411 -----SerCysAlaHisPro 415

RESULT 14
US-09-905-381A-290
; Sequence 290, Application US/0905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eacou, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
```

```
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,381A
CURRENT FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 290
LENGTH: 1059
TYPE: PRT
ORGANISM: Homo Sapien
US-09-905-381A-290

Alignment Scores:
Pred. No.: 1,35e-15 Length: 1059
Score: 269.50 Matches: 101
Percent Similarity: 42.78% Conservative: 56
Best Local Similarity: 27.52% Mismatches: 135
Query Match: 0.31% Indels: 75
DB: 4 Gaps: 15

US-09-396-985b-48 (1-50000) x US-09-905-381A-290 (1-1059)
QY 38390 GCCAATGTTTCTGCAATGCTCTGCGCAGGTGATCTATAAATATCTTAGAAGATGTTCTT 38449
    ::::::::::::::::::::
Db 61 AlaAsnIleThrLeuSerLeuAlaGlyAsnArgIle-----ValGluIleLeuPro 78
```

QY 38450 AACATTTCAAA---TGGCAATCCTTATCAATCATTAATGTCACATTAGACAG----- 38500
Db 79 GlnHisLeuLysGlnPheGlnSerLeuGlnThrLeuAspLeuSerSerAsnHisLeuSer 98
QY 38501 -----TTTCCAACTGTGATCTACCTCTTT----- 38527
Db 99 GluLeuGlnThrAlaPheProAlaLeuGlnLeuGlnSerLeuLysLeuAsnSerAsnArg 118
QY 38528 -----AAAATTGACTTAAT 38545
Db 119 ValThrSerMetGluProGlyTyrPheAspAsnLeuAlaAsnThrLeuLeuValLeuLys 138
QY 38546 ATGAACAAAGGGTCTATCAGTTT-----AAAAAGTGGCCCTTACCAAGTCTCAGC 38596
Db 139 LeuAsnArgAsnArgGlnLeuSerAlaLeuProProLysMetPheLeuLeuProGlnLeuGln 158
QY 38597 TATCTAGATCTTATAGAAATGCACTGAGCTTATAGTGGTCTGTTTATTTCTGATTTG 38656
Db 159 HisLeuGlnLeuAsnArgAsnLysLeuLysAsnValAspGlyLeuThrPheGlnGlyLeu 178
QY 38657 GGAACAAACAGCTGAGACCTTACAGCTTACAGCTTACAGTGGCCTC---ATTATGAGT 38713
Db 179 Gly-----AlaLeuLysSerLeuLysMetGlnArgAsnGlyValThrLysLeuMetAsp 196
QY 38714 GCCAATTTTCATGGTCTTGAAGAGCTGAGACCTGAGATTTTTCAGCACTTACTTAA 38773
Db 197 GlyAlaPheThrPrgLysLeuSerAsnMetGlnLeuGlnLeuAspHisAsnHisLeuThr 216
QY 38774 AGGTCACAAATTC----- 38788
Db 217 GluThrLysGlyTyrLeuLysGlyLeuLeuMetLeuGlnLeuHisLeuSerGln 236
QY 38789 -----TCAGCTTTCTATCCCTTGAAGAACTTACTT 38824
Db 237 AsnAlaIleAsnArgLysSerProAspAlaThrGluPheCysGlnLysLeuSerGlnLeu 256
QY 38825 GACATCTCTTACTACTAC---ACCAAAATGACTTCATGATTAATTTCTGGTCTGAC 38881
Db 257 AspLeuThrPheAsnHisLeuSerArgLeuAsp---AspSerSerPheLeuGlyLeuSer 275
QY 38882 AGTCTCAACACATTAATAATGCTGGCAATTTCTTCAAGAACAACACCTTTCAATGTC 38941
Db 276 LeuLeuAsnThrLeuHisIle---GlyAsnAsnArgValSerTyrIleAlaAspCysAla 294
QY 38942 TTTGCAAAACAAACAAATTTGACATCTCTGATCTTTTAATGTCATTTGGAACAATA 39001
Db 295 PheArgGlyLeuSerSerLeuLysThrLeuAspLeuLysAsn-----AsnGlnIle 311
QY 39002 TCTTGG-----GGGGTATTTGACACCTTCATAGACTTCAATTAATTA 39043
Db 312 SerThrThrIleGluAspMetAsnGlyAlaPheSerGlyLeuAspLysLeuArgLeu 331
QY 39044 AATATGAGTCAACAATCTATTTGTTGATTCATCCATTAATTAACACAGCTGATTTCC 39103
Db 332 IleLeuGlnGlyLeuAsnArgIleArgSerIleThrLysValPheThrGlyLeuAspAla 351
QY 39104 CTCGACACTCTTATTTGAGATTTGATGCGCATAGACATTAAGAATATCTGCAACAT 39163
Db 352 LeuGlnHisLeuAspLeuSerAspAsnAlaIleMetSerLeuGlnGlyAsnAlaPheSer 371
QY 39164 TTTTCAAAAGTCTAGCTTCTTCAATCTTAAACATTTGTTGCTGATATGTA 39223
Db 372 GlnMetLysLysLeuGlnGlnLeuHisLeuAsnThrSerSerLeuLysCysGln 391
QY 39224 CATAGAAATTTCTGAGTGGTCTAAGGACAGACAG---CAGTTCTTGATGATTTGAA 39280
Db 392 LeuLysThrLeuProGlnThrValAlaGluLysAsnPheGlnSerPheValAsnAla--- 410
QY 39281 CAATGACATGTGCAACCT 39301
Db 411 -----SerCysValAlaHisPro 415

RESULT 15
US-09-906-618-290
Sequence 290, Application US/09906618
Patent No. 6628146
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavir, Ivar J.
APPLICANT: Macher, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: 1046-14
CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 290
LENGTH: 1059
TYPE: PRT

```

: ORGANISM: Homo Sapien
US-09-906-618-290

Alignment Scores:
Pred. No.: 1.35e-15      Length: 1059
Score: 269.50           Matches: 101
Percent Similarity: 42.78%      Conservative: 56
Best Local Similarity: 27.52%    Mismatches: 135
Query Match: 0.31%             Indels: 75
DB: 4                       Gaps: 15

US-09-396-985b-48 (1-50000) x US-09-906-618-290 (1-1059)

QY 38390 GCGAATGTTTTCGCAATGCTCTGAGAGGTGATATCTAATAATCTAGAGATGTTCCCT 38449
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 61 AlaAsnIleThrLeuLeuSerLeuLeuIleAsnIleGlyLeu-----ValGluIleLeuPro 78

QY 38450 AAACATTTCAAA---TGGCAATCCTTATCAATCAATTAAGTGTCAACTTAACGAG----- 38500
    ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 79 GluHisLeuLysGluPheGlnSerLeuGlnThrLeuAspLeuSerSerAsnAsnIleSer 98

QY 38501 -----TTTCGACTCTGGATCTACCCCTTCTT----- 38527
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 99 GluLeuGlnThrAlaPheProAlaLeuGlnLeuLysTyrLeuAsnSerAsnArg 118

QY 38528 -----AAAAAGTTGACTTTTAACT 38545
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 119 ValThrSerMetGluProGlyTyrPheAspAsnLeuAlaAsnThrLeuLeuValLeuLys 138

QY 38546 ATGAACAAAGGGCTATCAGTTT-----AAAAAGTGGCCCTAACCAAGTCTGAGC 38596
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 139 LeuAsnArgAsnArgIleSerAlaIleProProLysMetPheLysLeuProGlnLeuGln 158

QY 38597 TATCTAGATCTTAGAGAAAGCAGCTGAGCTTGAAGTGTGCTGCTTCTATCTGATTTG 38656
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 159 HisLeuGlnLeuAsnArgAsnLysIleLysAsnValAspGlyLeuThrPheGlnGlyLeu 178

QY 38657 GGAACAAACAGCCTGAGACACTAGACCTTCAAGCTTGAGCCATC--ATTATGAGT 38713
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 179 Gly-----AlaLeuLysSerLeuLysMetGlnArgAsnGlyValThrLysLeuMetAsp 196

QY 38714 GCCAATTTCATGGGCTTAGAAGAGCTGAGCAGCCTGATTTTCAGCACTTACTTTAAA 38773
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 197 GlyAlaPheTrpGlyLeuSerAsnMetGluIleLeuGlnLeuAspHisAsnAsnLeuThr 216

QY 38774 AGGATCACAGAAATC----- 38788
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 217 GluIleThrLysGlyTrpLeuTyrGlyLeuLeuMetLeuGlnGluLeuHisLeuSerGln 236

QY 38789 -----TCAGCGTTCTTATCCCTGAAAGAGCTTACTTACCTT 38824
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 237 AsnAlaIleAsnArgIleSerProAspAlaTrpGluPheCysGlnLysLeuSerGluLeu 256

QY 38825 GACATCTCTTAATAAC--ACCAAAATTCAGTTGATGATATTTTGGCTTGACC 38881
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 257 AspLeuThrPheAsnHisLeuSerArgLeuAsp--AspSerSerPheLeuGlyLeuSer 275

QY 38882 AGTCTCAACATTAATAAAGCGTGGCAATCTTTCAAAGCAACACCCCTTCAAATGTC 38941
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 276 LeuLeuAsnThrLeuHisIle--GlyAsnAsnArgValSerTyrIleAlaAspCysAla 294

QY 38942 TTTGCAAAACACAAACAACTTACATTCCTGGATCTTCTTAATGTCATTTGGAACAATA 39001
    |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 295 PheArgGlyLeuSerSerLeuLysThrLeuAspLeuLysAsn-----AsnGluIle 311

QY 39002 TCTTGG-----GGGATATTGACACCCCTGCATAGACTTCAATTCAATTATTA 39043
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 312 SerTrpThrIleGluAspMetAsnGlyAlaPheSerGlyLeuAspLysLeuArgArgLeu 331

QY 39044 AATATGAGTCAACAATCTATTGTTTGGATTCATCCCATTTATACACAGCTGTATTCC 39103
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 332 IleuGlnGlnLysAsnArgIleArgSerIleThrLysLysAlaPheThrGlyLeuAspAla 351

```

```

QY 39104 CTCAGACCTCTTGATTGCAGTTTCAATCCGATAGACATCTAAAGGAATACTGCAACAT 39163
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 352 LeuGlnHisLeuAspLeuSerSerAspAsnAlaIleMetSerLeuGlnGlnLysAlaPheSer 371

QY 39164 TTTCAAAGAGTACGCTTCTTCAATCTTACTTAACAATTTGCTTGCTGTATATGTGA 39223
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 372 GlnMetLysLysLeuGlnGlnLeuHisLeuAsnThrSerSerLeuLeuCysAspCysGln 391

QY 39224 CATCAGAAATCTCTGAGTGGGTGCAAGAACAGAG--CAGTTCTTGGAATGTTGAA 39280
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 392 LeuLysTrpLeuProGlnTrpValAlaGluAsnAsnPheGlnSerPheValAsnAla--- 410

QY 39281 CAATGACATGTGCAACACCT 39301
    ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 411 -----SerCysAlaHisPro 415

```

Search completed: March 30, 2005, 03:08:44
 Job time : 2473 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:51:33 ; Search time 542 Seconds
(without alignments)
17752.170 Million cell updates/sec

Title: US-09-396-985B-48
Perfect score: 86900
Sequence: 1 ttccacatccatgtagtgc.....catttagtatttccaga 50000

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 28346 segs, 96216763 residues
Total number of hits satisfying chosen parameters: 1133664

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODL=frame+np.model -DEV=xlh
-Q=/cgn_1/USPTO_SPOOL/US09396985/runat_28032005_155743_21159/app_query.fasta-1.85098
-DB=PIR_79 -QFMT=fastan -SUFFIX=ipr -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODS=LOCAL
-OUTFMT=ptio -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09396985 @CGN_1_1_1364 @runat_28032005_155743_21159 -NCPV=6 -ICU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=150 -WARN TIMEOUT=30 -THRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	765.5	0.9	1281	1 GNM5L	retrovirus-related
C 2	732	0.8	1275	2 S21348	probable pol polyp
C 3	680.5	0.8	1281	1 GNM5L	retrovirus-related
C 4	568.5	0.7	1273	2 S21976	probable RNA-direc
C 5	575.5	0.7	1275	2 B28096	line-1 protein ORF
C 6	573.5	0.7	1280	2 B34087	hypothetical prote
C 7	572.5	0.7	1275	2 I38588	reverse transcript
C 8	567.5	0.7	1275	2 S65824	reverse transcript
C 9	563.5	0.6	712	2 S23650	retrovirus-related
C 10	547.5	0.6	1259	4 GNM5L	retrovirus-related
C 11	491.5	0.6	661	2 I56258	reverse transcript
C 12	492.5	0.6	1260	4 GNM5L	reverse transcript
C 13	487	0.6	1260	4 GNM5L	retrovirus-related
C 14	482.5	0.6	1275	2 B28096	line-1 protein ORF

15	483	0.6	1275	2 I38588	reverse transcript
16	480.5	0.6	1280	2 B34087	hypothetical prote
17	473.5	0.5	712	2 S23650	retrovirus-related
18	457.5	0.5	786	2 T08654	Toll protein-like
19	453	0.5	1259	4 GNM5L	retrovirus-related
20	445	0.5	317	2 S10151	transforming prote
21	441.5	0.5	1260	4 GNM5L	retrovirus-related
22	393.5	0.5	143	2 B41925	hypothetical prote
23	391	0.4	112	2 S21351	hypothetical prote
24	381	0.4	126	2 S33477	hypothetical prote
25	396	0.5	275	2 S21348	probable pol polyp
26	375	0.4	1097	2 A29943	Toll protein precu
27	372.5	0.4	392	2 S57662	hypothetical prote
28	336.5	0.4	562	2 JU0033	hypothetical prote
29	315.5	0.4	1389	2 T13852	chaoptin precursor
30	313.5	0.4	1385	2 T13887	insulin-like growt
31	318	0.4	392	2 S57662	hypothetical prote
32	301.5	0.3	99	2 S21350	hypothetical prote
33	292	0.3	1066	2 T15864	hypothetical prote
34	270	0.3	1134	1 A29944	chaoptin precursor
35	264.5	0.3	605	2 J05239	insulin-like growt
36	263.5	0.3	2026	1 OYB7	adenylate cyclase
37	261	0.3	1143	2 T10636	hypothetical prote
38	254.5	0.3	1051	2 T13174	gp150 protein - fr
39	251.5	0.3	603	2 T24315	hypothetical prote
40	252.5	0.3	994	2 H96510	probable disease r
41	245.5	0.3	603	2 J06128	insulin-like growt
42	251.5	0.3	1112	2 T10504	disease resistance
43	244.5	0.3	983	2 G84524	probable disease r
44	249	0.3	409	2 E86336	hypothetical prote
45	242.5	0.3	741	2 T05250	probable disease r

ALIGNMENTS

RESULT 1
GNM5L
retrovirus-related reverse transcriptase homolog - mouse retrotransposon
N.Alternate names: LMD repetitive element ORF-2; LINE-1 hypothetical protein; ORF 3900;
C.Species: Mus musculus (house mouse)
C.Date: 31-Mar-1999 #sequence revision 08-Jan-1999 #text change 09-Jul-2004
C.Accession: B58927; B24906; I49130; A23772; B23430
R.lobb, D.D.; Padgett, R.W.; Hardies, S.C.; Shehee, W.R.; Comer, M.B.; Edgell, M.H.; Hut
Mol. Cell. Biol. 6, 168-182, 1986
A.Title: The sequence of a large LMD element reveals a tandemly repeated 5' end and sev
A.Reference number: A93072; MUID:87064284; PMID:3023821
A.Accession: B58927
A.Status: translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-1281 <LOE1>
A.Cross-references: UNIPROT:P11369; UNIPROT:O60713; UNIPROT:O61787; GB:M13002; NID:g2008
A.Note: sequence constructed using the first potential start codon for ORF2
A.Accession: B24906
A.Molecule type: DNA
A.Residues: 'NNQESNHNSTNOKEDSHKNR', 1-1281 <LOE2>
A.Cross-references: GB:M13002; NID:g200849
A.Note: sequence shown in Fig. 2
R.Martin, S.L.; Martin, S.L.
Gene 153, 261-266, 1995
A.Title: Characterization of a LINE-1 cDNA that originated from RNA present in ribonucle
A.Reference number: 149129; MUID:95180729; PMID:7533116
A.Accession: 149130
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-85, 'L', 87-358, 'K', 360-706, 'F', 708-735, 'A', 737-760, 'W', 762-927, 'D', 929-1281
A.Cross-references: EMBL:U15647; NID:g558906; PIDN:AAA67727.1; PID:g558908
R.Motzer, E.; Rogan, P.K.; Manuelidis, L.
Nucleic Acids Res. 14, 3119-3136, 1986
A.Title: Conservation in the 5' region of the long interspersed mouse L1 repeat: implicat
A.Reference number: A23772; MUID:86176789; PMID:3008107
A.Accession: A23772
A.Molecule type: DNA
A.Residues: 'NNQESNHNSTNOKEDSHKNR', 1-245, 'K', 247-423, 'SYTQNMKTKTKTN', 439, 'WTDTRYQS' <MO

A:Residues: 1-1281 <LOEI>
A:Cross-references: UNIPROT:P11369, UNIPROT:O60713, UNIPROT:O61787, GB:M13002, NID:G2008
A:Note: Sequence constructed using the first potential start codon for ORF2
A:Accession: B24906
A:Molecule type: DNA
A:Residues: 'NNQSNHSTNOKEDSHKUR',1-1281 <LOE2>
A:Cross-references: GB:M13002, NID:G200849
A:Note: sequence shown in Fig. 2
R:Martin, S.L.; Martin, S.L.
Gene 153, 261-266, 1995
A:Title: Characterization of a LINE-1 CDNA that originated from RNA present in ribonucleic
A:Reference number: 149129, MUID:95180729, PMID:753116
A:Accession: 149130
A:Status: preliminary; translated from GB/EMBL/DBU
A:Molecule type: mRNA
A:Residues: 1-85, 'L', 87-358, 'K', 360-706, 'F', 708-735, 'A', 737-760, 'W', 762-927, 'D', 929-1281
A:Cross-references: EMBL:U15647, NID:G558906, NID:AA67727.1; PID:G558908
R:Motiez, E.; Rogan, P.K.; Manuelidis, L.
Nucleic Acids Res. 14, 3119-3136, 1986
A:Title: Conservation in the 5' region of the long interspersed mouse L1 repeat: implicated
A:Reference number: A23772, MUID:86176789, PMID:3008107
A:Accession: A23772
A:Molecule type: DNA
A:Residues: 'NNQSNHSTNOKEDSHKUR',1-245, 'K', 247-423, 'SYTQNMWTKTWKTN', 439, 'WTDTRYQS', <MO
A:Cross-references: GB:X03755, NID:G52829, PIDN:CA27363.1, PID:G1334115
C:Superfamily: pol polypeptide
:Keywords: reverse transcriptase

Pred. No.:	4.47e-44	Length:	1281
Score:	680.50	Matches:	174
Percent Similarity:	58.94%	Conservative:	37
Best Local Similarity:	48.60%	Mismatches:	77
Query Match:	0.78%	Indels:	73
DB:	1	Gaps:	9

US-09-396-98B-48 (1-50000) x GMSLL (1-1281)

OY	4937	CACCTGATCCTTTGAACAAGAGACTAAACCATCAGTGGAAAAAAGACAGCATTTTAA	4996
Dd	921	HISLEUILPEHEAPESGLIALALYSFTHRIIEGTINTP-LYSLSAPSERTIIEPHS	940
OY	4997	CAAAATGATGTCGCCTCAACTGTCTGTCCAGTCATGACAAAATAATGCAAAATGCCATTCTT	5056
Dd	940	NASNTIPYSTRIPIHSAENTRPLEULEUSERCYARGRGWETHRGILIEAPPROTYLE	960
OY	5057	ATTCCTTAGGCAAAAGCTCAAGTCCAAGTGATCAAGAACCCTTAACATAAACCGATAC	5116
Dd	960	USERPCYSTRHYSEVALVYSERYSTRIPLIELSGILEUENHSIILEYSPROGIUTH	980
OY	5117	CCTGAATATTTTAAAGAGAGAGAGTGGAGAAAGGCTTGAACACATNGGGAAGGGGAAA	5176
Dd	980	RLEULYSLEUIELGTUGLIVSVALIGLYSERIEULSNAPMETGLYTHRIGLYLU	1000
OY	5177	ATTCCTGACGAACACCAACGTG-----GCTTA-AGATCAAGATCTACAAATGGGGCT	5229
Dd	1000	SPELEUNSMARGHTHALAMETALACYSLALVALARGSERHRLIEASPSTPAEPLE	1020
OY	5230	CATAAAATTTGCAAAGCTTCTGTAATGCACAAAGACACTGTCAATAGACAAAAG---CA	5286
Dd	1020	UMELYSLEUDINSERPHECYSLYSALALYSAPTHTVALASNLYSTHRYSARGPROP	1040
OY	5287	AACGATTTGGAAAAAGATCTTTACCAATCCATACCAATGATGAGGGCTAATATCAATAT	5346
Dd	1040	CTHRAEPTIRLPJUKRGILIEPHENTRYRPROLYSESEHPRGILYLEUISERANIL	1060
OY	5347	ATACAAACACTCAAGAAATTAGACTCCAGAAACCAATACCCCTATTAA-AAATGGGG	5405
Dd	1060	EYLKLGSLULEUYSLYSVALASPHEARGLYSERASHNANPROIIEULYSYSTPGI	1080
OY	5406	TAC-AAGCTAAACAAAGATTTTCAGCTGAGAGATTTTGATGGCCAAAGATCACCTTAA	5464
Dd	1080	YSERTIUENSNLYSGIUNPESERPROGIUGLUTYTRMGTEKLAEGLYSHLSLEULY	1100

QY	5465	GAATAATTGAACATGTTAGTCA	TCA	TGACG	GAATAATGCAAAATGCAAACTGGAAGT	5524
Db	1100	slvscysserthser	thetserlellearglunetglnilevsththtrleuargpheni			1120
QY	5525	TATTCCTGAAGTGTAT	AAAAATGTCCTTAAAC	CTAATGACCTGAGAGATATACAG		5584
Db	1120	slveththproval		-----ArgMetAla-LysIleLysasnserg		1133
QY	5585	AAACATCT		-----GGGGAATTAACAACATAT		5610
Db	1133	lyaspserrargcys	trparxglycysgllylunrglyrhrlleuethiscys	trpTrpG		1153
QY	5611	-----TTACTATTTTAA	AAATAC	TGAAGAAATGTGGAATATTTTAATTTAA		5662
Db	1153	lucysargleuvalgln	Proleutrp	lysesserValtrpargPheleuArg-LysLeuAsp		1172
QY	5663	ATC				5665
Db	1173	IleValleuProglunsp	ProalaIleProleuLeuGlyIleTyrProglunsp	AlaPro		1192
QY	5666	-----ACATGCTATCTTA				5680
Db	1193	ThreIlylvslyasphtr	CysSerThnmetPheIleAlaIleuPheIleIleAlaArg			1212
QY	5681	-----AAATGTCATTTAA	CTATATCA	CCAAAGGCTATATGATATATAAAATG		5725
Db	1213	Sertrp	lysglunProahgCysProserThnglun	-----trpIleGlnIysmet		1229
QY	5726	TGTTATATGTATAC	CCATGATGATTTT	AGACAGAA--AAAAAAAGTAATATATACAATT		5782
Db	1230	TrptrylIeTyrthrm	etgIunryTyrserAlaIlelyelysasn	glunPhe	metLysPhe	1249
QY	5783	TTAGGAATGTGCATG	ATTTAAAAAATTA	ACTCAAGCTGGAATTACA		5830
Db	1250	leuAlaIys	trpmetaspLeu	ngIunIleIleLeu	serglunvalIthr	1265

RESULT 4

916738
probab]e

N; Altern

C;Date:

R; Kahre,

Submitted

A; Access

A; Residu

A; Experi

C; Genetic
A: Mohi 1a

C; Superf

•

Aligner
Pred. No

Score:
Percent

Best Loc

DB:

US-09-39

2

부

18

9

[illegible]

```
Dh 375 rlyetpCystrpPheantTPargAlathCyeargarmetGlnlleaerProCySe 395
Qy 5057 ATCCCTTAGGCAAGAGCTCAAGTCCAGTGGATCAAGAACTCTACATTAACCAAGATAC 5116
Dh 395 uSerProCystrpThrylsuSerlySerlyStrpIlelysaerPheutisIlelysaerPhe 415
Qy 5117 CCTGAATTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5176
Dh 415 rleuylleuileleuglulysleuGlylyshleuGlnihmetGlythryrGlyshs 435
Qy 5177 ATTCCTGACAGAACACCACTGGC-----TTAAGATCAAGAACTTACAAATGGGGCCT 5229
Dh 435 nPheleuamlystrpPrometalatYrAlaleuArSerarGlylleaplystrPaeple 455
Qy 5230 CATTAATTTGAAGAGCTTCTTATATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5287
Dh 455 uilleylsleuInserPheCylysaAlaAsprthValaValrthrylysaerGlnpr 475
Qy 5288 -ACAGATTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5346
Dh 475 othrasprtrpIulysIlePhehtrhAsnProthThrasprarglyleuileSerlysl 495
Qy 5347 ATACAAACTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5398
Dh 495 etYrlyeGlnleuylsleuylsleuAsparGargluthrAsnProIlelyS 512

RESULT 5
B28096
line-1 protein ORF2 - human
C/Species: Homo sapiens (man)
C/Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 09-Jul-2004
C/Accession: B28096
R:Skowronski, J.; Fanning, T.G.; Singer, M.F.
Mol. Cell. Biol. 8, 1385-1397, 1988.
A>Title: Unit-length line-1 transcripts in human teratocarcinoma cells.
A/Reference number: A28096; MUID:88246405; PMID:2454389
A/Accession: B28096
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-1275 <SKO>
A/Cross-references: UNIPROT:Q15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:Q00363; UNIPROT:Q9Y5K0; UNIPROT:Q00366; UNIPROT:Q8TE30; UNIPROT:Q00375
C/Superfamily: pol polyprotein

Alignment Scores:
Pred. No.: 7.77e-36 Length: 1275
Score: 575.50 Matches: 110
Percent Similarity: 72.73% Conservative: 34
Best Local Similarity: 55.56% Mismatches: 53
Query Match: 0.66% Indels: 2
DB: 2 Gaps: 1

US-09-396-985B-48 (1-50000) x B28096 (1-1275)
Qy 36378 ATTGAATAATGGGGGTACAGAACTAAAGAGAAATTCACATGAGATCTGATGACT 36319
Dh 1069 lIlelylsystrpAlaAlaAspMetAsnArghIsPheSerlysluAspIleTyrlaAla 1088
Qy 36318 GAAAGACTTAATAAAATGTTTAACATCTTACTGACAGAGAGAGAGAGAGAGAGAG 36259
Dh 1089 lylslyshIsmetlyslsCyseSerSerleuAlaIlearglImetGlnIlelystr 1108
Qy 36258 ACCGTGATATTCACCTTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 36199
Dh 1109 ThmetarglyrthlsleuIntrProvalArgmetAlaIlelelyslsSerGlyAsnAsn 1128
Qy 36198 AGATGCTGCAAGA-TGTAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 36140
Dh 1129 ArgCystrpArgGlyCyglGlnIleGlyThrleuLeuIhIsCystrpTrpAspCylyS 1148
Qy 36139 CTGATATACCACTCTGAGAAATCACTTTGGTGTCTCTCAAGAAATTTGACATGGTACTA 36080
Dh 1149 leuValGlnProleuTrpIlySerValItrpArgPheleuArGAspIleuGlnle 1168
```

```
Qy 36079 CTGAGGATCCAGCAATPACCACTCAAGGCAATATCCAGATGAT---GCTTACCTTGT 36023
Dh 1169 ProPheAspProAlaIleProleuLeuGlyIleTytrPheAsnAspTyrlsSerCyS 1188
Qy 36022 AATAGGACACATGCTCTACTATGTTTCATPAGCAGTTTATTTAAATAGCAGATGCTTG 35963
Dh 1189 TyrlsAspArhtrCyshtrArgmetPheIleAlaIleuPhehtrIleAlaIlystrtrp 1208
Qy 35962 AAAAGACTTGAATGTCCTCTCAACAGAGAAATGAGATACAAAATATGTCATTTGACA 35903
Dh 1209 AsnGlnProlyscysProthrmecIleAspTrpIlelyslsmetTrpIhIsIleTytr 1228
Qy 35902 GTGAGATCATGACGCTATTTAAACAGTGAATCTATGACATCTTACGAGAAATGAATG 35843
Dh 1229 MetGlnTytrAlaAlaIlelysaAsnAspGlnPhehSerIhValaGlythrmec 1248
Qy 35842 GACCTGAGGAGCATCATCTGACTGAGATGATACCACTCATTAAGAGAGACACAT 35789
Dh 1249 lylleuGlnuthrIleIleleuSerlyslsSerGlnGlnlystrhlyshIs 1266

RESULT 6
B34087
hypothetical protein (LIN 3' region) - human
C/Species: Homo sapiens (man)
C/Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
C/Accession: B34087
R:Scott, A.F.; Schmeckpeper, B.J.; Abdelrazik, M.; Comey, C.T.; O'Hara, B.; Rosolter, J.I
Genomics 1, 113-125, 1987
A>Title: Origin of the human LI elements: proposed progenitor genes deduced from a conser
A/Reference number: A34087; MUID:88085185; PMID:3692483
A/Accession: B34087
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-1280 <SCO>
A/Cross-references: UNIPROT:Q9Y5K0
C/Superfamily: pol polyprotein

Alignment Scores:
Pred. No.: 9.34e-36 Length: 1280
Score: 573.50 Matches: 110
Percent Similarity: 71.08% Conservative: 35
Best Local Similarity: 53.92% Mismatches: 58
Query Match: 0.66% Indels: 2
DB: 2 Gaps: 1

US-09-396-985B-48 (1-50000) x B34087 (1-1280)
Qy 36378 ATTGAATAATGGGGGTACAGAACTAAAGAGAAATTCACATGAGATCTGATGACT 36319
Dh 1074 lIlelylsystrpAlaAlaAspMetAsnArghIsPheSerlysluAspIleTyrlaAla 1093
Qy 36318 GAAAGACTTAATAAAATGTTTAACATCTTACTGACAGAGAGAGAGAGAGAGAGAG 36259
Dh 1094 AsnlyshIsmetlyslsCyseSerSerleuAlaIlearglImetGlnIlelystr 1113
Qy 36258 ACCGTGATATTCACCTTACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 36199
Dh 1114 ThmetarglyrthlsleuIntrProvalArgmetAlaIlelelyslsSerGlyAsnAsn 1133
Qy 36198 AGATGCTGCAAGA-TGTAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 36140
Dh 1134 ArgCystrpArgGlyCyglGlnIleGlyThrleuLeuIhIsCystrpTrpAspCylyS 1153
Qy 36139 CTGATATACCACTCTGAGAAATCACTTTGGTGTCTCTCAAGAAATTTGACATGGTACTA 36080
Dh 1154 leuValGlnProleuTrpIlystrhtrValItrpArgPheleuylsAspIleuGlnle 1173
Qy 36079 CTGAGATCCAGCAATPACCACTCAAGGCAATATCCAGATGAT---GCTTACCTTGT 36023
Dh 1174 ProPheAspProAlaIleProleuLeuGlyIleTytrProlysaAspTyrlsSerCyS 1193
Qy 36022 AATAGGACACATGCTCTACTATGTTTCATPAGCAGTTTATTTAAATAGCAGATGCTTG 35963
```

```
Db 1194 TyrlysaSprThrCysThrArgMetPheIleAlaIaleuphethrIleAlaIeThrTrrp 1213
Oy 35962 AAAGACCTAGATGTCCTCCACAGAGAAATGATACAAAATAATGTTGATCTTGACA 35903
Db 1214 AsnGlnProIysCysProMetIleAspTrpIleIysLysMetTrpHisIleTyrThr 1233
Oy 35902 GTGAGTACTATGACGTATTAAAACAGTGAATCTATGACATCTTGAAGCAATGAATG 35843
Db 1234 MetGlnTyrTrpAlaIleIleLysAsnAspGlnPheMetSerPheValGlyThrTrpMet 1253
Oy 35842 GACCTGAGGCGATCATCTGAGTGAAGTAAACCCAGTCATAAAAGAGACATGATATG 35783
Db 1254 LysLeuGlnThrIleIleLeuSerLysLeuSerGlnGlnGlnLysThrLysHisArgMet 1273
Oy 35782 CACTTAATCTG 35771
Db 1274 PheSerLeuIle 1277

RESULT 7
I38588
Reverse transcriptase homolog - human retrotransposon L1
N/Alternate names: ORF2 protein
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R/Dombroski, B.A.; Krebs, C.M.; Boehm, C.D.; Kazazian, H.H.
Nature Genet. 7, 143-148, 1994
A/Title: A new retrotransposable human L1 element from the LINE2 locus on chromosome 1q
A/Reference number: I38587; MUID:95004577; PMID:7920631
A/Accession: I38588
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1275 <RES>
A/Cross-references: UNIPROT:Q12881; EMBL:U09116; NID:g483914; PIDN:AAB60345.1; PID:g4839
C/Superfamily: pol polyprotein

Alignment Scores:
Pred. No.: 1,356-35 Length: 1275
Score: 572.50 Matches: 109
Percent Similarity: 72.73% Conservative: 35
Best Local Similarity: 55.05% Mismatches: 53
Query Match: 0.66% Indels: 2
Gaps: 1

US-09-396-985b-48 (1-50000) x I38588 (1-1275)
Oy 36378 ATTGAATAATGGGGTACAGAACTAAAGAAATTCACACTGAGATCTGAATGACT 36319
Db 1069 IleLysLysTrpAlaLysAspMetAsnArgHisPheSerLysGlnAspIleTyrAlaIa 1088
Oy 36318 GAAAGTACTAAATAAAATGTTTAAATCTTACTGATCAGGGAATGCAATCAATAACA 36259
Db 1089 LysLysHisMetLysLysCysSerSerLeuAlaIleArgLysMetGlnIleLysThr 1108
Oy 36258 ACCCTGATATTCCTTCAACCACTGATGATGATGATGATGATGATGATGATGATGATG 36199
Db 1109 ThrMetArgTyrHisLeuThrProValArgMetAlaIleLysLysSerGlyAsnAsn 1128
Oy 36198 AGATGTCGCAAGA-TGTAGAGAGAGAGAACACTCTTCATTTGCTGCGACAGATGTAA 36140
Db 1129 ArgCysTrpArgGlyCysGlyGlnIleLysThrLeuLeuHisCysTrpTrpAspCysLys 1148
Oy 36139 CTGATATACCACTCTGGAATATCAGTTGTGTCTCTCAGAAAATTTGACATGCTACTA 36080
Db 1149 LeuValGlnProLeuTrpLysSerValTrpArgPheLeuArgAspLeuGlnLeuGlnIle 1168
Oy 36079 CCTGAGATCCAGCAATACCACTCCAAAGCAATATTCAGATGAT---GCTTACCTTGT 36023
Db 1169 ProPheAspProAlaIleProLeuLeuGlnIleTyrProGlnAspTyrLysSerCysCys 1188
Oy 36022 AATAGACACATGCTCTACTATGTTTCATACAGTTTATTATTAATGACCAATGCTTG 35963
```

```
Db 1189 TyrlysaSprThrCysThrArgMetPheIleAlaIaleuphethrIleAlaIeThrTrrp 1208
Oy 35962 AAAGACCTAGATGTCCTCCACAGAGAAATGATACAAAATAATGTTGATCTTGACA 35903
Db 1209 AsnGlnProIysCysProMetIleAspTrpIleIysLysMetTrpHisIleTyrThr 1228
Oy 35902 GTGAGTACTATGACGTATTAAAACAGTGAATCTATGACATCTTGAAGCAATGAATG 35843
Db 1229 MetGlnTyrTrpAlaIleIleLysAsnAspGlnPheMetSerPheValGlyThrTrpMet 1248
Oy 35842 GACCTGAGGCGATCATCTGAGTGAAGTAAACCCAGTCATAAAAGAGACAT 35789
Db 1249 LysLeuGlnThrIleIleLeuSerLysLeuSerGlnGlnGlnLysThrLysHis 1266

RESULT 8
S65824
Reverse transcriptase homolog - human transposon L1.1
C/Species: Homo sapiens (man)
C/Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
R/Dombroski, B.A.
Submitted to the EMBL Data Library, January 1992
A/Description: Isolation of an active human transposable element.
A/Reference number: S65823
A/Accession: S65824
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1275 <DOM>
A/Cross-references: UNIPROT:Q15604; EMBL:M80340; NID:g339767; PIDN:AAA51622.1; PID:g3397
C/Superfamily: pol polyprotein

Alignment Scores:
Pred. No.: 3,376-35 Length: 1275
Score: 567.50 Matches: 108
Percent Similarity: 72.73% Conservative: 36
Best Local Similarity: 54.55% Mismatches: 53
Query Match: 0.65% Indels: 2
Gaps: 1

US-09-396-985b-48 (1-50000) x S65824 (1-1275)
Oy 36378 ATTGAATAATGGGGTACAGAACTAAAGAAATTCACACTGAGATCTGAATGACT 36319
Db 1069 IleLysLysTrpAlaLysAspMetAsnArgHisPheSerLysGlnAspIleTyrAlaIa 1088
Oy 36318 GAAAGTACTAAATAAAATGTTTAAATCTTACTGATCAGGGAATGCAATCAATAACA 36259
Db 1089 LysLysHisMetLysLysCysSerSerLeuAlaIleArgLysMetGlnIleLysThr 1108
Oy 36258 ACCCTGATATTCCTTCAACCACTGATGATGATGATGATGATGATGATGATGATGATG 36199
Db 1109 ThrMetArgTyrHisLeuThrProValArgMetAlaIleLysLysSerGlyAsnAsn 1128
Oy 36198 AGATGTCGCAAGA-TGTAGAGAGAGAGAACACTCTTCATTTGCTGCGACAGATGTAA 36140
Db 1129 ArgCysTrpArgGlyCysGlyGlnIleLysThrLeuLeuHisCysTrpTrpAspCysLys 1148
Oy 36139 CTGATATACCACTCTGGAATATCAGTTGTGTCTCTCAGAAAATTTGACATGCTACTA 36080
Db 1149 LeuValGlnProLeuTrpLysSerValTrpArgPheLeuArgAspLeuGlnLeuGlnIle 1168
Oy 36079 CCTGAGATCCAGCAATACCACTCCAAAGCAATATTCAGATGAT---GCTTACCTTGT 36023
Db 1169 ProPheAspProAlaIleProLeuLeuGlnIleTyrProGlnAspTyrLysSerCysCys 1188
Oy 36022 AATAGACACATGCTCTACTATGTTTCATACAGTTTATTATTAATGACCAATGCTTG 35963
Db 1189 TyrlysaSprThrCysThrArgMetPheIleAlaIaleuphethrIleAlaIeThrTrrp 1208
Oy 35962 AAAGACCTAGATGTCCTCCACAGAGAAATGATACAAAATAATGTTGATCTTGACA 35903
Db 1209 AsnGlnProIysCysProMetIleAspTrpIleIysLysMetTrpHisIleTyrThr 1228
```

QY 35902 GTGAGTACTATGAGCTATTAAACAGTGAATCTATGACATTCCTTAGGCAATGATG 35843
Db 1229 MetGluTyrTrpAlaAlaIleLysAsnAspGluPheValSerPheValGlyThrTrpMet 1248
QY 35842 GACCTGAGGGCATCTCTGAGTGAAGTAAACCGATCATTAAGAAAGACACAT 35789
Db 1249 LysLeuGluThrIleIleLeuSerLysLeuSerGlnGluGlnLysThrLysHis 1266

RESULT 9

S23650
retrovirus-related hypothetical protein II - human retrotransposon LINE-1
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C/Accession: S23650
R/Holm, H.; Minakami, R.; Sakaki, Y.
Nucleic Acids Res. 18, 4099-4104, 1990
A/Title: Selective cloning and sequence analysis of the human L1 (LINE-1) sequences which
A/Reference number: S23649; MUID:90332398; PMID:2165587
A/Accession: S23650
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-712 <HON>
A/Cross-references: UNIPROT:Q15604; UNIPROT:Q9UN80; UNIPROT:Q12881; UNIPROT:O00363; UNIPROT:Q14754; UNIPROT:Q9Y5K0; UNIPROT:O00366; UNIPROT:O8TB30; UNIPROT:O00375; EMBL:X52235
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990
C/Keywords: reverse transcriptase; pseudogene
A/Mobile element: LINE-1
A/Start codon: GTG
C/Superfamily: pol polyprotein

Alignment Scores:

Pred. No.:	5,54e-35	Length:	712
Score:	563.50	Matches:	109
Percent Similarity:	71.72%	Conservative:	33
Best Local Similarity:	55.05%	Mismatches:	55
Query Match:	2	Indels:	2
DB:	2	Gaps:	1

US-09-396-985b-48 (1-50000) x S23650 (1-712)

QY 36378 ATTGAATAATGGGGTACAGAACTTAAGAGAAATTTCTCACTGAGAAATCTGAATGACT 36319
Db 506 TleLysLysTrpAlaLysAspMetAsnArgHisPheSerLysGluAspIleTyrAlaAla 525
QY 36318 GAAAGTAACTTAATAAATGTTTAACATCTTACTGATCAAGGAAATGCAATCAAAACA 36259
Db 526 LysLysHisMetLysLysCysSerProSerLeuAlaIleArgGlnMetGlnIleLysThr 545
QY 36258 ACCCTGATATTCACCTTCACACAGTCAAGATGATGAATCAAAATCTCAATGACAGC 36199
Db 546 ThrMetArgTyrHisLeuThrProValArgMetAlaIleIleLysLysSerGlyAsnAsn 565
QY 36198 AGATGCTCGCAGA-TGTAGAGAGAGAGAACTTTCTTCATTCCTGGCAGAACTGTAA 36140
Db 566 ArgCysTrpArgGlyCysGlyGluIleGlyThrLeuLeuHisCysTrpTrpAspCysLys 585
QY 36139 CTGATATTAACACCTCTGGAATCACTTGTGGTCTCTCAAGAAATGAGACATGACTA 36080
Db 586 LeuValGlnProLeuTrpLysSerValTrpArgPheLeuArgAspLeuGluProGluIle 605
QY 36079 CCTGAGATCCAGCAATCACTCCAAAGCAAAATATCCAGATGATGCT---TCACTTGT 36023
Db 606 ProPheAspProAlaIleProLeuLeuGlyIleTyrProLysAspSerLysSerCysLys 625
QY 36022 AATAGACACATCTCTACTATGTTTCATAGCAGTTTATTTATTAATAGCCAGATGCTTG 35963
Db 626 TyrLysAspThrCysThrArgMetPheIleAlaIleAsnPheThrIleAlaLysThrTrp 645
QY 35962 AAAAGACCTAGATGCTCCCTCAACAGAGAAATGATACAAAATATGATGATTTGACA 35903
Db 646 AsnGlnProLysCysProThrMetIleAspTrpIleLysLysMetLysThrPheHisIleTyrThr 665
QY 35902 GTGAGTACTATGAGCTATTAAACAGTGAATCTATGACATTCCTTAGGCAATGATG 35843

Db 666 MetGluTyrTrpAlaAlaIleLysAsnAspGluPheValSerPheValGlyThrTrpMet 685
QY 35842 GACCTGAGGGCATCTCTGAGTGAAGTAAACCGATCATTAAGAAAGACACAT 35789
Db 686 LysLeuGluThrIleIleLeuSerLysLeuSerGlnGluGlnLysThrLysHis 703

RESULT 10

GNHUL1
retrovirus-related reverse transcriptase pseudogene - human
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1988 #sequence_revision 04-Jan-1996 #text_change 09-Jul-2004
C/Accession: A25313
R/Hattori, M.; Kohara, S.; Takenaka, O.; Sakaki, Y.
Nature 321, 625-628, 1986
A/Title: L1 family of repetitive DNA sequences in primates may be derived from a sequence
A/Reference number: A93381; MUID:86230917; PMID:2423883
A/Accession: A25313
A/Status: conceptual translation of pseudogene
A/Molecule type: DNA
A/Residues: 1-1259 <HAT>
A/Cross-references: UNIPROT:P08547
A/Note: this sequence was constructed from an alignment of published and unpublished seq
C/Keywords: reverse transcriptase; pseudogene

Alignment Scores:

Pred. No.:	1.1e-33	Length:	1259
Score:	547.50	Matches:	106
Percent Similarity:	72.40%	Conservative:	33
Best Local Similarity:	55.21%	Mismatches:	52
Query Match:	4	Indels:	2
DB:	4	Gaps:	1

US-09-396-985b-48 (1-50000) x GNHUL1 (1-1259)

QY 36378 ATTGAATAATGGGGTACAGAACTTAAGAGAAATTTCTCACTGAGAAATCTGAATGACT 36319
Db 1068 TleLysLysTrpAlaLysAspMetAsnArgHisPheSerLysGluAspIleTyrAlaAla 1087
QY 36318 GAAAGTAACTTAATAAATGTTTAACATCTTACTGATCAAGGAAATGCAATCAAAACA 36259
Db 1088 LysLysHisMetLysLysCysSerProSerLeuAlaIleArgGlnMetGlnIleLysThr 1107
QY 36258 ACCCTGATATTCACCTTCACACAGTCAAGATGATGAATCAAAATCTCAATGACAGC 36199
Db 1108 ThrMetArgTyrHisLeuThrProValArgMetAlaIleIleLysLysSerGlyAsnAsn 1127
QY 36198 AGATGCTCGCAGA-TGTAGAGAGAGAGAACTTTCTTCATTCCTGGCAGAACTGTAA 36140
Db 1128 ArgCysTrpArgGlyCysGlyGluIleGlyThrLeuLeuHisCysTrpTrpAspCysLys 1147
QY 36139 CTGATATTAACACCTCTGGAATCACTTGTGGTCTCTCAAGAAATGAGACATGACTA 36080
Db 1148 LeuValGlnProLeuTrpLysSerValTrpArgPheLeuArgAspLeuGluLeuGluIle 1167
QY 36079 CCTGAGATCCAGCAATCACTCCAAAGCAAAATATCCAGATGATGCT---GCTTCACTTGT 36023
Db 1168 ProPheAspProAlaIleProLeuLeuGlyIleTyrProLysAspTrpLysSerCysLys 1187
QY 36022 AATAGACACATCTCTACTATGTTTCATAGCAGTTTATTTATTAATAGCCAGATGCTTG 35963
Db 1188 TyrLysAspThrCysThrArgMetPheIleAlaIleAsnPheThrIleAlaLysThrTrp 1207
QY 35962 AAAAGACCTAGATGCTCCCTCAACAGAGAAATGATACAAAATATGATGATTTGACA 35903
Db 1208 AsnGlnProLysCysProThrMetIleAspTrpIleLysLysMetLysThrPheHisIleTyrThr 1227
QY 35902 GTGAGTACTATGAGCTATTAAACAGTGAATCTATGACATTCCTTAGGCAATGATG 35843
Db 1228 MetGluTyrTrpAlaAlaIleLysAsnAspGluPheMetSerProValGlyThrTrpMet 1247
QY 35842 GACCTGAGGGCATCTCTGAGTGAAGTAAACCGATCATTAAGAAAGACACAT 35789

Db 1248 LysleuGIuThrIleIleLeuSerIylLeuSerGln 1259

RESULT 11

156258 RPI05 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: I56258

R:Myake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.

J:Immunol. 154, 3333-3340, 1995

A:Title: RPI05, a novel B cell surface molecule implicated in B cell activation, is a me

A:Reference number: I56258; MUID:95204928; PMID:7897216

A:Accession: I56258

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-661 <RES>

A:Cross-references: UNIPROT:Q62192; GB:D37797; NID:9761711; PIDN:BAA07043.1; PID:9761712

Alignment Scores:

Pred. No.:	Length:	661
Score:	491.50	Matches: 155
Percent Similarity:	44.48%	Conservative: 115
Best Local Similarity:	25.54%	Mismatches: 288
Query Match:	0.57%	Indels: 49
DB:	2	Gaps: 15

US-09-396-985B-48 (1-50000) x I56258 (1-661)

QY 37706 ATATTGGTATCTCTTTGGCCAT-----AGTGTGAATTTGAAACATTTGAAGACAG 37759

Db 76 LeuIleAsnLeuThrPheLeuAspLeuThrArgCysGlnIleYrIleIleGluAsp 95

QY 37760 GCATGGCATGGCTTAACACCATCTGCAAACTTGATGACAGAGAAACCTTACAGAGT 37819

Db 96 ThrPheGlnSerGlnHisArgLeuAspThrLeuValLeuThrIleAsnProLeuIlePhe 115

QY 37820 TTTTCCCGAGAGAGTTCTCTGCACTAACAAGTTTAGAAGATCTGTGGCTGTGGAGACA 37879

Db 116 MetAlaGluThrAlaLeuSerGlyProlysalLeuIleuHisLeuPhePheIleGlnThr 135

QY 37880 AAATTGGCTCTTGAAGAAAGCTTCCCTATTTGACAGCTTATTAACCTTAAAGAACTCAAT 37939

Db 136 GlyIleSerSerIleAspPheIleProLeuHisAsnGlnIleYrLeuGlnSerLeuIleYr 155

QY 37940 GTGGCTCAACATTTTATATCATCTCTGTAATTAAGTTTACCTGATTTTTCACATCTGACGAC 37999

Db 156 LeuGlySerAsnHisIleSerSerIleYleuProlysglyPheProthr--GluIys 174

QY 38000 CTAGTACATGTGATCTTTCTTATATCATATTAATCAAACTTATCTGACAGCTTACAG 38059

Db 175 LeuIleValLeuAspPheGlnAsnAsnAlaIleHisIleYrLeuSerIylGluAspMetSer 194

QY 38060 TTTTCTAGTGAAGAAATCCACAAGTCAATCTCTTTAGACATGTCTTTGAACCAATTGAC 38119

Db 195 SerIleuGlnGln-----AlaThrAsnLeuSerLeuAsnGlnIleAsnAspIleAla 212

QY 38120 TTCAATCAAGACCAAGCTTTGAGGAATTAAAGTCCATGACATGACCTTAAGAGTTAAT 38179

Db 213 GlyIleLeuProGlyAlaPheAspSerAlaValPheGlnSerLeu-----Asn 228

QY 38180 TTTTAATGCTCAAAATATATATGAAGAACTTGCTTCAAACTGCTGTTTACAGTTCAT 38239

Db 229 PheIleGlyIleThrGlnAsnLeuValIlePheIleGlyLeuIleuAsnSerThrIleGln 248

QY 38240 CGGTGATCTTTGGAGAAATTTAAAGATGAAGAAATCTGCAAAATTTTGAACCTCTATC 38299

Db 249 SerIleuThrLeuGlyIleThrPheGlnAspMetAspAspGluIle-----SerProAlaVal 267

QY 38300 ATGAGAGACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38359

Db 268 PheGlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 287

QY 38360 TCAGATGATATTTGTAAGTTCCATGCTGTGGCAATGTTTCTGCAATGCTCTGCGAGGT 38419

Db 288 AsnIleSerSerAsnThrPheHisCysPheSerGlyLeuGlnGluLeuAspLeuThrAla 307

QY 38420 GTATCTATAAATATCTTAAGAAATGTTCTTAACATTTCC----- 38458

Db 308 Thr-----HisLeuSerGlnLeuProSerGlyLeuValGlyLeuSerThrLeuIys 324

QY 38459 -----AAATGGCAATCTTTATCAATCATATGATGCAACTT--- 38494

Db 325 LysLeuValLeuSerAlaAsnIleYsPheGluAsnLeu-----CysGlnIleSer 340

QY 38495 ---AAGAGTTTCCAACTGTGATCTTAACCTTTGTAAGTTGACTTAACTTAACAGAC 38551

Db 341 AlaSerAsnPheProSerLeuThrHisLeuSerIleYsGlyAsnThrIleYsArgLeuGlu 360

QY 38552 AAAGGCTCTATCACTTTTAAAAAGTGCCCTTACCAAGTCTCACTATCTGATCTTATG 38611

Db 361 LeuGlyThrGlyCysLeuGluAsn-----LeuGluAsnLeuArgGluLeuAspLeuSer 378

QY 38612 AGAATGACATGACCTTGAAGTGTGCTGTTCTTATCTGATTTGGGAACAACAGCCTG 38671

Db 379 HisAspAspIleGluThrSerAspCysAsnLeuGlnLeuAlaGlnLeuSerHisLeu 398

QY 38672 AGACACTTGAACCTCACTCAATGATGACATTAATGAGTGCAT--TTCAATGGGT 38728

Db 399 GlnSerLeuAsnLeuSerIylAsnGluProLeuSerLeuIleYrThrGluAlaPheIleGlu 418

QY 38729 CTAGAAGCTGCGACGACCTGATTTTACAGACCTCTTATTAAGAGGTACAGAAATTC 38788

Db 419 CysProGlnIleuGlnIleuLeuAspLeuAlaPheThrArgLeuValIleYsAspAlaGln 438

QY 38789 TCAGCTTTTATACCTTGAAGGCTTATTAACCTTGAACATCTGTTATCTTAACACCAA 38848

Db 439 SerProPheGlnAsnHisIleuLeuIleValLeuAsnLeuSerHisIleuLeuAsp 458

QY 38849 ATTGACTTGAATGATATTTCTTGGCTTGAACAGCTTCAACAATTAAGATGAGTGC 38908

Db 459 IleSerSerGlnIleuPheAspGlyLeuProAlaLeuGlnHisIleuAsnLeuGlnGly 478

QY 38909 AATTCTTTCAAGACCAACCCCTT-----TCAATGCTTTTGAACAACAACAACCTTG 38962

Db 479 AsnHisPheProlysglyAsnIleGlnIleYsThrAsnIleuGlnThrLeuGlyArgLeu 498

QY 38963 ACATCTGTGATCTTTTAATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39022

Db 499 GluIleuValLeuSerPheCysAspLeuSerSerIleAspGlnHisAlaPheThrSer 518

QY 39023 CTCATGACCTCAATATTAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39076

Db 519 LeuIleMetMetAsnHisValAspLeuSerHisAsnArgLeuThrIleSerSerIleGlu 538

QY 39077 ---TCATCCATTAATCAACAGCTGATCTCCCTGACAGCTTGTGATGCAATTCATGCC 39133

Db 539 AlaLeuSerHisIleuIleYr-----LeuAsnLeuAlaSerAsnHis 554

QY 39134 ATAGAGACATCTAAAGAAATATGCAACATTTTCAAAAGGTGAGCTTCTTAACCTT 39193

Db 555 IleSerIleIleLeuProSerLeuProIleuSerGlnGlnAlaGlnThrIleAsnLeu 574

QY 39194 ACTTAACATCTGTGCTTATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39253

Db 575 ArgGlnAsnProLeuAspCysThrCysSerAsnIleYrPheLeuGluThrIlePheGlu 594

QY 39254 CAGAAGCATTTCTTGGATGTTGAACAATGATGATGATGATGATGATGATGATGATGATGATGAT 39313

Db 595 AsnMetGlnIleuLeuGluAspThrGluAspThrLeuIleuIleuAsnProLeuLeuArg 614

QY 39314 -----ACCTCTTAAGTGTGATTTTAATATCTACCTGTTATATGATGATGATGATGATGATGAT 39361

Db 615 GlyValArgLeuSerAspValThrLeuSerCysSerMetAlaAlaValGlyIlePhePhe 634

QY 39362 ACAATCATCACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39421


```
Db      1216 etlleasp-----TripleLysLysMetTrpHisIleTyrThrMetGluTyrTyrA 1233
QY      5754 CAGAA---AAAAAAGTGAATATATACAAATTTAGGAAATGTCATGCGATTATAAAATT 5810
Db      1233 laalaileLysAsnAspGluPheIleSerPheValGlyThrTrpMetLysLysGluThrI 1253
QY      5811 ATACTCAGACTGGAATTACAAAAATTTCAGAACTGAGCAATAGTCCTTATTCAGAAAG 5870
Db      1253 lelle-----LeuSerLysLeuSerGlnGlu-----GlnLysT 1264
QY      5871 ACAATACTATATATATATACCTC 5893
Db      1264 hrlYshIleArgIlePheSerLeu 1271
```

Search completed: March 30, 2005, 03:00:40
Job time : 2473 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 29, 2005, 11:30:23 ; Search time 2837 Seconds
(without alignments)
18050.024 Million cell updates/sec

Title: US-09-396-985B-48

Perfect score: 86900
Sequence: 1 ttccacatcatgatagatgc.....catttagtattattccaga 50000

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6449512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame_n2p_model -DEV=xlh
-Q=/cgm2_1/USFPO.spool/US09396985/runcat_28032005_155743_21146/app_query.fasta_1.85098
-DB=uniprot_03 -QMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blowsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USRR=US09396985 @CNC 1.1 5213 @runcat_28032005_155743_21146 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	ID	Description
1	3895	4.5	835	1	TIR4_MOUSE
2	3876	4.5	835	2	Q8K2T5
3	3382	3.9	835	1	TIR4_RAT
4	3155	3.6	838	1	TIR4_CRICR
5	2607	3.0	839	1	TIR4_HUMAN
6	2607	3.0	839	1	TIR4_PANPA
7	2597	3.0	826	1	TIR4_PANPA
8	2582	3.0	837	2	Q8SPF8
9	2580	3.0	828	1	TIR4_PONPY
10	2578	3.0	841	1	TIR4_BOVIN
11	2575	3.0	841	2	Q8S0S5
12	2573	3.0	841	2	Q6WCDS
13	2571	3.0	841	2	Q6WCDS
14	2567	3.0	843	1	TIR4_HORSE
15	2522.5	2.9	833	1	TIR4_FELCA
16	2507	2.9	841	1	TIR4_PIG

17	2374	2.7	839	2	Q8MIQ2
18	1967	2.3	636	2	Q8SCH3
19	1576.5	1.8	843	2	Q7ZTGS
20	1118	1.3	819	2	Q6T541
21	1107	1.3	817	2	Q6NV08
22	897	1.0	1015	2	Q7TMA9
23	767.5	0.9	477	2	Q7R857
24	765.5	0.9	1281	2	Q91288
25	765.5	0.9	1281	2	Q91289
26	765.5	0.9	1300	1	BOL2_MOUSE
27	765.5	0.9	1300	2	Q61785
28	764	0.9	432	2	Q7R714
29	762	0.9	1281	2	Q88915
30	769.5	0.9	258	2	Q70EKA
31	760.5	0.9	627	2	Q7RAY6
32	761	0.9	1300	2	Q08906
33	756	0.9	1219	2	Q9QIM3
34	756	0.9	1281	2	Q54850
35	756	0.9	1281	2	Q88913
36	756	0.9	1281	2	Q88914
37	756	0.9	1281	2	Q79219
38	756	0.9	1281	2	Q9QIT2
39	756	0.9	1281	2	Q9QWY0
40	756	0.9	1281	2	Q9QWY3
41	751	0.9	1714	2	Q6Q178
42	745	0.9	1446	2	Q7TP07
43	743	0.9	621	2	Q6Q153
44	741	0.9	516	2	Q6Q192
45	738.5	0.9	1217	2	Q6TUP6

ALIGNMENTS

RESULT 1
ID TIR4_MOUSE
AC Q9QUK6; Q9D691; Q9QZFS; Q9Z203; PRT; 835 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=Tlr4; Synonyms=Lps;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ;
RX MEDLINE=99167984; PubMed=10087992; DOI=10.1006/bcmd.1998.0201;
RA Poltorak A., Smirnova I., He X., Liu M.-Y., Van Huffel C., Du X.,
RA Birdwell D., Alejos E., Silva M., Du X., Thompson P., Chan E.K.L.,
RA Ledesma J., Roe B., Clifton S., Vogel S.N., Beutler B.,
RT "Genetic and physical mapping of the lps locus: identification of the
RT Toll-4 receptor as a candidate gene in the critical region."
RT Blood Cells Mol. Dis. 24:340-355(1998).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANT LPS-TOLERANT HIS-712.
RC STRAIN=C3H/HeJ;
RX MEDLINE=9905627; PubMed=9851930; DOI=10.1126/science.282.5396.2085;
RA Poltorak A., He X., Smirnova I., Liu M.-Y., Van Huffel C., Du X.,
RA Birdwell D., Alejos E., Silva M., Galanos C., Freudenberg M.,
RA Ricciardi-Castagnoli P., Layton B., Beutler B.,
RT "Defective LPS signaling in C3H/HeJ and C57BL/10ScCr mice: mutations
RT in Tlr4 gene."
RT Science 282:2085-2088(1998).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT LPS-TOLERANT HIS-712.
RC STRAIN=C57BL/6J;
RX MEDLINE=99145502; PubMed=9989976;
RA O'Neill S.T., Laviere L., Leveque G., Clermont S., Moore K.U.,
RA Gros P., Malo D.,
RT "Endotoxin-tolerant mice have mutations in Toll-like receptor 4

RT (TLR4).";

RL J. Exp. Med. 189:615-625 (1999).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Macrophage;

RX MEDLINE=0014145; PubMed=10548109; DOI=10.1038/44605;

RA Underhill D.M., Ozolsky A., Hajjar A.M., Stevens A., Wilson C.B.,

RA Bassetti M., Adereem A.;

RT "The Toll-like receptor 2 is recruited to macrophage phagosomes and

RT discriminates between pathogens.";

RL Nature 401:811-815 (1999).

RN [5]

RP SEQUENCE FROM N.A., AND VARIANTS ASN-94; ILE-209; GLY-219; ILE-254;

RP LRU-423; SER-477; ALA-516; ASP-593; ILE-600; VAL-607; ILE-637; HIS-761

RP AND LYS-811.

RC STRAIN=Various strains;

RX MEDLINE=20558910; PubMed=1104518;

RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;

RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4

RT locus (TLR4).";

RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10 (2000).

RN [6]

RP SEQUENCE OF 1-154 FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Skin;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki I., Furuno M., Kaanaka T., Adachi J., Bono H., Kondo S.,

RA Nikaiko I., Osato N., Saico R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schindach C., Gojohori T.,

RA Baldecelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Schirral L.M., Kanapin A., Matsumoto H., Batalov S., Beisel K.W.,

RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,

RA Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J.,

RA Grimmerand T., Gustinch S., Hirokawa N., Jackson I.J., Jarvis E.D.,

RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Kanagaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,

RA Meglath D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Nimata K., Okido T., Pavan W.J., Petrea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontus J.U., Qi D., Ramchandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Saitana R., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Wainstedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wymshaw-Boris A., Yanagisawa M., Yang L., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

RA Yaumishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573 (2002).

RN [7]

RP FUNCTION.

RX MEDLINE=20507837; PubMed=10952994; DOI=10.1074/jbc.M007386200;

RA Rhee S.H., Hwang D.;

RT "Murine Toll-like receptor 4 confers lipopolysaccharide responsiveness

RT as determined by activation of NF kappa B and expression of the

RT inducible cyclooxygenase.";

RL J. Biol. Chem. 275:34035-34040 (2000).

RN [8]

RP FUNCTION: Cooperates with LY96 and CD14 to mediate the innate

RP immune response to bacterial lipopolysaccharide (LPS). Acts via

RP MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine

RP secretion and the inflammatory response (By similarity).

CC -1 SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a

CC multi-protein complex containing at least CD14, LY96 and TIRAP.

CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via

CC their respective TIR domains.

CC -1 SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -1 TISSUE SPECIFICITY: Highly expressed in heart, spleen, lung and

CC muscle. Lower levels are found in liver and kidney.

CC -1 POLYMORPHISM: Interstrain analyses reveals that TLR4 is a

CC polymorphic protein and that the extracellular domain is far more

CC variable than the cytoplasmic domain, which is variable at the C-

CC terminal.

CC -1 DISEASE: The protein is encoded by the Lps locus, an important

CC susceptibility locus, influencing the propensity to develop a

CC disseminated Gram-negative infection.

CC -1 SIMILARITY: Belongs to the Toll-like receptor family.

CC -1 SIMILARITY: Contains 19 leucine-rich (LRR) repeats.

CC -1 SIMILARITY: Contains 1 TIR domain.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF095353; AAC9411.1; -;

DR EMBL; AF185285; AAF04278.1; -;

DR EMBL; AF110133; AAD29272.1; -;

DR EMBL; AF17767; AAF05317.1; -;

DR EMBL; AK014533; -; NOT_ANNOTATED_CDS.

DR HSSP; Q15399; 1FVY.

DR MGD; MGI:96824; Tlr4.

DR GO; GO:0046596; C:lipopolysaccharide receptor complex; ISS.

DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.

DR GO; GO:0004888; F:transmembrane receptor activity; ISS.

DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; NAS.

DR GO; GO:0016046; P:detection of fungi; ISS.

DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.

DR GO; GO:0042116; P:macrophage activation; ISS.

DR GO; GO:0045576; P:negative regulation of osteoclast different. . . ; ISS.

DR GO; GO:0045571; P:negative regulation of interleukin-1 biosyn. . . ; NAS.

DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; NAS.

DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.

DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; NAS.

DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; NAS.

DR GO; GO:0042088; P:helper 1 type immune response; ISS.

DR InterPro; IPR001611; LRR.

DR InterPro; IPR000483; LRR_Cterm.

DR InterPro; IPR00157; TIR.

DR Pfam; PF00560; LRR; 10.

DR Pfam; PF01582; TIR; 1.

DR PRINTS; PR00019; LEURICRPT.

DR SMART; SM00082; LRRCT; 1.

DR SMART; SM00255; TIR; 1.

DR PROSITE; PS50104; TIR; 1.

DR Disease mutation; Glycoprotein; Immune response;

KW Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;

KW Repeat; Signal; Transmembrane.

KM SIGNAL 1 25 Potential.

FT CHAIN 1 835 Toll-like receptor 4.

FT DOMAIN 26 638 Extracellular (Potential).

FT TRANSMEM 639 659 Potential.

FT DOMAIN 660 835 Cytoplasmic (Potential).

FT REPEAT 29 52 LRR 1.

FT REPEAT 53 75 LRR 2.

FT REPEAT 76 99 LRR 3.

FT REPEAT 100 123 LRR 4.

FT REPEAT 127 148 LRR 5.

FT REPEAT 149 172 LRR 6.

FT REPEAT 173 196 LRR 7.

FT REPEAT 201 224 LRR 8.

FT REPEAT 227 251 LRR 9.

FT REPEAT 305 330 LRR 10.

FT REPEAT 348 370 LRR 11.

FT REPEAT 371 393 LRR 12.

FT REPEAT 396 419 LRR 13.

FT REPEAT 420 443 LRR 14.

FT REPEAT 468 492 LRR 15.

FT REPEAT 494 516 LRR 16.

FT REPEAT 517 540 LRR 17.
 FT REPEAT 542 563 LRR 18.
 FT REPEAT 565 589 LRR 19.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 34 34 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 75 75 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 172 172 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 204 204 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 237 237 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 307 307 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 492 492 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 495 495 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 524 524 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 572 572 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 575 575 N-linked (G1cNAc. . .) (Potential).
 FT CARBOHYD 613 613 N-linked (G1cNAc. . .) (Potential).

Alignment Scores:

Pred. No.: 3.76e-277 Length: 835
 Score: 3895.00 Matches: 750
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 4.48% Indels: 0
 DB: 1 Gaps: 0

US-09-396-985b-48 (1-50000) x TLR4_MOUSE (1-835)

QY 37730 AGGTGTGAATTTGAACAATTGAAGACAGGACGATGCTTACACCACTTCTCAAC 37789
 DB ArgGySglnIleGlnThrIleGlnAspLysAlaTrpHisGlyLeuHisSLeuSerAsn 105
 QY 37790 TTGTACTGACAGGAACCCATGCTCAGAGTTTCCCAGGAAGTTTCTCTGACATACA 37849
 DB LeuIleuThrGlyAsnProIleGlnSerPheSerProGlySerPheSerGlyLeuThr 125
 QY 37850 AGTTAGAGATCTGTGCTGTGAGACAAATTTGCGCTCTAGAAAGCTTCCCTATT 37909
 DB SerLeuGlnLeuLeuValAlaValAlaGlnThrIleLeuHisSerLeuGlnSerPheProIle 145
 QY 37910 GGACAGCTTTACCTTAAGAACTCAATGTGGCTCAACAATTTTATACATTTCTGTAG 37969
 DB GlyGlnIleuIleThrIleuLysLysLeuAsnValAlaHisAsnProIleHisSerCysLys 165
 QY 37970 TTACCTGCATATTTTCCATCTGACGAACTAGATGATGATCTTTCTTAACTAT 38029
 DB LeuProAlaTyrPheSerAsnLeuThrAsnLeuValHisValAspLeuSerTyrAsnTyr 185
 QY 38030 ATTCAACTATTAAGTCAAGCACTTACAGTTTCTACGTGAATAATCCAAAGCAATCTC 38089
 DB IleGlnThrIleThrValAsnAspLeuGlnPheLeuArgLysAsnProGlnValAsnLeu 205
 QY 38090 TCTTTAGACATGCTTTGAAACCAATGACTTCAATCAAGCAAGCTTTGAGGAATT 38149
 DB SerLeuAspMetSerLeuAsnProIleAspPheIleGlnAspGlnAlaPheGlnGlyIle 225
 QY 38150 AAGTTCATGAACGACTTAAGAGTAATTTTATAGCTCAATTAATGAAGAACTTGC 38209
 DB LysLeuHisGlnLeuThrIleArgGlyAsnPheAsnSerSerAsnIleMetLysThrCys 245
 QY 38210 CTTCAAAACCTGGCTGTTTACAGCTCAATGCTGATCTTTGGAGAGATTTAAAGATGAA 38269
 DB LeuGlnAsnLeuHisGlyLeuHisValHisArgLeuIleLeuGlnGlyLysPheLysArgGln 265
 QY 38270 AGGAATCTGAATTTTGAACCTCTATCAATGAGAGACTATGTGATGACCATTTGAT 38329
 DB ArgAsnLeuGlnIlePheGlnProSerIleMetGlnGlyLeuCysAspValThrIleAsp 285
 QY 38330 GAGTTCAGTTAATATACAAATGATTTTCAATGATATGTTAGTCCATGCTTG 38389
 DB GluPheArgLeuThrTyrThrAsnAspPheSerAspIleValLysPheHisCysLeu 305
 QY 38390 GCGAATGTTTCTGCAAGTCTCTGGCAGGTGATCTATAAATATCTAGAAAGATGTTCT 38449
 DB

DB 306 AlaAsnValSerAlaMetSerLeuAlaGlyValSerIleLeuThrGlnAspValPro 325
 QY 38450 AAACATTTCAAAAGCGCAATCTTATATCAATGATGATGCTTAAGCACTTCCAACT 38509
 DB LysHisPheLeuThrGlnSerLeuSerIleIleArgCysGlnLeuLysGlnPheProThr 345
 QY 38510 CTGGATCTACCCCTTTCTTAAAGTTTACCTTTAATCTATGAACAAAGGATCTATCAGTTT 38569
 DB LeuAspLeuProPheLeuLysSerLeuThrLeuThrMetCysLysGlySerIleSerPhe 365
 QY 38570 AAAAAGTGGCCCTTACCAAGTCTTACGATCTAGATCTTAGTGAATGACATGAGCTTT 38629
 DB LysLeuValAlaLeuProSerLeuSerTyrLeuAspLeuSerArgAsnAlaLeuSerPhe 385
 QY 38630 AGTGTGCTGTTCTTATTTCTGATTTTGGGAAACAAAGCCTGAGACCTTATGACCTGAC 38689
 DB SerIleCysCysSerTyrSerAspLeuGlyThrAsnSerLeuArgHisLeuAspLeuSer 405
 QY 38690 TTCAATGTCATCATTTATGAGTGCATTTTCAATGAGGCTTGAAGAGCTGACACCTG 38749
 DB PheAsnGlyAlaIleIleMetSerAlaAsnPheMetCysLeuGlnLysLeuGlnHisLeu 425
 QY 38750 GATTTTCAGACCTCTACTTTAAAGGTCACAGAAATTTCTACGCTTCTTATCCCTGAA 38809
 DB AspPheGlnHisSerThrLeuLysArgValThrGlnPheSerAlaPheLeuSerLeuGln 445
 QY 38810 AAGCTACTTATCTTGAATCTTATATCTTATATCAACCAAAATTTGATCTGATGATATTT 38869
 DB LysLeuLeuTyrLeuAspIleSerTyrThrAsnThrLysLysAspPheAspGlyIlePhe 465
 QY 38870 CTTGGCTTGAACAGTCTCAACATTAATAAATGGCTGCAATCTTTCAAGAACACACC 38929
 DB LeuGlyLeuThrSerLeuAsnThrLeuLysMetAlaGlyAsnSerPheLysAsnThr 485
 QY 38930 CTTTCAATGCTCTTGGCAACACAACTTACATTTCTGTGATCTTTTAAATGTCAA 38989
 DB LeuSerAsnValPheAlaAsnThrThrAsnLeuThrPheLeuAspLeuSerLysCysGln 505
 QY 38990 TTGGAAACAAATATCTTGGGGGATTTTGAACACCTCCATGACTTCAATTTAAATATG 39049
 DB LeuGlnGlnIleSerTrpGlyValPheAspThrLeuHisArgLeuGlnLeuLeuAsnMet 525
 QY 39050 AGTCACAAACATCTATTTTGGATTTTCAATCCATATTAACAGCTGTATTCCTCAGC 39109
 DB SerHisAsnAsnLeuLeuPheLeuAspSerSerHisLysAsnGlnLeuTyrSerLeuSer 545
 QY 39110 ACTCTTGATTTGACGTTTCAATGTCATAGACATCTTAAGAAATCTGCAACATTTTCA 39169
 DB ThrLeuAspCysSerPheAsnAlaGlyIleThrSerLysGlyIleLeuGlnHisPhePro 565
 QY 39170 AAGAGTACGCTTTCTTCAATCTTACTAACAATTTCTGTGCTTGATATGTAACATCAG 39229
 DB LysSerLeuAlaPhePheAsnLeuThrAsnAsnSerValAlaCysIleCysGlnHisGln 585
 QY 39230 AAATTCCTGAGTGGGCAAGAAAGCAAGACAGTCTTGGTGAATGTTGAACAAATGCA 39289
 DB LysPheLeuGlnTrpValLysGlnGlnLysGlnPheLeuValAsnValGlnGlnMetThr 605
 QY 39290 TGTGCAACCTGTAGATGAATATACCTCTTATGTTGATGATTTTAATTTCACTGT 39349
 DB CysAlaIleThrProValGlnMetAsnThrSerLeuValLeuAspPheAsnAsnSerThrCys 625
 QY 39350 TATATGTACAAACATCATCATGATGTGTCAATGTGTGATGATTTGGATGATCACTGTA 39409
 DB TyrMetTyrIleThrIleIleSerValSerValValSerValIleValAlaSerThrVal 645
 QY 39410 GCATTTCTGATATACCACTCTTATTTTCACTGATCTTATGCTGGCTGTAATAAAGTAC 39469
 DB AlaPheLeuIleTyrHisPheThrPheHisLeuIleLeuIleAlaGlyCysLysLysTyr 665
 QY 39470 AGCAGAGAGAAAGCATATGATGATGATTTGTGATCTACTGAGTCAAGATGAGACTGG 39529
 DB SerArgGlyGlnSerIleTyrAspAlaPheValIleTyrSerSerGlnAsnGlnAspTrp 685

QY 39530 GTGGAAGATGAGCTGTAAGATTTTGAAGAGAGGCGCCGCTTTCACCTTGCTTC 39589
DB 686 ValArgsnlnuLeuValValAsnleuGlnGlnValValProAlaPheHisLeuCySleu 705
QY 39590 CACTACAGAGACTTATTCCTGCTGTGAGCCATTGCTCCCAACATCATCCAGAGAGCTTC 39649
DB 706 HisArgArgAspPheIleProGlyValAlaIleHisAlaHisIleIleGlnGlnGlyPhe 725
QY 39650 CACAGAGCCGGAAGGTTATTTGTGTAGTCTGACACTTATTCAGAGCCGCTTGCTGT 39709
DB 726 HisLysSerArgLysValIleValValSerArgHisPheIleGlnSerArgTyrCys 745
QY 39710 ATCTTGAATGATGATTCCTCAACATGCGAGTTTCTGAGCAGCCGCTTGCAATATC 39769
DB 746 IlePheGlnTyrGlnIleHisGlnThrTyrPheGlnPheLysSerArgHisGlyIleIle 765
QY 39770 TTCATTGCTTGAAGAGTTGAGAGTCCCTGCTGAGCAGCAGGTGGAATGTATCGC 39829
DB 766 PheIleValleuGlnLysValGlnLysSerLeuLysArgGlnGlnValGlnLeuTyrArg 785
QY 39830 CTTTTCAGCAAAACACTTACCTGATGAGAGCAATCTCTGCGGAGGACATCTTC 39889
DB 786 LeuLysSerArgAsnThrTyrLeuGlnTyrPheGlnAspAsnProLeuGlyArgHisIlePhe 805
QY 39890 TGGAGAGACTTAATAATGCGCTTGTGATGAGAAAGCTTGATCTGAGCAACAGCA 39949
DB 806 TyrArgArgLeuLysAsnAlaLeuLeuAspGlyLysAlaSerAsnProGlnGlnThrAla 825
QY 39950 GAGGAGAGCAAGAACGGCACTTGAGAC 39979
DB 826 GlnGlnGlnGlnGlnThrAlaThrTyrThr 835

RESULT 2
Q8K2T5 PRELIMINARY; PRT; 835 AA.
ID Q8K2T5;
AC Q8K2T5;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Toll-like receptor 4.
GN Name=TLR4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stadelton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein J., Ustin T.B., Toshlyuk S., Carrinci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska J., Smalins D.B., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N. A.
RC STRAIN=CZECH II; TISSUE=Mammary tumor;

RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029856; AAH29856.1; -.
DR HSSP; O60603; 1077.
DR MGD; MGI:96824; TLR4.
DR GO; GO:0005615; C:extracellular space; TMS.
DR GO; GO:0016021; C:integral to membrane; TMS.
DR GO; GO:004872; F:receptor activity; IDA.
DR GO; GO:0007249; P:1-kappaB kinase/NF-kappaB cascade; IDA.
DR GO; GO:0008663; P:Toll signaling pathway; IDA.
DR Interpro; IPR000867; Aldase_KDPe_KHG.
DR Interpro; IPR001611; LRR.
DR Interpro; IPR000483; LRR_Cterm.
DR Interpro; IPR00157; TIR.
DR Pfam; PF00560; LRR_1; 10.
DR Pfam; PF01582; TIR_1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00082; LRRCT; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS00159; ALDOLASE_KDPe_KHG_1; UNKNOWN_1.
DR PROSITE; PS50104; TIR; 1.
KM RECEPTOR.
SQ SEQUENCE 835 AA, 95488 MW, A103C3997A59CF5B CRC64;
Alignment Scores:
Pred. No.: 9,41e-276 Length: 835
Score: 3876.00 Matches: 745
Percent Similarity: 99.87% Conservative: 4
Best Local Similarity: 99.33% Mismatches: 1
Query Match: 4.46% Indels: 0
Gaps: 0
US-09-396-985b-48 (1-50000) x Q8K2T5 (1-835)
QY 37730 AGGTGGAATTTGAACAACTTGAAGACAGGAGCTGATGCTTACACCACTTCAAC 37789
DB 86 ArgCysGlnIleGlnThrIleGlnAspLysAlaTyrHisIleGlnHisLeuSerAsn 105
QY 37790 TTGATCTGACAGAAACCTATCCAGAGTTTCCCGAGAGTTTCTGTGAGCTAACA 37849
DB 106 LeuIleLeuThrGlnLysProIleGlnSerPheSerProGlySerPheSerGlyLeuThr 125
QY 37850 AGTTGAGAGATCTGAGCTGCTGAGACAAATTTGCTCTAGAAAGCTTCCCTATT 37909
DB 126 SerLeuGlnLysLeuValAlaValGlnThrLysLeuAlaSerLeuGlnSerPheProIle 145
QY 37910 GAGACGCTTAAACCTTAAAGAACTCAATGCTGCCTCAATTTTATCTCTGTAAG 37969
DB 146 GlnGlnLeuIleThrLeuLysLysLeuAsnValAlaHisAsnPheIleHisSerCysLys 165
QY 37970 TTACCTGCATATTTTCCCAATCTGAGCAACCTATGATCATGTGATCTTCTTAATAT 38029
DB 166 LeuProLalArgPheSerAsnLeuThrAsnLeuValHisValAspLeuSerTyrAsnTyr 185
QY 38030 ATTCAACTTAACTGTGCAAGCACTTACAGTTTCTAGGTAAATCCAAAGTCAATCTC 38089
DB 186 IleGlnThrIleThrValAsnAspLeuGlnPheLeuArgGlnAsnProGlnValAsnLeu 205
QY 38090 TCTTTAGACATGCTTTTGAACCCCAATGATCTTCAATCAACCAAGCCTTTCAGGAAAT 38149
DB 206 SerLeuAspLysSerLeuAsnProIleAspPheIleGlnAspGlnAlaPheGlnGlyLe 225
QY 38150 AAGTCATGATGCTGCTCAAGAGGTAATTTAATAGCTCAATTAAGAAACTTGC 38209
DB 226 LysLeuHisGlnLeuThrLeuValArgLysAsnPheAsnSerSerAsnIleCysLys 245
QY 38210 CTTCAAAACCTGCTGCTGTATACAGCTTCATCGGTTGATCTTGGAGAAATTTAAGATGAA 38269
DB 246 LeuGlnAsnLeuHisGlyLeuHisValHisArgLeuIleLeuGlnGlyPheLysAspGln 265
QY 38270 AGGAATCGAAATTTTGAACCTTATCATGAGAAAGACTTATGTGATGACCATTTGAT 38329
DB 266 ArgAsnLeuGlnIlePheGlnProSerIleMetGlnGlyLeuCysAspValThrIleAsp 285

```

QY 38330 GAGTTCAGGTTAACAATATACAAATGATTTTCAGATGATATATGTTAGTCCATGCTTG 38389
D 286 GlutheutrgleuthrhiethrAsnAspSerSerAspArgIleValysrPhehiCysleu 305
QY 38390 GCGAATGTTTCTGCAATGCTCTGCGACGCTGATCTATATAAATATGAGAAGATGTTCT 38449
D 306 AlaasnValSerIleAmcSerleuAlaGlyValSerIleIysTyrLeuGlnAspValPro 325
QY 38450 AAAAATTCAATAGGCAATCTTTATCATCATGATGATGTCATAGCACTTGAAGCACTTCCACT 38509
D 326 LysHisPheIysTyrPginSerleuSerIleIleArgCysGlnLeuLysGlnPheProThr 345
QY 38510 CTGATCTACCTCTTCTTAAAGTTTGACTTAACTATGACAAAGAGGTCTATCAGTTT 38569
D 346 LeuAspLeuProPheleuLysSerleuThrleuThrMetAnLysGlySerIleSerPhe 365
QY 38570 AAAAAAGTGGCCCAACCAAGTCTCAGCTATGATCTTATGATGAGAATGCACTGAGCTTT 38629
D 366 LysLysValAlaIleuProSerleuSerTyrleuAspLeuSerArgAsnAlaIleuSerPhe 385
QY 38630 AGTGGTTCCTGTTCTTATCTGATTTGGGAAACAAACAGCTGAGACACTTGAACCTCAGC 38689
D 386 SerGlyCysCysSerTyrSerAspLeuGlyThrAsnSerleuArgHisLeuAspLeuSer 405
QY 38690 TTCAATGGTGCATCATATGAGTGCAGCAATTCAGGGCTTGAAGAGCTGCAGCAGCTG 38749
D 406 PheAsnGlyAlaIleIleMetSerAlaAsnPheMetGlyLeuGlnLeuGlnHisleu 425
QY 38750 GATTTGACGACTCTACTTTAAAAAGGCTCACAGAAATCTCAGCGTTCTTATCCCTTGA 38809
D 426 AspheGlnHisSerThrleuLysArgValIthrGlnPheSerAlaPheleuSerleuGln 445
QY 38810 AAGCTACTTACCTTGACATCTCTTACTTAAACACCAAAATGACCTTGATGATATTT 38869
D 446 LysleuLeuTyrleuAspIleSerTyrThrAsnThrLysIleAspPheAspGlyIlePhe 465
QY 38870 CTTGGCTTGACAGCTCTCAACACATTTAAATGGCTGCAATCTTCAAGAACACACCC 38929
D 466 LeuGlyleuThrSerleuAsnThrleuLysMetAlaGlyAsnSerPheLysAspAsnThr 485
QY 38930 CTTTCAATGTCCTTTGCAACACAACTGACATTCCTGATCTTCTTAAATGTCAA 38989
D 486 LeuSerAsnValPheAlaAsnThrThrAsnleuThrPheleuAspLeuSerLysCysGln 505
QY 38990 TTGAAACAAATATCTTGCGGGGTATTTGACACCTCCATACACTTCAATTATTAATATG 39049
D 506 LeuGlnGlnIleSerTyrGlyValPheAspThrleuHisArgLeuGlnLeuLeuAsnMet 525
QY 39050 AGTCACAACATCTATGTTTGGATTGATCCCATTAATACGAGCTGATTCCTCAGC 39109
D 526 SerHisAsnAsnLeuLeuPheLeuAspSerSerHisTyrAsnGlnLeuTyrSerleuSer 545
QY 39110 ACTCTGATGTCAGTTTCAATCGATAGAGACATCTAAGAAATAGTCACATTTTCCA 39169
D 546 ThreuleuAspCysSerPheAsnArgIleGlnThrSerLysGlyIleleuGlnHisPhePro 565
QY 39170 AAGAGCTAGCCTTCTTCAATCTTACTAACAATTCGTGCTTGATATATGAAATCAG 39229
D 566 LysSerleuAlaPhePheAsnleuThrAsnAsnSerValAlaCysIleCysGlnHisGln 585
QY 39230 AAAATCTGAGTGGGTCAACAGAACAGAAAGATTTTGGTGATGTTGAAACAATGACA 39289
D 586 LysPheleuGlnThrValLysAspGlnLysGlnPheleuValAsnValGlnGlnMetThr 605
QY 39290 TGTGCAACACCTGTAGATGAATACCTCTTATGTTGATTTTAAATTTTCACTCTGT 39349
D 606 CysAlaThrProValGlnMetAsnThrSerleuValLeuAspPheAsnAsnSerThrCys 625
QY 39350 TATATGACAGACATATATAGTGTGTCAGTGTGCTGAGTGTGATTTGATTCACCTGTA 39409
D 626 TyrmetyLysThrIleIleSerValSerValIleSerValIleValValSerThrVal 645

```

```

QY 39410 GCATTTCTGATATACACCTTCTATTTTACCTGATACTTATGCTGCGGTGAAAAAGTAC 39469
D 646 AlaPheleuIleTyrHisPheTyrPhehiIleuIleleuIleAlaGlyCysLysLysTyr 665
QY 39470 AGCAGAGAGAAAGACATCTATGATGCAATTTGTGATCTTACTGAGTCAAGATGAGACTCG 39529
D 666 SerArgGlyGlnSerIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTyr 685
QY 39530 GTGAGAAATGAGCGGTGAAAGAAATTTAGAAAGAGAGAGTCCCGCTTCACTCGCTTC 39589
D 686 ValArgAsnGlnLeuValLysAsnLeuGlnGlnIleValProArgPheHisLeuCysleu 705
QY 39590 CACTACAGAGACTTATTCCTGTGTAGCCATTCCTGCTCCCAACATCATTCAGAAAGCTTC 39649
D 706 HisTyrThrAspPheIleProGlyValAlaIleAlaIleAlaHisIleIleGlnGlnLysPhe 725
QY 39650 CACAAAGCCGGAGGTTATTTGTGAGTCTTGAACAATTATTCAGAGCGCTTGCTGT 39709
D 726 HisLysSerArgLysValIleValValSerArgHisPheIleGlnSerArgTyrCys 745
QY 39710 ATCTTGAATATGAGATTTGCTCAACACCTGCAAGTCTTGAAGACCGCTCGGATCATC 39769
D 746 IlePheGlnLysTyrGlnIleAlaGlnThrTyrPginPheleuSerSerArgSerGlyIleIle 765
QY 39770 TTCAATGCTCTGAGAGGTTGAGAAAGTCCCTGCTGAGGACAGAGTGAATTTATCGC 39829
D 766 PheIleValLeuGlnLysValGlnLysSerleuLeuArgGlnGlnValGlnLeuTyrArg 785
QY 39830 CTTCTTACAGAAACACCTTACCTGGAATGGAGAGACAAATCTCTGGGAGGACACATCTTC 39889
D 786 LeuLeuSerArgAsnThrTyrLeuGlnTyrPginLysAspAsnProleuGlyArgHisIlePhe 805
QY 39890 TGGAGAGACTTAAATGGCCCTTATGATGAGAAAGCCTCGATCTCTGAGCAACGCA 39949
D 806 TyrArgArgLeuLysLysValAlaLeuLeuAspGlyLysAlaSerAsnProGlnGlnThrAla 825
QY 39950 GAGGAAAGACAGAAACGCAACTTGAGCC 39979
D 826 GlnGlnGlnGlnGlnThrAlaThrTyrThr 835

```

```

RESULT 3
ID TLR4 RAT STANDARD; PRT; 835 AA.
AC 09X005;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor (Toll14).
GN Name=TLR4;
OS Rattus norvegicus (Rat).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, TISSUE=Heart;
RX MEDLINE=9362487; PubMed=10430608;
RA Frenzt S., Kobzik L., Kim Y.-D., Fukazawa R., Medzhitov R., Lee R.T.,
RA Kelly R.A.;
RT "Toll14 (TLR4) expression in cardiac myocytes in normal and failing
myocardium";
RL J. Clin. Invest. 104:271-280(1999).
CC -1- FUNCTION: Cooperates with Lys96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, Lys96 and TIRAP.
CC Binds Lys96 via the extracellular domain. Binds MyD88 and TIRAP via
CC their respective TIR domains (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 17 leucine-rich (LRR) repeats.

```



```

Db      371  oSerLeuArgTyrLeuSpleuSerArgSnaLmeSerPheArgGlyCysCysSerTy 391
Qy      38647  TTTGATTTGGGAAACAAAGCCTGAGACACTTACCTGAGCTTCAATGCTGACATC 38706
Db      391  rSerAspPheGlyThrAsnAsnLeuLysTyrLeuAspLeuSerPheAsnGlyValIleLe 411
Qy      38707  TATGAGGCCAATTCATGGGTCTAGAAAGAGCTGAGACCTGGATTTCAGACCTTAC 38766
Db      411  uMeSerAlaAsnHmeTgLyLeuGluGluLeuGluTyrLeuAspPheGlnHISerTh 431
Qy      38767  TTTTAAAGAGGTCAAGAAATTCAGAGCTTATTCCTTGAAGAAAGTACTTATCTTGA 38826
Db      431  rLeuLysValThrGluPheSerValPheLeuSerLeuGluLysLeuLeuTyrLeuAs 451
Qy      38827  CATCTCTTATTAACCAACCAAAATTCAGATGATATATTCCTGGCTGACAGCTC 38886
Db      451  pLleSerTyrThrAsnThrLysIleAspPheAspGlyIlePheLeuGluLeuIleSerLe 471
Qy      38887  CAACACATTAATAAATGGCTGGCAATCTTTCAAAGACACACCTTCAATGTCTTTCG 38946
Db      471  uAsnThrLeuLysMetAlaGlyAsnSerPheLysAspAsnThrLeuSerAsnValPheTh 491
Qy      38947  AAACACACAAACCTTGACATTCCTTGATCTTTCATATGTCATATGGAACAATATCTTG 39006
Db      491  rAsnThrThrAsnLeuThrPheLeuAspLeuSerLysCysGlnLeuGluGlnIleSerAr 511
Qy      39007  GGGGGTATTGAGACCCCTCCATAGACTTCAATTAATTAATTAATGAGTACAAATATAT 39066
Db      511  gGlyValPheAspThrLeuTyrArgLeuGlnLeuLeuAsnMetSerIleAsnAsnLeuLe 531
Qy      39067  GTTTTGATTCATCCATTAATAACAGCTGATTCCTCGACACTCTTGATGTCAGATT 39126
Db      531  uPheLeuAspProSerHisTyrLysGlnLeuTyrSerLeuArgThrLeuAspCysSerTh 551
Qy      39127  CAATCGATAGAGACATTTAAGAAATTCGCAACATTTTCAAAGAGTCTAGCTTCTT 39186
Db      551  eAsnArgIleGluThrSerLysGlyIleLeuGlnHISpHeProLysSerLeuAlaValPh 571
Qy      39187  CAATCTTACAAACAATCTGTTGTTGATTAATTAATTAATTAATTAATTAATTAATTA 39246
Db      571  eAsnLeuThrAsnAsnSerValAlaCysIleCysGlnTyrIleAsnPheLeuGlnTTPVa 591
Qy      39247  CAAGGAACAGAGAGAGTCTTGATGATGATGATGATGATGATGATGATGATGATGATG 39306
Db      591  lLysAspGlnLysMetPheLeuValAsnValGluGlnMetLysCysAlaSerProIleAs 611
Qy      39307  GATGAATACCTCCTTAGTGTGATTTTAATTAATTCATCTGTTATATGATCAAGACAT 39366
Db      611  pMetLysAlaSerLeuValLeuAspPheThrAsnSerThCysTyrIleTyrIleThrII 631
Qy      39367  CATCAGGTGTGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 39426
Db      631  eLleSerValSerValValSerValLeuValAlaThrValAlaPheLeuIleTyrHIS 651
Qy      39427  CTTCTATTTTCACTGATTAATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 39486
Db      651  sPheTyrPheHisLeuLeuLeuIleAlaGlyCysLysLysTyrSerArgGlyLysSerII 671
Qy      39487  CTATGATGATCTTGTGATCTTCTGAGTCAAGATGAGAGTGGGTGAGAAATGAGCTGT 39546
Db      671  eTyrAspAlaPheValIleTyrSerSerGlnAsnGluAspTyrValArgAsnGluLeuVa 691
Qy      39547  AAAGAAATTTGAAGAAGAGAGTCCCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTTAT 39606
Db      691  lLysAsnLeuGlnGluGlyValProArgPheGlnLeuCysLeuHISerTyrArgAspPheII 711
Qy      39607  TCCGTGTGTAGCACTTGTGCAATCATCATCAGGAAGGCTTCACAAAGAGCCGAGAGGT 39666
Db      711  eProGlyValAlaIleAlaAlaAsnIleIleGlnGlnGlyPheHisLysSerArgLysVa 731
Qy      39667  TATTGTGTGTGTGTGATGACATTTATTCAGAGCGTGTGTGTATCTTTGATATGAGAT 39726

```

```

Db      731  lIleValValSerArgHisPheIleGlnSerArgTyrCysIlePheGluTyrGluII 751
Qy      39727  TGCTCAACATGAGAGATTTCTGAGACAGCCCTGTCGATCATCTTCAATGCTTGAAGA 39786
Db      751  eAlaGlnThrTyrPheGlnPheLeuSerSerArgSerGlyIleIlePheIleValLeuGluTy 771
Qy      39787  GGTGAGAGTCCCTGCTGAGAGCAGCAGGTGGAATTTATTCGCTTTCAGACAAACAC 39846
Db      771  sValGluLysSerLeuLeuArgGlnGlnValGluLeuTyrArgLeuLeuSerArgAsnTh 791
Qy      39847  CTACCTGGAATGGAAGACAAATCTCTGGGAGGACAAATCTTTCGAGAAAGACTTAAAA 39906
Db      791  rTyrLeuGluTyrPheGluAspAsnAlaLeuGlyArgHisIlePheThrArgArgLeuLysLy 811
Qy      39907  TGCCCTATGATGAGAAAGCCTCGAATCTCGAATCTCGAACAACAGAGAAAGAAAGAAC 39966
Db      811  sAlaLeuLeuAspGlyLysAlaLeuAsnProAspGluThrSerGluGluGlnGluAl 831
Qy      39967  GGCACATTTGAGAC 39979
Db      831  aThrThrLeuThr 835

RESULT 4
ID      TLK4 CRIGR STANDARD; PRT; 838 AA.
AC      Q9WV82;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DE      05-JUL-2004 (Rel. 44, Last annotation update)
GN      Toll-like receptor 4 precursor.
OS      Cricetus griseus (Chinese hamster).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC      Cricetulus.
OX      NCBI_TaxID=10029;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Macrophage;
RX      MEDLINE=2014868; PubMed=10683379;
RA      Lien E., Means T.K., Heine H., Yoshimura A., Kusumoto S., Fukase K.,
RA      Fenton M.J., Oikawa M., Qureshi N., Monks B., Finberg R.W.,
RA      Ingalls R.R., Golombok D.T.;
RT      "Toll-like receptor 4 imports ligand-specific recognition of bacterial
RT      lipopolysaccharide."
RL      J. Clin. Invest. 105:497-504(2000).
CC      -!- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC      immune response to bacterial lipopolysaccharide (LPS). Acts via
CC      MYD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC      secretion and the inflammatory response (By similarity).
CC      -!- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC      multi-protein complex containing at least CD14, LY96 and TLR4.
CC      Binds LY96 via the extracellular domain. Binds MYD88 and TIRAP via
CC      their respective TIR domains.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC      -!- TISSUE SPECIFICITY: Detected in macrophages and the Chinese
CC      hamster ovary fibroblast cell line.
CC      -!- SIMILARITY: Belongs to the Toll-like receptor family.
CC      -!- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC      -!- SIMILARITY: Contains 1 TIR domain.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC      or send an email to license@ebi-sib.ch).
DR      EMBL, AF153676; MIM:1891.1; -.
DR      HSP, Q15399; IPIV.
DR      InterPro, IPR001611; LRR.
DR      InterPro, IPR000483; LRR_Cterm.

```


Query Match:	1	3.00%	Gaps:	8	Mismatches:	172
US-09-396-985B-48 (1-50000) x TLR4_HUMAN (1-839)						
QY 37400	TGGAAGAAATGCAATTAATTAATCTAAGACATCAATTAATCAATCTTATGTAACCCA					37455
Db 26	TTpIuPProCyValGIuValProAsnIleThrTyrGln-----					39
QY 37460	GTATATGATCTTGAATGATATTTTCTATAGATATTTGCGCTGACATAGTGATGATGTT					37519
Db 40	CysMetGIuLeuAsnRhePheTyrGlySileProAspAsnLeuPro-----					53
QY 37520	ATCATCACTGTAGCAAGGTGAAATAGCAAAATCTGCAGAGTTCCCTCGCTCAACC					37579
Db 54	-----PheSerThrIlyAsnLeuAspLeuSerPheAsnProLeuArgHis---					68
QY 37580	ATCATCACTGTTTGTGCTGTACAGTTTCTCTTACAAATACATGATATCATATCT					37639
Db 69	-----LeuGlySerTyrSerPhe-----					74
QY 37640	GTATTGATCATAGTATGATGTAGGACACTGTATATGATTAAGAAAGGTTTTTTTTCGAA					37699
Db 75	-----PheSerPheProGlu 79					
QY 37700	AAATATCAATATGGTATCTCTTTTGGCCCATAGGTGTGAAATGAAATTAAGACAG					37759
Db 80	LeuGlnValLeuAspLeuSer-----ArgCysGlnIleGlnThrIleGlnAspGly 96					
QY 37760	GCATGCAATGCTTACACCAACCTTCAAACTGATATCTGACAGAAACCTTATCCAGAT					37819
Db 97	AlaTyrGlnSerLeuSerSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSer 116					
QY 37820	TTTTCCCAAGAGTTTCTCTGACATCAAGTTTAAAGATATGGGTGGTGGAGACA					37879
Db 117	LeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIlyLeuValAlaGlnThr 136					
QY 37880	AAATGGCTCTCTAGAAAGCTTCCCTATTGACAGCTTAATTAACCTTAAAGAACTCAAT					37939
Db 137	AsnLeuAlaSerLeuGlnAsnPheProIleGlyHisLeuIlySerThrLeuGlyGluLeuAsn 156					
QY 37940	GTGGCTCACAATTTTATATACATCTCTGTAAAGTACCTGCATATTTTCCAACTGACGAAC					37999
Db 157	ValAlaHisAsnLeuIleGlnSerPheIlyLeuProGluTyrPheSerAsnLeuThrAsn 176					
QY 38000	CTAGTACATGGATCTTCTCTTAATCACTATATCAACATTAATCTCAACAGACTTACAG					38059
Db 177	LeuGlnIlyHisLeuAspLeuSerSerPheAsnIlyIleGlnSerIleTyrCysThrAspLeuAsp 196					
QY 38060	TTTTCTAGGTAAATCCACAGTCAATCTCTCTTGAACATGTGCTTGAACCAATTCAC					38119
Db 197	ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsn 216					
QY 38120	TTTCAATTAAGACCAAGCTTTCAGGGAATTAAGCTCCATGAACATGACTCTTAAGAGGTAAT					38179
Db 217	PheIleGlnProGlyAlaPheIlyAsnGluIleArgLeuHisIlySerLeuThrLeuArgAsnAsn 236					
QY 38180	TTTTAATGGCTCAATTAATTAAGAAATCTGCTCAAACTGGCTGGCTTTCACGGTCAAT					38239
Db 237	PheAspSerLeuAsnValMetIlySileCysIleGlnGlyLeuAlaGlyLeuGlnValHis 256					
QY 38240	CGGTGATCTTGGAGAAATTAAGATGAAGAAAGATCTGAAATTTTGAACCCCTATATC					38299
Db 257	ArgLeuValLeuGlyGlnPheArgAsnGlnGlyAsnLeuGlnIlySerPheAspLeuSerAla 276					
QY 38300	ATGAAGAGACTATGTGATGTGACCATGTATGAGTTTCAAGTTTACATCAATCAAAATGATTTT					38359
Db 277	LeuGlnIlyLeuCysAsnLeuThrIleGlnGlnPheArgLeuAlaTyrLeuAspRlyTyr 296					
QY 38360	TCAGATATATTTGTTAG--TTCCATATGGCTTGGAGAAATTTTTCGCATATGCTCTGGCA					38416
Db 297	LeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuVal 316					

QY	38417	GGGTATCTATTAATAATCTCAGAAAGATGGTCTTCAAACTTTCAAAAGGCAATCTTATCA	38417
Db	317	ServalintriallegluaagvallyshapneserTyrasPheciYlrrplnhi sleuGu	336
QY	38477	ATCATTAAGATGCAACTTAAAGAGCTTAAAGCTTCAACTGATCTACCTTTCTTAAAGTTTG	38536
Db	337	LeuValnencysylsPhegllyglnPheProthLeuIlyLeuIylserLeuIylsArgLeu	356
QY	38537	ACTTTAATCTAGAACCAAAAGGCTCTACGTTTAAATAAAAGTGCCCTTACCAAGTCTCACG	38596
Db	357	ThrePheTherSerasnysgllyglYaaenAlaPheSerGlnValAspLeuProSerLeuGln	376
QY	38597	TATTTAATCTAGTAGAATATGACAGAGCTTAAAGTGGTGGTCTTATTTCTGATTTTG	38656
Db	377	PheLeuaspLeuSerzhangenGlyLeuSerPheIylGlyCyeCySerelInSerasphe	396
QY	38657	GGAAACAACAGCTGAGACACTTAAGACCTTACGCTCAATGTCGCATTTATGAGTCC	38716
Db	397	GlyThrTherSerLeuysrTyleuAspLeuSerPheasnGlyValIleTherMetSerSer	416
QY	38717	AATTATGAGTGTCTAGAGAGCTGAGACCTGAGATTTTACAGACCTTCTTAAAGG	38776
Db	417	AsnPheLeuGlyLeuGlnLeuGlnLeuGlnIshLeuAspPheGlnhiSerasnLeuysgln	436
QY	38777	GTCACAGAAATCTCAGCGTCTTATCCCTTGAAAAGCTACTTACCTTGACATCTTAT	38836
Db	437	MetSerGlnPheSerValPheLeuSerLeuArgasnLeuIleTyrLeuaspIleSerhis	456
QY	38837	ACTTAACCAACCAAAATTAAGTCCATGATTAATTTCTTGCGTTGACAGCTTCAACACATTA	38896
Db	457	ThnIsthrTrArgValAlaPheasnGlyIlePheasnGlyLeuSerSerLeuGlnValleu	476
QY	38897	AAATGCGCTGGCAATCTTTCAAGACCAACACCCCTTGAAAGTCTTTGCAACAACA	38956
Db	477	LyeMetelIadIyasnSerPheGlnGlnuasnPheLeuProaspIlePheThrGlyLeuArg	496
QY	38957	AACTTGACATTTCTCGATCTTTTAAATGTCAATTTGAAACAATAATTTGGGGGCTATTT	39016
Db	497	AsnLeuThrPheLeuaspLeuSerGlnCysGlnLeuGlnLeuSerProThraIaPhe	516
QY	39017	GACACCCCTGCATGAGCTCACTTAATTAATTAAGAGCAACAACATTAATGTTTTGGAT	39076
Db	517	AsnSerLeuSerSerLeuGlnValLeuasnMetSerhisAsnaspPheSerLeuasp	536
QY	39077	TCAATCCATTAATAACAGCTGTATTTCCCTCAGACACTTGTATGTCAGTTTCAATGCGATA	39136
Db	537	ThrPheProIyIylsCysLeuasnSerLeuGlnValLeuaspTyrSerLeuasnHisIle	556
QY	39137	GAGACATCT--AAAGAAATATCTGCAACATTTTCCAAAGATCTAGCCTTTCTTCAATCTT	39193
Db	557	MetThrSerIylsGlnGlnLeuGlnIshPheProSerSerLeuAlaPheLeuasnLeu	576
QY	39194	ACTTAACATTTCTGTGCTTGATATATGTGAACAATCAAGAATTTCTGACAGGCGTCAAGAA	39253
Db	577	ThnGlnasnaspPheIadCysThrCysGlnIshGlnSerPheLeuGlnIrrplIeysasp	596
QY	39254	CAGAAAGCATTTCTTGCGTAATGTTGAACAATAATGACATGTGCAACACTGTAGAGATGAAT	39313
Db	597	GlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAlaIThrProSeraspIylsGln	616
QY	39314	ACCTCCTTAATGTTGGATTTTAATATTTCTACCTGTTATATATACAAAGCATTAACAGT	39373
Db	617	GlyMetProValLeuSerLeu--AsnIleThrCysGlnMetAsnIylsIleIleGly	635
QY	39374	GTGTCAATGTCAGTGTGAATTTGTGTATCCACTGTAGACATTTCTGATATCAACTTAT	39433
Db	636	ValSerValLeuSerValLeuValValSerValValAlaValLeuValTyrIylsPheTyr	655
QY	39434	TTTTCACCTGATTAATTTGCTGCGCTGTAATAAGTCAAGAGAGGAGAAAGCATTAAT	39493
Db	656	PheIshLeuMetLeuLeuAlaGlyCysIleIylsTyrGlyArgGlyGlnasnIleTyrasp	675

QY 39494 GCATTGTGATCTACTGAGTCAGATAGAGAGCTGGTGAGAAATGAGCTGTAAAGAT 39553
 DB 676 AlahetValletierSerserSerginApclubSptrValahargangulueuVallyabn 695
 QY 39554 TTGAAGAGAGAGTGGCCCGCTTACCTCTGCTTCACTACAGAGACTTTATTCCTGGT 39613
 DB 696 LeudlunluglyValPropropheGlnLeuCySeruHstRyRargapPheilleProgly 715
 QY 39614 GTAGCCATTGCTGCACATCATCATCCAGAGCCCTTCCACAGAGCCGGAAGGTTATGTG 39673
 DB 716 ValAlaIlealaaIaaanIlelleHieGlnIlyPheHstRySerserAglVallIleVal 735
 QY 39674 GTAGCTCTAGACACTTATTCAGAGCCGTGTGTATCTTGAATATGAGTCTCA 39733
 DB 736 ValValserGlnHstPheilleGlnSerRargRtrpSlePheGlnIlyrgIullealGln 755
 QY 39734 ACATGCGAGTTTCTGAGAGCCGCTGGCATCATCTTCATTTCTCTTGAGAGCTTGAG 39793
 DB 756 ThrTrpGlnPheleuSerSeraRgIaglyIlellePheilleValleGlnlyValGln 775
 QY 39794 AAGCCCTGCTGAGAGAGAGCTGGAATTTGATGCTTCTTACAGAAAACCTACTG 39853
 DB 776 LysThrleuLeuAglGlnIleuValGlnleuTyRtrgLeuLeuSerAglSerThrTyRleu 795
 QY 39854 GAATGAGAGAGCAATCTCTGGAGAGGACATCTTCTGAGAGAACTTAAATGCCCTA 39913
 DB 796 GluTrpGlnuapSerserValleuGlyRargHstlellePheRtrpAgluAglValleu 815
 QY 39914 TTGGATGAAAAGCCTGGAATCTCTGAGCAACA 39946
 DB 816 LeuApglyLysSerTrpAsnProGlnIlyThr 826
 RESULT 6
 TLR4_PANPA STANDARD; PRT; 839 AA.
 ID TLR4_PANPA
 AC Q9TTNO;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Pan paniscus (Pygmy chimpanzee) (Bonobo).
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 NC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pan.
 NX NCBI_TaxID=9597;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20558910; PubMed=11104518;
 RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
 RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
 locus (TLR4).";
 RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
 CC -1- FUNCTION: Cooperates with MyD88 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, IRAK and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, MyD88 and TLR4.
 CC Binds Lys6 via the extracellular domain. Binds MyD88 and IRAK via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.ebi.ac.uk/announcements/](http://www.ebi.ac.uk/announcements)
 CC or send an email to license@ebi-sib.ch).
 CC -----

DR EMBL; AF179220; AAF05320.1; -.
 DR EMBL; AF179219; AAF05320.1; JOINED.
 DR EMBL; AF179219; AAF05320.1; JOINED.
 DR HSSP; Q15399; 1FVY.
 DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045576; P:negative regulation of osteoclast different. . .; ISS.
 DR GO; GO:0045671; P:negative regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045362; P:positive regulation of interleukin-12 biosyn. . .; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-13 biosyn. . .; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-6 biosyn. . .; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR00483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR; 12.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_TYP; 2.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 DR KX Glycoprotein; Immune response; Inflammatory response;
 DR Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT CHAIN 1..23
 FT DOMAIN 24..839
 FT TRANSMEM 632..652
 FT DOMAIN 653..839
 FT REPEAT 52..76
 FT REPEAT 77..100
 FT REPEAT 101..124
 FT REPEAT 128..149
 FT REPEAT 150..173
 FT REPEAT 174..197
 FT REPEAT 203..225
 FT REPEAT 228..252
 FT REPEAT 277..303
 FT REPEAT 307..330
 FT REPEAT 332..350
 FT REPEAT 351..372
 FT REPEAT 373..398
 FT REPEAT 400..421
 FT REPEAT 422..445
 FT REPEAT 447..469
 FT REPEAT 470..494
 FT REPEAT 495..518
 FT REPEAT 520..541
 FT REPEAT 543..566
 FT REPEAT 568..592
 FT REPEAT 672..818
 FT DOMAIN 819..839
 FT CARBOHYD 173..173
 FT CARBOHYD 205..205
 FT CARBOHYD 282..282
 FT CARBOHYD 309..309
 FT CARBOHYD 497..497
 FT CARBOHYD 526..526
 FT CARBOHYD 575..575
 FT CARBOHYD 624..624
 FT CARBOHYD 630..630
 FT SEQUENCE 839 AA; 95637 MW; 3B328C5682127D37 CRC64;
 Alignment Scores: 2,46e-182 Length: 839
 Pred. No.:

Dd	656	PheHisIseuMetLeuLeuAlaIagIyCySIIeIyTyrGIyArgIyGIuIaenIIeTyrAsp	675
Qy	39494	GCATTGTGATCTTACTGAGTCAAGATAGAGACTGGGTGAGAAATGAGTGGTAAAGAT	39553
Dd	676	AlaIheValIIeTyrSerSerGIuAspTTrpValArgbngIuLeuValIySAsn	695
Qy	39554	TTAAGAAGAAGAGTGGCCCCCTTTCACCTCTGCTTCACTACAGAACTTTATCTGTGT	39613
Dd	696	LeuIuGIuGIuValProPProPheGInLeuCyValenIIeTyrTrArgAspHeIIeProGly	715
Qy	39614	GTAGCCATGTGGCCACATCATCATCAGAGAGGCTCCACAAAGGCCGAAAGGTTATGTG	39673
Dd	716	ValAlaIIeAlaAlaAlaenIIeIIeIIeIaGIuGIyPheIIeIySerTrgIySValIIeVal	735
Qy	39674	GTAAGTCTAGACACTTATTCACAGCCGTTGTGTATCTTTGAATATAGATTGTCTCA	39733
Dd	736	ValValSerGInIIePheIIeGInSerArgTrpCyeIIePheGInuTrgIuIIeIaGIn	755
Qy	39734	ACATGSCAGTTTCTGACAGCCGCTCTGGCATCATCTTCACTTGTCTTGAGAAAGTTGAG	39793
Dd	756	ThrTrpGInPheLeuSerSerArgIaGIyIIeIIePheIIeValIeGInIySValGIn	775
Qy	39794	AAGCCCGCTGGAGCAGCAGGTGAATTTGTATGCGCTTTTAGCAGAAACCTTACCTG	39853
Dd	776	LysTrhIreuIeuIaArgIaGInValGInIeTrpArgIeIuIeuSerTrgAsnTrhIyIreu	795
Qy	39854	GAATGGAGAGCAATCCTCTGTGGAGGAGCAGCATCTTCTGAGAGAACTTAAATAGCCCTA	39913
Dd	796	GIuTrpGInAspSerValIeGInIyArgIIeIIePheTrpArgTrgIeuTrgIySAlaIeu	815
Qy	39914	TTGGATGAAAGAGCCTCGAATCCTGAGCAACA	39946
Dd	816	LeuAspGIySerTrpAsnProGInGIyThr	826

RESULT 7

TIR4_PAPAN STANDARD; PRT; 826 AA.

AC Q9TSP2; 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Toll-like receptor 4 precursor.

GN Name=TLR4;

OS Papio anubis (Olive baboon).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopitheciinae; Papio.

NCBI_TaxId=9555;

EN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20558910; PubMed=11104518;

RA SmItnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;

RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4 locus (TLR4).";

RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).

CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate immune response to bacterial lipopolysaccharide (LPS). Acts via MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response (By similarity).

CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via their respective TIR domains (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -1- SIMILARITY: Belongs to the Toll-like receptor family.

CC -1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.

CC -1- SIMILARITY: Contains 1 TIR domain.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

CC	entities requires a license agreement (See http://www.ibb-sib.ch/announce/ or send an email to license@ibb-sib.ch).		
CC	-----		
DR	EMBL; AF180964; AAF07059.1; -		
DR	EMBL; AF180962; AAF07059.1; JOINED.		
DR	EMBL; AF180963; AAF07059.1; JOINED.		
DR	HSSP; O15199; IEFV.		
DR	GO; GO:0046686; C:lipopolysaccharide receptor complex; ISS.		
DR	GO; GO:0001530; F:lipopolysaccharide binding; ISS.		
DR	GO; GO:0004888; F:transmembrane receptor activity; ISS.		
DR	GO; GO:0007260; P:activation of NF-kappaB-inducing kinase; ISS.		
DR	GO; GO:0016046; P:detection of fungi; ISS.		
DR	GO; GO:0009598; P:detection of pathogenic bacteria; ISS.		
DR	GO; GO:0042116; P:macrophage activation; ISS.		
DR	GO; GO:0045576; P:mast cell activation; ISS.		
DR	GO; GO:0004567; P:negative regulation of osteoclast different. . .; ISS.		
DR	GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.		
DR	GO; GO:0045084; P:positive regulation of interleukin-12 biosy. . .; ISS.		
DR	GO; GO:0045368; P:positive regulation of interleukin-13 biosy. . .; ISS.		
DR	GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.		
DR	GO; GO:0042088; P:T-helper 1 type immune response; ISS.		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR000483; LRR_Cterm.		
DR	InterPro; IPR003591; LRR_Typ.		
DR	InterPro; IPR000157; TIR.		
DR	Pfam; PF00560; LRR; 13.		
DR	Pfam; PF01463; LRRCT; 1.		
DR	Pfam; PF01582; TIR; 1.		
DR	PRINTS; PRO0019; LEURICRPT.		
DR	SMART; SM00369; LRR_Typ; 2.		
DR	SMART; SM00082; LRRCT; 1.		
DR	SMART; SM00255; TIR; 1.		
DR	PROSITE; PS0104; TIR; 1.		
KW	Glycoprotein; Immune response; Inflammatory response;		
KW	leucine-rich repeat; Receptor; Signal; Transmembrane.		
FT	SIGNAL	1	23
FT	CHAIN	24	826
FT	DOMAIN	24	631
FT	TRANSMEM	632	652
FT	DOMAIN	653	826
FT	REPEAT	53	76
FT	REPEAT	77	100
FT	REPEAT	101	124
FT	REPEAT	128	149
FT	REPEAT	150	173
FT	REPEAT	174	197
FT	REPEAT	203	225
FT	REPEAT	228	252
FT	REPEAT	277	303
FT	REPEAT	327	350
FT	REPEAT	351	372
FT	REPEAT	373	398
FT	REPEAT	400	421
FT	REPEAT	422	445
FT	REPEAT	447	469
FT	REPEAT	470	494
FT	REPEAT	495	518
FT	REPEAT	520	541
FT	REPEAT	543	569
FT	REPEAT	571	592
FT	DOMAIN	672	818
FT	CARBOHYD	35	35
FT	CARBOHYD	173	173
FT	CARBOHYD	205	205
FT	CARBOHYD	282	282
FT	CARBOHYD	309	309
FT	CARBOHYD	497	497
FT	CARBOHYD	526	526
FT	CARBOHYD	525	525
FT	CARBOHYD	624	624
FT	CARBOHYD	630	630
SEQ	SEQUENCE	826 AA; 94678 MW; 442277318E5F1769 CRC64;	

Alignment Scores:

Prod. No.:	1.34e-181	Length:	826
Score:	2597.00	Matches:	523
Percent Similarity:	73.41%	Conservative:	101
Best Local Similarity:	61.53%	Mismatches:	174
Query Match:	2.99%	Indels:	52
DB:	1	Gaps:	8

US-09-396-985B-48 (1-50000) x TLR4_PAPAN (1-826)

```

QY 37400 TGGAAAAATGATTAATTAATCTAGACTACTATCAATATCAATCTCTTTATGACCCCA 37459
   |||:::|
Db 26 TtrpGluProCysValGluValAlaProAsnIleThrTyGln----- 39
QY 37460 GTTATGATCTGAATTTATTTTCTTAATGATTTGCGCCGACATGATGATGATTT 37519
   |||:::|
Db 40 CysMetGluLeuAsnPhenTyLysIleProAsnIlePro----- 53
QY 37520 ATCATCTAGTACGAGTGTGAAAAATGACAAATGACAGATTCTCTGCTCACACC 37579
   |||:::|
Db 54 -----PheSerThrLysAsnLeuAspLeuSerPheAsnProLeuArgHis--- 68
QY 37580 ATCATCACTGTTTGGCTCTGCTGACGTTTCTTTTCAATTAACATGGTATATCATATCT 37639
   |||:::|
Db 69 -----LeuGlySerTyLysSerPheLeu----- 75
QY 37640 GTTTGTATCATATGATGTAGGAGACTGTATGTATTAAGAAAGGTTTTTTTCAGCAA 37699
   |||:::|
Db 76 -----ArgPheProGlu 79
QY 37700 AAATACATTAATGTGATCTCTTTTGCCTAGTGTGTAATGAAACAAATTGAAGACAAAG 37759
   |||:::|
Db 80 LeuGlnValLeuAspLeuSer-----ArgCysGluIleGlnThrIleGluAspGly 96
QY 37760 GCATGCGATGCGCTTACACCACTCTCAACTGATGACGAGAAACCTTATCCAGACT 37819
   |||:::|
Db 97 AlAtyrgInserLeuSerHisLeuSerThrLeuIleuThrGlyAsnProIleGlnSer 116
QY 37820 TTTTCCCGAGAGATTTCTCTGACCTACACAGTTTAGAATCTGGTGGCTGTGAGACA 37879
   |||:::|
Db 117 LeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIlyLeuValAlaValGlnThr 136
QY 37880 AAATGGCTCTCTAGAAAGCTTCCCTTATTTGACAGCTTATTAACCTTAAAGAACTCAAT 37939
   |||:::|
Db 137 AsnLeuAlaSerLeuGlnAsnPhenProIleGlyHisLeuTySthIleuGlyLeuAsn 156
QY 37940 GTGCTCACAATTTTATTCATCTCTGTAAAGTTTACCTGCATATTTTCCATCTGACGAAAC 37999
   |||:::|
Db 157 ValAlaHisAsnLeuIleGlnSerPheTyLeuProGluTyPheSerAsnLeuThrAsn 176
QY 38000 CTACTACATGTGATCTTCTTATTAACATATTCATACTATTAATCTGTCACAGACTTACAG 38059
   |||:::|
Db 177 LeuAluHisLeuAspLeuSerSerAsnIlyIleGlnAsnIleTyCysLysAspLeuGln 196
QY 38060 TTTCTACGTGAAAAATCCACAGATCAATCTCTTTAGACATGTCTTTGAAACCCCAATTGAC 38119
   |||:::|
Db 197 ValLeuHisGlnMetProLeuProAsnLeuSerLeuAspLeuSerLeuAsnProIleAsn 216
QY 38120 TTCTATTCAAGCAAGCTTTTCAGGGAATTAGCTCCATGACATGACTTAAAGAGTTAT 38179
   |||:::|
Db 217 PheIleGlnProGlyAlaPheLysGluIleArgLeuHisLysLeuThrIleuArgSerSer 236
QY 38180 TTTATATGCTCAATATATATGAAATTTGCTTCAAAACCTGGTGCTTACAGTCCAT 38239
   |||:::|
Db 237 PheAspAspLeuAsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHis 256
QY 38240 CGGTGATCTTTGGAGAAATTTAAAGATGAAGAAATCTGAAATTTTGAACCTCTATC 38299
   |||:::|
Db 257 ArgLeuValLeuGlnGluPheArgAsnGluArgAsnLeuGlnGluPheAspLysSerAla 276
QY 38300 ATGGAAGCATATGTATGATGACCAATGATGATGATGATGATGATGATGATGATGATGATGAT 38359
   |||:::|
Db 277 LeuGlnGlyLeuCysAsnLeuThrIleGlnGlnPheArgLeuThrTyLeuAspTyLys 296

```

```

QY 38360 TCAGATGATATGTTAAG---TTCATGCTTTGGGGAATGTTTTCGAATGCTCTGGACA 38416
   |||:::|
Db 297 LeuAspAsnIleIleAspLeuPheAsnCysLeuAlaAsnAlaSerPheSerLeuVal 316
QY 38417 GGTGTATCTATTAATAATCTAGAAAGATGTTCTTAAACATTTCAATGGCAATCTTATCA 38476
   |||:::|
Db 317 SerValAsnIleLysArgValGluAspPheSerTyLysAsnPheArgTyGlnHisLeuGln 336
QY 38477 ATCATTAATGTCACATTTACAGATTTTCACATCTGATCTTACCTTTTAAAAAGTTTG 38536
   |||:::|
Db 337 LeuValAsnCysLysPheGlnGlnPheProThrLeuGlnLeuGlnSerLeuLysArgLeu 356
QY 38537 ACTTTAATGAAACAAAGGCTATACGTTTAAAAAAGGCGCCCTCAAGCTCAGC 38596
   |||:::|
Db 357 ThrPheThrAlaAsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGln 376
QY 38597 TATCTAGATCTTATGAGAAATGACATGAGCTTTAGTGTGCTGTCTTATTTCTGATTTG 38656
   |||:::|
Db 377 PheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCysSerGlnSerAspPhe 396
QY 38657 GGAAACAAACAGCTCGACACATTTAGACCTCAAGCTTCAATGTCATATTAATGATGCC 38716
   |||:::|
Db 397 GlyThrThrSerLeuLysTyLeuAspLeuSerPheAsnAspValIleThrMetGlySer 416
QY 38717 AATTTCAAGGCTTAGAAGAGCTGACAGACCTGGATTTTCGACCTTCTTAAAAAGG 38776
   |||:::|
Db 417 AsnPheLeuGlyLeuGlnGlnLeuGlnIlyLeuAspPheGlnHisAsnLeuLysGln 436
QY 38777 GTCAAGAAATCTCAGGCTTTTATTCCTTGAAGAAAGCTTCTTACCTTGACATCTTAT 38836
   |||:::|
Db 437 MetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyLeuAspIleSerHis 456
QY 38837 ACTTAACACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38896
   |||:::|
Db 457 ThrHisThrThrValAlaPheAsnGlyIlePheAspGlyLeuLeuSerLeuLysValLeu 476
QY 38897 AAAATGGCTGCAATTTCTTCAAGAACAAACCCCTTCAAAATGCTTTGAAACAAACACA 38956
   |||:::|
Db 477 LysPheAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIlePheThrAspLeuLys 496
QY 38957 AACTTGACATTTCTGATCTTCTTAAATGTCAATTTGAAACAAATATCTTTGGGGGATATT 39016
   |||:::|
Db 497 AsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPhe 516
QY 39017 GACACCTCCATAGACTTCAATTAATTAATATGATGACAAACAATCTTATGTTTGGAT 39076
   |||:::|
Db 517 AspThrLeuAsnLysLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAsp 536
QY 39077 TCATCCATTAATTAACGAGCTGATTCCTCAGACACTGTGATTCAGATTCAATTCGATA 39136
   |||:::|
Db 537 ValPheProTyLysCysLeuProSerLeuGlnValLeuAspTyLysLeuAsnHisIle 556
QY 39137 GAGACATCTAAAGAA---ATACTGCAACATTTTCCAAAGAGTCTAGACCTTCTCAATCTT 39193
   |||:::|
Db 557 MetHisSerLysAsnGlnGluProGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 576
QY 39194 ACTTAACATTTCTGCTTGTATATGGAACATGAAATTTCTGCAAGTGGCTCAAGGAA 39253
   |||:::|
Db 577 ThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnTyIleLysAsp 596
QY 39254 CAGAGAGATCTTTGGGAATGTTGAAACAAATGACATGTCGAAACACCTGTAAGATGAT 39313
   |||:::|
Db 597 GlnArgGlnLeuLeuValGluAlaGluArgMetLysSalAlaThrProSerAspLysGln 616
QY 39314 ACCTCTTAGTGTGATTTTAAATATCTTACCTGTTATATGTAACAAGACATATCATGAT 39373
   |||:::|
Db 617 GlyMetProValLeuSerVal---AsnIleThrCysGlnMetAsnLysThrIleIleGly 635
QY 39374 GTGTGATGCTCAGTGTGATGTTGGTATTCATCTGATACATTTCTGATATACCACTTCTAT 39433
   |||:::|
Db 636 ValSerValPheSerValLeuValValSerValValAlaValLeuValTyLysPheTyLys 655

```

Oy		39434	TTTACCGTGAACTATTATGTCGGCGGTGAAAAAGATGACGCAGACGAGAAGAACACTATGAT	39434
Dd		656	PhehiSleuuecttleulewAlagLYCySiTelystyrcLYArGdiYgIuSenlletYraP	675
Oy		39494	GCAATTGTGATCTACTCGAGTCAGAAATGAGACTGGGTGAATAATGCTGTAAAGAT	39553
Dd		676	AlahelValllletYrSerSerGIInApGluNepTrValArgsnblueuVallyBan	695
Oy		39554	TTAAGAGAGAGAGTGCCCGCCTTACCTCTGCCCTTCACTACAGAGACTTTATCTGGT	39613
Dd		696	LeuGlugluglyValProPropheGlnLeuCysleuhtltyrArgAspPheilleProgly	715
Oy		39614	GTACCCTATGTCGCACATCATCCAGAGCGCTTCACAAGACCGGAAAGCTTAATGTCG	39673
Dd		716	VAlAlatlelaalaaSnllelehtlEhtlgldlyPhehtlsySerxrglyBAllleval	735
Oy		39674	GTAAGTGTAGACACTTATTTACAGAGCGCGTGTGTATCTTTGAATATGAGATTGCTCAA	39733
Dd		736	VAlValserGlnhlSpheilleGlnSerARgtPrCYalehehdunyrGluilealaGln	755
Oy		39734	ACATGGCAGTTTCTGAGCACGCCGCTCTGGGCATCATCTTCAATTGCTTGGAGAGGTTGAG	39793
Dd		756	ThrtPrGlnPheluSerSerzArgAlagLYleAletheilleValleuGlnlyBValGlu	775
Oy		39794	AAGTCCTGCTGAGCGACGACAGTGGAAATTGTATGCGCTTTTGCGAAAACACTTACCTG	39853
Dd		776	LysThrleuEuARGnglnInValGluLeuryrArgleuSeerArgsnhTrYrlieu	795
Oy		39854	GAATGGAGGACAACTCCTCTGGGGAGCACATCTTCTGAGGAAGACTTAAATAGCCCTTA	39913
Dd		796	GIutPrGluNepSerValleuGlyGlnhllePhehtPrArgArgleuArglySalaleu	815
Oy		39914	TTGGATGAGAAAAGCCTGAATCCTGAGCAA	39943
Dd		816	LeuAepGLyArgSerTPraNeproGluGlu	825
<hr/>				
RESULT 8				
ID	Q8SPER		PREDIMINARY;	PRT; 837 AA.
AC	Q8SPER;			
DT	01-JUN-2002 (TREMBLrel. 21, Created)			
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Toll-like receptor 4.			
GN	Name=TLR4;			
OS	Gorilla gorilla (gorilla).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.			
OX	NCBI_TaxId=9593;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE I., Hamblin M.T., McBride C., Di Rienzo A.;			
RA	Smitrnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;			
RT	"Excess of rare amino acid polymorphisms in the Toll-like receptor 4			
RL	in humans.";			
RL	Genetics 158:1657-1664(2001).			
RP	[2]			
RP	SEQUENCE FROM N.A.			
RA	Beutler B., Smitrnova I., Hamblin M.T., McBride C., Di Rienzo A.;			
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF497565; AAM18617.1; -			
DR	EMBL; AF497563; AAM18617.1; JOINED.			
DR	EMBL; AF497564; AAM18617.1; JOINED.			
DR	HSSP; O60603; 1077.			
DR	GO; GO:0046696; C.lipopolysaccharide receptor complex; ISS.			
DR	GO; GO:0001530; F.lipoplysaccharide binding; ISS.			
DR	GO; GO:0004888; P.transmembrane receptor activity; ISS.			
DR	GO; GO:0007250; P.activation of NF-kappaB-inducing kinase; ISS.			
DR	GO; GO:0016046; P.detection of fungi; ISS.			
DR	GO; GO:0009598; P.detection of pathogenic bacteria; ISS.			
DR	GO; GO:0042116; P.macrophage activation; ISS.			
DR	GO; GO:0045576; P.mast cell activation; ISS.			
DR	GO; GO:0045671; P.negative regulation of osteoclast different. . ; ISS.			

DR	GO; GO:0045362; P:positive regulation of interleukin-1 biosyn.	..	ISS.
DR	GO; GO:0045084; P:positive regulation of interleukin-12 biosy.	..	ISS.
DR	GO; GO:0045368; P:positive regulation of interleukin-13 biosy.	..	ISS.
DR	GO; GO:0045410; P:positive regulation of interleukin-6 biosyn.	..	ISS.
DR	GO; GO:0042088; P:T-helper 1 type immune response; ISS.		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR000483; LRR_Cterm.		
DR	InterPro; IPR003591; LRR_Cyp.		
DR	InterPro; IPR001571; TIR.		
DR	Pfam; PF01463; LRCT; 1.		
DR	Pfam; PF00560; LRCT; 1.		
DR	Pfam; PF01582; TIR; 1.		
DR	PRINTS; PR00019; LEURICRPT.		
DR	SMART; SM0082; LRCT; 1.		
DR	SMART; SM00369; LRR_Typ; 2.		
DR	SMART; SM00255; TIR; 1.		
DR	PROSITE; PS0104; TIR; 1.		
KM	Receptor		
SQ	SEQUENCE 837 AA; 95497 MW; 5A177BAB341396DD CRC64;		
 Alignment Scores:			
Pred. No.:	1,7e-180	Length:	837
Score:	2582.00	Matches:	523
Percent Similarity:	73.44%	Conservative:	102
Best Local Similarity:	61.46%	Mismatches:	172
Query Match:	2.97%	Indels:	54
DB:	2	Gaps:	9
 US-09-396-985B-48 (1-50000) x Q8SPB8 (1-837)			
QY	37400 TGGAAAAATGCATAATTATCTGAAGACTACATCATCACTGTCCTTATGTACC	CCCA	37455SS
Db	26 TrpLipProcysVal-----ValProAsnIleThrTyrln-----		37
QY	37460 GTTAGATCTGGATGATGTTTCTTAATGGATTGCTCGTGACATAGTGATGTT		37519
Db	38 CysHecGlueubsnPheryrLyIleProaspAsnLeupro-----		51
QY	37520 ATCATCAGCTGAGCAAGTGGAATAATGACAACCTGCAGAGTTCCTCGCTCACACC		37579
Db	52 -----PheSerThrlysaenLeuaspLeuSer-PheasnProleuanrghs---		66
QY	37580 ATCATCAGCTGTTTGTCTGTACAGTTTCTCTTAAATACATGATGATATCATGCT		37638
Db	67 -----LeuGIserTyrserepe-----		72
QY	37640 GTTGTATCANATGATNGATGGAGACGTGTATGTCATTAGAAGAGCTTTTTTTCAGCA		37699
Db	73 -----PheSerPheProGU---		77
QY	37700 AATATCAATATGGATCTCTTTGGCCATAGTGATGAATGAACAATGAGAACAAG		37758
Db	78 LeuGIvalLeuaspLeuSer-----ArgCyGIuIIleGIlnThrlleGIuapGLy		94
QY	37760 GCATGCAGTGGCTTACACACCTCTCAACTGTGATACGACAGAAAACCTTATCCAGAGT		37819
Db	95 AlatyrcIInserleuSerHIsleuSerThrlenuIleuthncIylasnProlleGIInser		114
QY	37820 TTTTCCCCAGAAATTTCTCTGCATCAACAAGTTTGAGAAATCTGGTGGCTGTGGAGCA		37879
Db	115 LeuAlaleuGIalylapPheSerGIylLeuSerSeIleuGIlnlybLeuValAlavalGIuTr		134
QY	37880 AAAATGGCCCTCTGAGAAAGCTTCCATATGGACAGCTTATACCTTAAAGAACTCAAT		37939
Db	135 AsnLeuAlaserleuGIuasnPherProIIleGIlyHIleuLystrHreulySGluLeuasn		154
QY	37940 GTGGCTCACATTTTATACATTCCTGTAAAGTTACCTGCATATTTTCCATCTGACGAAC		37999
Db	155 ValAlahIasnLeuIleGIInserPheLybleuProGIuTyPheSerasnLeuThraen		174
QY	38000 CTAGTACATGTGATCTTTTATTAACATATATTCAAATTAATCTGACAGACTTACAG		38058SS
Db	175 LeuGIuIryrIeuaspLeuSerSerAsnLyvIlleGIInserIleTyrcyThrAspleuay		194

OY	38060	TTTGTACGAGAAATTCACAAGCTACCTGCTTTGACATGCTTTGAACCCATATGAC	38113
Db	195	ValLeuHnIsgIlnMetPProLeuLeuAAsnLeuSerLeuAspLeuSerLeuAsnProMetThr	214
OY	38120	TTTCATCAAGACCAAGCCCTTCAAGGAAATTAACTCCATGACATGCTCTAAAGAGTAAT	38179
Db	215	PhelIleGlnProGlyAlaPheLeuGluIleArgLeuHnIleGlySerThrLeuArgAsn	234
OY	38180	TTTAAATAGCTCAATATATATGAAGAAACCTTGCTTCAAAACCTGGCTGGTTTACACGTCAT	38239
Db	235	PheAspSerLeuAsnValMetLeuSerThrCysAlaIleGlnGlyLeuAlaGlyLeuGluValArg	254
OY	38240	CGGTGTGATCTGTGGAGAAATTTAAAGATGAAGAAAGATCTGGAAATTTTGAACCCCTATAC	38299
Db	255	ArgLeuValLeuGlnGlyLupPheArgAsnGlnGlyAsnLeuGluLysPheAspLysSerAla	274
OY	38300	ATGGAAGACATATGTGATATGTGACCATGTGATGAGTTCAGGTTAACATATACAAATGATTTT	38359
Db	275	LeuGlnGlyLeuCysAsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspTyrTyr	294
OY	38360	TCAGATGATATGTGTAAAG--TTCCATGTGTGGCGAAGTTTCTGCAATAGCTCTGGCA	38416
Db	295	LeuAspSerPheIleIleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuVal	314
OY	38417	GGGTATCTATAAATAATCTAGAAGATGTTCCTAAACATTTCAATGACATCTTATATCA	38476
Db	315	SerValThrIleGlnArgValLysAspPheSerTyrAsnPheGlyTyrGlnHnIleuGlu	334
OY	38477	ATCATATGATGATCACTTAAGACAGCTTTCACATCTGGATATACCTTTTCTTAAAGTTTG	38536
Db	335	LeuValAsnCysLysPheGlnGlnPheProThrLeuLysLeuLysSerLeuLysArgLeu	354
OY	38537	ACTTATACATATGAACAAGAGGTCTATCATGTTTAAAAAAGTGCCCTTCAACATGCTACGC	38596
Db	355	ThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlu	374
OY	38597	TATCTAAGATCTTAGTAAATATGCATGACGCTTAAAGTGTTGCTGTCTTATTTGTGATTTG	38656
Db	375	PheLeuAspLeuSerAlaGlnGlnGlyLeuSerPheLysGlyCysArgSerGlnSerAspPhe	394
OY	38657	GGAAACAACAGCCCTGACGACACTTAAGACCTGACGCTTCAAGGAGGCCATTTATTTGAGTGC	38716
Db	395	GlyThrThrSerLeuLysTyrLeuAsnLeuSerPheAsnGlyAlaIleThrMetSerSer	414
OY	38717	AATTTCATGGGCTTAGAAGAGCTGCACACCATCGAATTTTCAGACACTCTTATTAAGAAAG	38776
Db	415	AsnPheLeuGlnGlyLeuGlnGlnLeuGlnHnIleAsnAspPheGlnHnIleSerAsnLeuLysGln	434
OY	38777	GTCAACAATAATTCACAGGTTCTTATCCCTTGAAGACTATTAACCTTGACATCTCTTAT	38836
Db	435	MetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspLysIleSerHis	454
OY	38837	ACTTAACAACAATAATTCGATGAGATGATTTCTTGAGCTTGACAGCTGACACATTA	38896
Db	455	ThrIleThrArgValAlaPheAsnGlnGlyIlePheAsnGlnGlyLeuSerSerLeuGluValLeu	474
OY	38897	AAAAATGCTGCGAATTTCTTCAAGAACAACACCCCTTCAAAATGTCTTGGCAACAACA	38956
Db	475	LysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGluLeuArg	494
OY	38957	AACCTGACATTCCTCGATCTTTCTTAATATGTCAATATGGAACAATATCTTGAGGGGGATTT	39016
Db	495	AsnLeuThrThrPheLeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPhe	514
OY	39017	GACACCCCTTCATAGACTTCATATTAATTAATATGATGACACACATCTATATGTTTGGAT	39076
Db	515	AsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAsp	534
OY	39077	TCAATCCATATATACACAGCTGTATCTCCCTACAGACTCTTGATTTGACAGTTTCAATGCGAT	39136
Db	535	ThrPheProTyrLysCysLeuAsnSerLeuArgValLeuAspLysSerLeuAsnHisIle	554

QY	39137	GAGCATCT---	AAAGAAATATCGCAACATTTTCCAAAGAGTGTACCTTTCAATCTT	39193
Db	555	MetTherizonyxlyngingiuleGlnhlysrProSerSerleuAlaPheleuAsnLeu	574	
QY	39194	ACTAACAAATTCGTGTGCTGTATATATGAAATCATCAGAAATTCCTGCAGTGGGTCAAGAA	39253	
Db	575	ThriGlnhAsnPrPheAlaCysThrCySgUlnhISGlnSerPheleuGlnTrpIlelyAsp	594	
QY	39254	CAGAAAGCATTTCTGGTGGAATGTTTGAACAAATGACATGTGCACACCTGTAGAGATGAAT	39313	
Db	595	GlnArgGlnleuLeuValIGluValIGluArgMetGluCysAlaThrProSerAspLySgln	614	
QY	39314	ACCTCCCTTAGGTGGATTTTAATTAATTCACCTGTATATATGAAAGAAATCATCAGAT	39373	
Db	615	GlyMetProValleuSerLeu---	AsnIleThrCySgGlnMetAsnLyThrIleIleGly	633
QY	39374	GTCACAGTGGTCAGATGTGATGTGGATATCCATCGTACAGCATTTTCTGTATATACACTTCTAT	39433	
Db	634	ValSerValleuSerValleuValValSerValValAlaValleuValLyTrpLySphetyr	653	
QY	39434	TTTCACTGTATTTATTTGCTGTGCTGTAAAAAGTACAGACAGAGAGAAAGCATTTATGAT	39493	
Db	654	PhehisleuMetSerleuAlaGlyCysIleLyTyGlyArgLyGluAsnValTyAsp	673	
QY	39494	GCAATTTGTATCTATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	39553	
Db	674	AlaPheValIleTySerSerGlnAspGlnAspTrpValArgAsnIleuValIlyAsn	693	
QY	39554	TTTAAAGAGAGAGAGCCCGCTTTCACCTGTGCTTTCACATACAGAGACTTTATTCCTGCT	39613	
Db	694	LeuGlnGlnGlyAlaProPheGlnGlnLeuCySgUlnhISGlnArgAspPheIleProGly	713	
QY	39614	GTACCCATTCCTGTGCAACATCATCCAGAAAGCTTTCACAGAGCCGGAAGGTATTATGTC	39673	
Db	714	ValAlaIleAlaAlaAsnIleIleISGlnGlyPhehisIlySerAspGlyValIleVal	733	
QY	39674	GTAAGTGTCTAGACACTTTATTCAGAGCCGTTGGTGTATCTTTGAATATGAGATTGCTCA	39733	
Db	734	ValValSerGlnhlysrPheIleGlnSerArgTrpCySgIlePheGlnLyGlnIleAlaGln	753	
QY	39734	ACATGGAGAGTTTCTGAGACAGCCGCTGGGATCATCTTATTTGCTTGAAGAGTTGAG	39793	
Db	754	ThrTrpGlnPheleuSerSerArgAlaGlyIleIlePheIleValleuGlnIlyValGln	773	
QY	39794	AAAGCTCTGTGTGAGGAGCAGCAGTGTGAATGTATCGCTTTTACAGAAACACTACCTG	39853	
Db	774	LythrIleuLeuArgGlnGlnIleValIGluLeuTyArgLeuLeuSerArgAsnThrLyxleu	793	
QY	39854	GAATGGAGAGCAATCTCTGTGGGAGGACACATTTTCTGAGAAAGACTTAAAAATGCTCTA	39913	
Db	794	GluTrpGlnAspSerValleuGlnArgHisIlePheTrpArgArgGlnArgLySAlaLeu	813	
QY	39914	TTTGATGGAAGAAAGCCTCGAATCTTACGCAACCA	39946	
Db	814	LeuAspGlyLySerTrpAsnProGlnGlyThr	824	
RESULT 9				
ID	TIR4_PONPY	STANDARD:	PRT:	828 AA.
AC	Q8SP69;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DE	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Toll-like receptor 4 precursor.			
GN	Name=TIR4;			
OS	Pongo pygmaeus (Orangutan).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pongo.			
OX	NCBI_TaxId=9600;			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=21405531; PubMed=11514453;			
RA	Smirnova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;			

RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
 RL in humans.";
 CC Genetics 158:1657-1664(2001).
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MYD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TIRAP.
 CC Binds LY96 via the extracellular domain. Binds MYD88 and TIRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL: AF497562; AAM18616.1; -.
 DR EMBL: AF497560; AAM18616.1; JOINED.
 DR EMBL: AF497561; AAM18616.1; JOINED.
 DR HSSP: O60603; LEW.
 DR GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO: GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
 DR GO: GO:0016046; P:detection of fungi; ISS.
 DR GO: GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO: GO:0042116; P:macrophage activation; ISS.
 DR GO: GO:0045576; P:mast cell activation; ISS.
 DR GO: GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO: GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO: GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO: GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 DR GO: GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Cyp.
 DR InterPro: IPR001571; TIR.
 DR Pfam: PF00560; LRR_12.
 DR Pfam: PF01463; LRRCT_1.
 DR Pfam: PF01582; TIR_1.
 DR PRINTS: PR00019; LEURICRPT.
 DR SMART: SM00369; LRR_TYP_1.
 DR SMART: SM00082; LRRCT_1.
 DR SMART: SM00255; TIR_1.
 DR PROSITE: PS50104; TIR_1.
 DR GlycoProtein: Immune response; Inflammatory response;
 KM Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 1 828 Toll-like receptor 4.
 FT DOMAIN 24 828 Extracellular (Potential).
 FT TRANSMEM 630 650 Potential.
 FT DOMAIN 651 828 Cytoplasmic (Potential).
 FT REPEAT 50 74 LRR 1.
 FT REPEAT 75 98 LRR 2.
 FT REPEAT 99 122 LRR 3.
 FT REPEAT 126 147 LRR 4.
 FT REPEAT 148 171 LRR 5.
 FT REPEAT 172 195 LRR 6.
 FT REPEAT 201 223 LRR 7.
 FT REPEAT 226 250 LRR 8.
 FT REPEAT 275 301 LRR 9.
 FT REPEAT 325 348 LRR 10.
 FT REPEAT 349 370 LRR 11.
 FT REPEAT 371 396 LRR 12.

FT REPEAT 398 419 LRR 13.
 FT REPEAT 420 443 LRR 14.
 FT REPEAT 445 467 LRR 15.
 FT REPEAT 468 492 LRR 16.
 FT REPEAT 493 516 LRR 17.
 FT REPEAT 518 539 LRR 18.
 FT REPEAT 541 564 LRR 19.
 FT REPEAT 566 590 LRR 20.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 33 33 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 171 171 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 203 203 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 280 280 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 307 307 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 524 524 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 573 573 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 622 622 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 628 628 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 828 AA; 94340 MW; 51AC0984E5970DFD CRC64;
 Alignment Scores:
 Pred. No.: 2.39e-180 Length: 828
 Score: 2580.00 Matches: 521
 Percent Similarity: 73.33% Conservative: 103
 Best Local Similarity: 61.22% Mismatches: 173
 Query Match: 2.97% Indels: 54
 DB: 1 Gaps: 9
 US-09-396-985b-48 (1-5000) x TLR4_PONPY (1-828)
 QY 37400 TGGAAATAATGCAATTAATGATCACTACTAGACATGATCACTGCTTATGACCCCA 37459
 Db 26 TGGGlnProCysVal-----ValProAsnIleThyrGln----- 37
 QY 37460 GTTATGATCTGGAATGATTTTCTTAATGATTTGCTGCGACATAGTGATAGTTT 37519
 Db 38 CysMetC1LeuAsnPhenTyrlsIleProAsnLeuPro----- 51
 QY 37520 ATCATCACTAGACAGTGGAAATGACAATCTGCAGAGTCTCTCTGCTCACACC 37579
 Db 52 -----PheSerThrIysAsnLeuAspLeuSerPheAsnProLeuArgHis--- 66
 QY 37580 ATCATCACTGTTTGTCTGTGACAGTTTCTCTTACAAATGATGATATCATCT 37639
 Db 67 -----LeuGlySerTyrSerPhe----- 72
 QY 37640 GTTGTATCATGATAGTAGGAGCATGTTATGATTAAGAAAGGTTTTTTTTCAGCAA 37699
 Db 73 ----- 77
 QY 37700 AATATCAATATGATATCTTTTGGCCCATAGGTGGAATGGAACATATGAAGACAG 37759
 Db 78 LeuGlnValLeuAspLeuSer-----ArgCysGlnIleGlnThrIleGlnAspGly 94
 QY 37760 GCATGGAGTGCCTTACACACCTCTCAACTGTGATGACAGAAACCTATCCAGAGT 37819
 Db 95 AlaTyrGlnSerLeuSerHisLeuSerThrLeuIleuThrGlnAsnProIleGlnAsn 114
 QY 37820 TTTTCCCGAAGATTTCTGTGACATTAACAGTTTATGAGATCTGTGCTGTGAGACA 37879
 Db 115 LeuAlaLeuGlnAlaPheSerGlyLeuSerSerLeuGlnIleuValAlaValGlnThr 134
 QY 37880 AATATGCTCTCTTACAAACCTCCATATGACAGCTTAACTTAACCTTAAGAACTCAAT 37939
 Db 135 AsnLeuAlaSerLeuGlnIleuAsnProIleGlyHisIleuLysThrLeuLysGlnLeuAsn 154
 QY 37940 GTGGCTCACAATTTATACATCTCTGTAAGTACCTGATATTTTCCATCTGACGAC 37999
 Db 155 ValAlaHisAsnLeuIleGlnSerPheLysLeuProGlnIlePheSerAsnLeuThrAsn 174
 QY 38000 CTAGTACATGATCTTTCTTAACTATATTTCAACTATTACTGTCACAGACTTACAG 38059
 Db 38000 CTAGTACATGATCTTTCTTAACTATATTTCAACTATTACTGTCACAGACTTACAG 38059

Db 175 LeuGluHISLeuAAspLeuSerSerAsnLysIleGlnSerIleTyrCysLeuAAspLeuGln 194
 QY 38060 TTCTACAGTGAATAATCCACAATGCAATCTCTTAGACATATGCTTTTAAACCAATGAC 38119
 Db 195 ValLeuHISGlnMetProLeuLeuAsnLeuSerLeuAAspLeuSerLeuAAspLeuAAsn 214
 QY 38120 TTCAATTAAGACCAAGCCTTTAGGGAATTAAAGCTCCAGTAACTGACTCTTAAGAGTAA 38179
 Db 215 PheIleGlnProGlyAlaPheLeuGlnIleArgLeuHISLysLeuThrLeuAAspLeuSer 234
 QY 38180 TTTAAATGCTCAATATATATAAACTGCTTCAAAACCTGGCTGGTTTACAGTCCAT 38239
 Db 235 PheAspSerLeuAAsnValMetLysThrCysIleGlnLysLeuAlaGlyLeuGlnValHIS 254
 QY 38240 CGGTGATCTTGGGGAATTAAAGATGAAGAATGGAATTTTGAACCCCTATAC 38299
 Db 255 HisLeuValLeuGlnLysPheArgAsnGlnLysAsnLeuGlnLysPheAspThrSerAla 274
 QY 38300 ATGGAAGACTATGATGATGATGACCAATGATGAGTTGAGTTTAACTATATACAAATGATTT 38359
 Db 275 LeuGlnGlyLeuCysAsnLeuThrIleGlnLysPheArgLeuAlaTyrLeuAAspTyr 294
 QY 38360 TCAGATGATATGTTAG--TTCCATTGCTTGGCGAATGTTTTCGCAATGCTTGCGCA 38416
 Db 295 LeuAspIleIleLeuAAspLeuAAsnLysCysLeuAlaAsnValSerSerPheSerLeuVal 314
 QY 38417 GGTGATCTATATAATATCTAGAAGATGCTCTAAACATTTCAATGGCAATCCCTTACA 38476
 Db 315 SerValThrIleLysSerValLysAspPheSerTyrAsnPheGlyTyrGlnHISLeuGln 334
 QY 38477 ATCATAGATGCAACTTAACAGTTTCACTGATCTGATCTACCTTTCTTAAAGTTTG 38536
 Db 335 LeuValAsnLysPheGlyGlnPheProThrLeuGlnLysSerLeuLysArgLeu 354
 QY 38537 ACTTTAATGAAACAAGGCTTATCACTTTTAAAGGCGCCCTTCAAGTCTCAAGC 38596
 Db 355 ThrPheThrAlaAsnLysGlyAlaAsnAlaPheSerGlnValAAspLeuProSerLeuGln 374
 QY 38597 TATCATAGTCTTAGAGAAAGCACTGAGCTTGTGCTGCTGCTTATCTTATCTGATTTG 38656
 Db 375 PheLeuAAspLeuSerArgAsnGlyLeuSerPheLysGlyCysGlySerGlnSerAspPhe 394
 QY 38657 GGAACAACAGCCTGAGACACTGACCTTCACTGATGCTGATCATATTGATGAGTCC 38716
 Db 395 GlyThrThrSerLeuLysTyrLeuAAspLeuSerPheAsnAspValIleThrMetGlySer 414
 QY 38717 AATTTCATGGCTTGAAGAGCTGACAGCACTGATTTTCACTGACTTCACTTAAAGG 38776
 Db 415 AsnPheLeuGlnLysGlnLysLeuGlnIleAsnAspPheGlnHISerAsnLeuLysGln 434
 QY 38777 GTACAGAAATCTGAGGCTTCTTATCCCTTGAAGAACTTCTTCACTGATCTTAT 38836
 Db 435 MetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAAspIleSerHIS 454
 QY 38837 ACTAACAACAAATGACTTGTGATGATATTTCTTGGCTTGAACAGTCTCAACATTA 38896
 Db 455 ThrIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuLysValLeu 474
 QY 38897 AAAATGGCTGGCAATTTCTTCAAGACAACACCTTTCAATATGCTTTGCAACAACA 38956
 Db 475 LysMetAlaGlyAsnSerPheGlnLysAsnPheProAspIlePheThrGlnLeuArg 494
 QY 38957 AACTTGACATCCCGATCTTCTTAAATGCAATTTGAACAATAATCTTGGGGGATTTT 39016
 Db 495 AsnMetThrPheLeuAAspLeuSerGlnCysGlnLeuGlnLysSerProThrAlaPhe 514
 QY 39017 GACACCTTCATAGACTTCAATTAATTAATGATGATCAACAATCTTATTTTGGAT 39076
 Db 515 AsnMetLeuSerSerLeuGlnValLeuAAsnMetSerHISAsnAsnPhePheSerLeuAAsp 534
 QY 39077 TCATCCCATTAATAACAGCTGATTTCCCTGACAGCTTGTGATGCAATGATGCAATA 39136
 Db 535 ThrPheProTyrLysCysLeuAAsnSerLeuGlnValLeuAAspTyrSerLeuAAsnHISile 554

QY 39137 GAGACATCT---AAGAATACTGCAACATTTTCCAAAGAGTCAAGCTTCTTCAATCTT 39193
 Db 555 MetThrSerLysLysGlnGlnLeuGlnHISerPheProSerSerLeuAlaPheLeuAAsnLeu 574
 QY 39194 ACTTAACAATCTGCTGCTTGTATATGTAACATGACAAATTCCTGACAGTGGCTCAAGAA 39253
 Db 575 ThrGlnAsnAspPheAlaCysThrCysGlnIleGlnSerPheLeuGlnTyrIleLysAsp 594
 QY 39254 CAGAGAGATTTCTGGGAATGTTGAACAATGACATGTCGAACACCTGTGAGATGAT 39313
 Db 595 GlnArgGlnLeuLeuValGlnValGlnArgMetLysSalThrProSerAspLysGln 614
 QY 39314 ACTCTCTAGTGTGGAATTTTAAATTTCACTGATTAATGTAACAACAATCACTAGT 39373
 Db 615 GlyMetProValLeuSerLeu---AsnIleThrCysGlnMetAsnLysThrValIleGly 633
 QY 39374 GTGTCAGTGTCACTGTGATTTGTGATTCACATGATCTTGTATATACACTTCTAT 39433
 Db 634 ValSerValPheSerValLeuValValSerValValAlaValLeuValTyrLysPheTyr 653
 QY 39434 TTTTACCTGATCTTATTTGCTGGCTGATAAAAGTACAGAGAGAAAGATCTATGAT 39493
 Db 654 PheHisLeuMetLeuLeuAlaGlyCysIleLysTyrGlyArgGlyAsnThrTyrAsp 673
 QY 39494 GCATTTGATCTTCACTGAGTCAAGATGAGAGAGAGTGGGGAATGAGCTGTAAAGAT 39553
 Db 674 AlaPheValIleTyrSerSerGlnAspIleAspThrValArgAsnGlnLeuValLysAsn 693
 QY 39554 TTGAAGAAGAGAGTCCCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 39613
 Db 694 LeuGlnGlnGlyValProThrPheGlnLeuLysCysLeuHISerTyrArgAspPheIleProGly 713
 QY 39614 GTAGCCATGCTGGCAACATCATCCAGAGAGCTTCCACAAGAGCCGGAAGGTATTGTG 39673
 Db 714 ValAlaIleAlaAsnIleIleLeuGlnLysPheHisLysSerArgLysValIleVal 733
 QY 39674 GTAGTGTCTGACACTTATTTACAGAGCGCTGGTGGTATCTTTGAATATGAGATGCTCAA 39733
 Db 734 ValValSerGlnHISerIleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGln 753
 QY 39734 ACATGAGATTTCTGACAGCAGCTGTCGATCATCTTCAATGCTTGAAGAGTGTAG 39793
 Db 754 ThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGln 773
 QY 39794 AAGTCCCTGCTGAGGAGGAGGATGATTTGATGCTTCTTGAAGAAACCTTACCTG 39853
 Db 774 LysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeu 793
 QY 39854 GAATGGAGGACATCCTGCGGAGGACACATCTTCTGGAAGACCTTAAATATGCCCTA 39913
 Db 794 GlnTyrGlnAspSerValLeuGlnLysGlnIlePheThrTyrArgLeuArgLysAlaLeu 813
 QY 39914 TTGATGAAAGAGCTTGAATCTTGAACAACA 39946
 Db 814 LeuAspGlyLysSerThrAsnProGlnGlyThr 824

RESULT 10
 TLR4_BOVIN
 ID TLR4_BOVIN STANDARD; PRT; 841 AA.
 AC O96L65;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Toll-like receptor 4 precursor.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBT_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Guionaud C.T., Dubey C., Jungi T.W. ;
 RT "Ovine Toll-like receptor 4 (TLR4)." ;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TRAF4.
 CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAF6 via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 18 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL: AF310952; AAC32061.2; -.
 DR HSSP: O60603; LFYX.
 DR GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO: GO:0007250; P:activation of NF-kappa-B-inducing kinase; ISS.
 DR GO: GO:0016046; P:detection of fungi; ISS.
 DR GO: GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO: GO:0042116; P:macrophage activation; ISS.
 DR GO: GO:0045576; P:macrophage activation; ISS.
 DR GO: GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO: GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO: GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO: GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 DR GO: GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR004831; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Cyp.
 DR InterPro: IPR001571; TIR.
 DR Pfam: PF00560; LRR_13.
 DR Pfam: PF01463; LRRCT_1.
 DR Pfam: PF01582; TIR_1.
 DR PRINTS: PR00019; LEURICRPT.
 DR SMART: SM00369; LRR_TYP_1.
 DR SMART: SM00082; LRRCT_1.
 DR SMART: SM00255; TIR_1.
 DR PROSITE: PS50104; TIR_1.
 KW Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 841 Toll-like receptor 4.
 FT DOMAIN 24 632 Extracellular (Potential).
 FT TRANSMEM 633 653 Potential.
 FT DOMAIN 654 841 Cytoplasmic (Potential).
 FT REPEAT 53 76 LRR 1.
 FT REPEAT 77 100 LRR 2.
 FT REPEAT 102 124 LRR 3.
 FT REPEAT 149 173 LRR 4.
 FT REPEAT 174 197 LRR 5.
 FT REPEAT 203 225 LRR 6.
 FT REPEAT 277 300 LRR 7.
 FT REPEAT 310 334 LRR 8.
 FT REPEAT 350 372 LRR 9.
 FT REPEAT 373 398 LRR 10.
 FT REPEAT 400 421 LRR 11.
 FT REPEAT 422 445 LRR 12.
 FT REPEAT 446 469 LRR 13.
 FT REPEAT 471 494 LRR 14.

FT REPEAT 495 518 LRR 15.
 FT REPEAT 520 542 LRR 16.
 FT REPEAT 544 566 LRR 17.
 FT REPEAT 568 592 LRR 18.
 FT DOMAIN 673 819 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 73 73 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 238 238 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 282 282 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 625 625 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 841 AA; 96026 MW; C5E17CB9C798CD16 CRC64;
 Alignment Scores:
 Pred. No.: 3,36e-180 Length: 841
 Score: 2578.00 Matches: 520
 Percent Similarity: 72.02% Conservative: 103
 Best Local Similarity: 60.12% Mismatches: 188
 Query Match: 2.97% Indels: 54
 DB: 1 Gaps: 8
 US-09-396-985b-48 (1-50000) x TLR4_BOVIN (1-841)
 QY 37400 TGGAAAAAATGTAATTAATGTAAGACTGATCAATGATGCTTTATGTAACCCCA 37459
 Db 26 TTPASPProcyvalGlnValValProaenIleSerTyrIn----- 39
 QY 37460 GTTATGATCTTGAAATGATTTTCTTAATGATTTCTGCTGCATGATGATGTTT 37519
 Db 40 CyMeGcluleuSsnleuTyrIlySleIProaSpAnIlePro----- 53
 QY 37520 ATGATCATGTAAGCAAGTGTGAAATGCAATCTGCAAGATCTCTGCTCACACC 37579
 Db 54 -----IleSerThrIlySmetLeuApsLeuSerPheAnTyrIleuArgHis--- 68
 QY 37580 ATGATCACCTGTTTGTCTGTACATGTTTCTCTTAAATTAACATGATATCATATCT 37639
 Db 69 -----LeuGlySerHisAsnPheSer----- 75
 QY 37640 GTTGTATCATGATGATGTAAGGACTGTATGTCATTAAGAAAGGTTTTCACGAA 37699
 Db 76 -----SerPheProGlu 79
 QY 37700 AAATGATTAATGATATCTCTTTGCCCATAGTGTAATGAAATGTAAGACACAG 37759
 Db 80 LeuGlnValIleuApsLeuSer-----ArgCysGluIleIlySleIleGluApsAsp 96
 QY 37760 GCATGCAATGCTTACACCAACCTCTGAACTGATCTGACAGAAACCTATCCAGAGT 37819
 Db 97 ThrPheGlnIlyleuSsnHISleuSerThrIleuIleuThrIlySsnProIleGlnSer 116
 QY 37820 TTTTCCCGAAGATTTCTGTGACTTACAAAGTTTGAAGATCTGTGCTGTGAGACA 37879
 Db 117 LeuAlaIleTyrIlyAlaPheSerGlyLeuSerSerLeuGlnIlySleuValAlaValGluThr 136
 QY 37880 AAATGGCTCTCTAGAAAGCTTCCCTATTGACAGGTTTAAACCTTAAAGAAATGCAAT 37939
 Db 137 AsnIleuValSerIleuApsLeuPheProIleGlyHisIleuIlySsnLeuIlySglIleuApsN 156
 QY 37940 GTGGCTTACAAATTTTATACATCTCTGTAATTAACCTGCAATTTTCCATTCGACGAC 37999
 Db 157 ValAlaHisAsnPheIleHisSerPheIlySleuProGluIlyrPheSerIleuProAsn 176
 QY 38000 CTAGTACATGATGATCTTTCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 38059
 Db 177 LeuGlnHisIleuApsLeuSerAsnIlySleIleGlnIlySleIlyrIlyIlyApsValIlyS 196
 QY 38060 TTTCTACGTAATAATCCACAAATGCAATCTCTTTTACATGATGTTTGAACCAATTTGAC 38119
 Db 177 LeuGlnHisIleuApsLeuSerAsnIlySleIleGlnIlySleIlyrIlyIlyApsValIlyS 196

Db 197 ValLeuHISglMetProLeuLeuSerLeuAspSerLeuAsnProLeuAsp 216
 QY 38120 TTCAATCAAGACCAAGCTTTCAGGGAATTAAGCTCCATGAAGTCACTTAAGAGTAA 38179
 Db 217 PheIleGluProGlyThrPheLeuSgluIleuLeuAsnGlyLeuThrLeuArgSerAsn 236
 QY 38180 TTTAAATAGCTCAATATAATGAATAAAGCTTCAAAACCTGGCTGGTTTACACGTCAT 38239
 Db 237 PheAsnSerSerHISValMetLeuThrCysIleGlnGlyLeuAlaGlyLeuLeuThrAsn 256
 QY 38240 CGGTGATCTTGGGGAATTTAAAGATGAAGAACTGGAATTTTGAACCCCTCTATC 38299
 Db 257 ArgLeuValLeuGlyGluPheLeuSasngluArglyLeuGlnArgPheAspArgSerPhe 276
 QY 38300 ATGAAGGACTATGATGATGACATGATGATGATGATGATGATGATGATGATGATGAT 38359
 Db 277 LeuGluGlyLeuCysAsnLeuThrIleGluGlnPheAsnGlyAlaIleuLeuAspArgPhe 296
 QY 38360 TCA--GATGATATGTTAAAGTTCCATGCTTGGCGAATGTTTGCACATGCTCGCA 38416
 Db 297 SerGlyAspAspThrAspLeuPheAsnCysLeuAlaAsnValSerValIleSerLeuLeu 316
 QY 38417 GGTGATATCTATAAATATCTAGAAGATGCTTAAACATTTTGAATGGCAATCCTTATCA 38476
 Db 317 SerIleSerLeuGlySerLeuGlnAlaLeuLeuLysAspPheArgTrpGlnHISLeuGlu 336
 QY 38477 ATCATTAGATGTCATTAAGCAGTTCCTCAACTGATGATCTACCTCTTCTTAAAGTTTG 38536
 Db 337 IleIleAsnCyAspPheAspArgPheProAlaLeuLysLeuSerSerLeuLysArgPhe 356
 QY 38537 ACTTTAATATGACAAAGAGGCTCTATCAGTTTAAAAAAGTGGCCCTTACCAAGTCTCAGC 38596
 Db 357 ValPheThrAspAsnLysAspIleSerThrPheThrGluPheGlnLeuProSerLeuGln 376
 QY 38597 TATCTAGATCTTAGTGAAGAAATGCACTGAGCTTAAAGTGGTGTCTTCTTATTCGATTTG 38656
 Db 377 TyrLeuAspLeuLysArgAsnHISLeuAspLeuSerPheLysGlyCysSerHISThrAspPhe 396
 QY 38657 GGAACCAACAGCCTGAGACACTTAGACCTTCAATGGTGCATCATTAATGAGTGC 38716
 Db 397 GlyThrThrAsnLeuLysHISLeuAspLeuSerPheAsnAspValIleThrLeuLysSer 416
 QY 38717 AATTTCATGGCTTGAAGAGCTGAGACCTGATTTTCAGACTTCACTTAAATGAAAG 38776
 Db 417 AsnPheMetGlyLeuGluGlnLeuGlnHISLeuAspPheGlnHISerThrLeuLysGln 436
 QY 38777 GTCCACGAATCTCAGCCTTCTATCCCTTGAAGAAAGCTTACTTACCTTGAATCTTAT 38836
 Db 437 IleAsnAlaPheSerAlaPheLeuSerLeuLysArgAsnLeuArgTyrLeuAspIleSerTyr 456
 QY 38837 ACTTAACACCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 38896
 Db 457 ThrAsnIleArgIleValPheHISGlyIlePheThrGlyLeuValSerLeuGlnThrLeu 476
 QY 38897 AAAATGGCTGCAATCTTTCGAAAGCAACACCTTTCGAAATGCTTTCGAAAGCAACA 38956
 Db 477 LysMetAlaGlyAsnSerPheGlnAsnAsnLeuLeuProAlaIlePheThrGlnLeuThr 496
 QY 38957 AACTTGACATCTCGGATCTTCTTAATGATGATGATGATGATGATGATGATGATGATGAT 39016
 Db 497 AsnLeuThrValLeuAspLeuSerTyrCysGlnLeuGlnValAlaGlnThrAlaPhe 516
 QY 39017 GACACCTCCATAGACTCAATTAATTAATGATGATGATGATGATGATGATGATGATGATGAT 39076
 Db 517 HISerLeuSerSerLeuGlnValLeuAsnMetSerHISAsnLysLeuLeuSerLeuAsp 536
 QY 39077 TCATCCATTATTAACACAGCTGATTCCTCGACACTTTCGATGATGATGATGATGATGATGAT 39136
 Db 537 ThrPheLeuTyrGluProLeuHISerLeuArgIleLeuAspCysSerPheAsnArgIle 556
 QY 39137 GAGACATCTAA---GGAATCTGCAACATTTTCCAAAGATCTAGCCTTCTTCAATCTT 39193
 Db 557 MetAlaSerLysGluGlnGlnLeuGlnAsnLeuProArgSerLeuThrTrpLeuAsnLeu 576

QY 39194 ACTTAACAAATCTGTTGCTTGTATATGATGATGATGATGATGATGATGATGATGATGAT 39253
 Db 577 ThrGlnAsnAlaPheAlaCysValCysGluHISglInsSerPheLeuGlnTrpValLysAsp 596
 QY 39254 CAGAAAGACTTCTTGGTGAATGTTGGAACAAATGACATGATGCAACACTGATAGATGAAT 39313
 Db 597 GlnArgGlnLeuLeuValGlyAlaGluGlnMetMetCysAlaGluProLeuAspMetGlu 616
 QY 39314 ACCTCTTAATGTTGGATTTTAAATATCTTACCTGTATATGATGATGATGATGATGAT 39373
 Db 617 AspMetProValLeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrIleLeuSer 636
 QY 39374 GTGTGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39433
 Db 637 ValSerValValThrValLeuLeuValSerValValGlyValLeuValTyrLysPheTyr 656
 QY 39434 TTTCACTGATATCTTATTTGCTGGCTGTAAAGTACAGCAGAGGAAAGCATCTTATGAT 39493
 Db 657 PheHISLeuMetLeuLeuAlaGlyCysLysLysTyrGlyArgGlyGluSerIleTyrAsp 676
 QY 39494 GCATTTGATCTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39553
 Db 677 AlaPheValIleTyrSerSerGlnAspGlyAspTrpValArgAsnGlnLeuValLysAsn 696
 QY 39554 TTGAAGAAGAGAGTGGCCCGCTTCACTGATGATGATGATGATGATGATGATGATGATGAT 39613
 Db 697 LeuGluGlnGlyValProProPheGlnLeuCysLeuHISLysArgAspPheIleProLys 716
 QY 39614 GTAGCATTGCTGCAACATCATCCAGAAAGCTTCCACAGAGCCGGAAGTTATGTTG 39673
 Db 717 ValAlaIleAlaAlaAsnIleIleGlnGlnLysPheHISLysSerArgGlyValIleVal 736
 QY 39674 GTAGTGTCTAGACATTTATTCAGAGCCGTTGGTGTATCTTGAATATGATGATGCTCA 39733
 Db 737 ValValSerGlnHISPheIleGlnSerArgTrpCysIlePheGlnTyrGluIleAlaGln 756
 QY 39734 ACATGGAGCTTTCGAGAGCCGCTGAGCACTCATCTTCAATGCTTGAAGAGTGGAG 39793
 Db 757 ThrTrpGlnPheLeuSerSerArgAlaGlyIlePheIleValLeuGlnLysLeuGln 776
 QY 39794 AAGTCCCTGTGAGGACAGAGTGAATGTGATGCTTCTTACAGAAACACTTACCTG 39853
 Db 777 LysSerLeuLeuArgGlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyrLeu 796
 QY 39854 GAATGGAGAGCAATCTCTGGGAGGACATCTTCTGAGAAACATTTAAATGCCCTTA 39913
 Db 797 GluTrpGluAspSerValLeuGlyArgHISValPheTrpArgLeuArgLysAlaLeu 816
 QY 39914 TTGATGGAAGAAAGCTCGAATCTCGAGCAACAGCAGAGGAAGAA-----CAAGAA 39964
 Db 817 LeuAlaGlyLysProGlnSerProGluGlyThrAlaAspAlaGluThrAsnProGlnGln 836
 QY 39965 ACGGCAACTTGAGC 39979
 Db 837 AlaThrThrSerThr 841

RESULT 11
 Q8S055 ID Q8S055 PRELIMINARY; PRJ: 841 AA.
 AC Q8S055; ID Q8S055;
 DT 01-JUN-2002 (TREMBLERel. 21, Created)
 DT 01-JUN-2002 (TREMBLERel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBLERel. 26, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC NCBI_TaxID=9913;
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.


```

Db 477 LysMetAlaGlyAenSerPheGlnAsnAsnLeuProAspIlePheThrGlnLeuThr 496
QY 38957 AACTTGACATTCCTGATCTTTAAATGTCAATTTGGAACAATATCTTGCGGGGATATT 39016
Db 497 AsnLeuThrValLeuAspLeuSerLysCysGlnLeuGlnValAlaGlnThrAlaPhe 516
QY 39017 GACACCTCCATAGACTCAATTAATTAATATGATGACAAACAATCTATTGTTTGGAT 39076
Db 517 HisSerLeuSerLeuGlnValLeuAsnMetSerHisAsnLeuLysLeuSerLeuAsp 536
QY 39077 TCATCCCATTAATACAGCTGTATTCCTCAGACCTGTGATTTGAGATTTCATTCGATA 39136
Db 537 ThrPheLeuYrGlnProLeuHisSerLeuArgIleLeuAspCysSerPheAsnArgIle 556
QY 39137 GAGACATCTAA--GGAACTAGTCAACATTTTCCAAAGATCTAGCCTTCTTCATCTT 39193
Db 557 MetAlaSerLysGlnGlnGlnLeuGlnAsnLeuProArgSerLysThrTrpLeuAsnLeu 576
QY 39194 ACTACAAATCTGTGCTTGTATATGTGACATGACAAATTCCTGACAGTGGTCAGAGAA 39253
Db 577 ThrGlnAsnAlaPheAlaCysValCysGlnHisGlnSerPheLeuGlnTrpValLysAsp 596
QY 39254 CAGAGACATCTTCTGATGATGTGGAACAATGACATGTGCAACACTGTAGAGATGAT 39313
Db 597 GlnArgGlnLeuLeuValGlyAlaGlnMetMetCysAlaGlnProLeuAspMetGln 616
QY 39314 ACCTCCTTAGTGTGATTTAATTAATTTCTACCTGTTATATGATCAAGACAAATCATAGT 39373
Db 617 AspMetProValLeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrIleIleSer 636
QY 39374 GTGACAGTGTGCTGATGTATGTGATTCACATGATGATTTCTGATATACACTTCTAT 39433
Db 637 ValSerValValThrValLeuLeuValSerValGlyValLeuValTyrLysPheTyr 656
QY 39434 TTTGACCTGATCTTATTTGCTGCTGCTGTAAGAAAGTACAGCAGAGAGAAAGCATATGAT 39493
Db 657 PheHisLeuMetLeuLeuAlaGlyCysLysLysTyrGlyArgGlyGlnSerIleTyrAsp 676
QY 39494 GCATTTGATCTACTGAGTCAAGTCAAGTGAAGAGAGCTGGGAGAAATGAGTGGTAAGAT 39553
Db 677 AlaPheValIleTyrSerSerGlnAspGlnAspTrpValAlaArgAsnGlnLeuValLysAsn 696
QY 39554 TTGAGAGAGAGAGTCCCGCTTTCACCTGCTGCTTCACTACAGAGACTTATTCCTGCT 39613
Db 697 LeuGlnGlnGlyValProProPheGlnLeuLysLysHisTyrArgAspPheIleProGly 716
QY 39614 GTAGCCATTTGCTGCCAATCATATCCAGAGAGCTTCCACAAAGAGCCGAGATTATGCTG 39673
Db 717 ValAlaIleLeuAlaAsnIleIleGlnGlnGlyPheHisLysSerArgLysValIleVal 736
QY 39674 GTAGTGTCTGACACTTATTCAGAGCCGTGGTGTATCTTGAATATGATGATGCTCA 39733
Db 737 ValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGln 756
QY 39734 ACATGAGATTTCTGACAGCCGCTGCTGCTGATCTTCAATTTGCTTGAAGAGTTGAG 39793
Db 757 ThrTrpGlnHisLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeuGln 776
QY 39794 AAGTCCCTGCTGAGCAGCAGGTGGAATGTATGCTTCTTTCAGAGAAACACTTACTG 39853
Db 777 LysSerLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeu 796
QY 39854 GAATGGAGAGACATCTCTGGGAGGACATCTTCTGAGAGAACTTAAATAAGCCCTTA 39913
Db 797 GlnTrpGlnLysSerValLeuGlyArgHisValAlaPheTrpArgAlaGlyValAlaLeu 816
QY 39914 TTGATGAGAAAGCTGGAATCTCTGACAAACAGCAGAGAGAGAA-----CAAGAA 39964
Db 817 LeuAlaGlyLysProGlnSerProGlnGlyThrAlaAspAlaGlnThrAsnProGlnGln 836
QY 39965 ACGGCAACTTGAGCC 39979
Db 837 AlaThrThrSerThr 841

```

```

RESULT 12
06WCDS PRELIMINARY; PRT; 841 AA.
ID 06WCDS
AC 06WCDS
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Toll-like receptor 4.
GN Name:TLR4;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2833971; PubMed=12915733; DOI=10.1073/pnas.1333957100;
RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.E.;
RT "Haplotype variation in bovine Toll-like receptor 4 and computational
RT prediction of a positively selected ligand-binding domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
DR EMBL; AY297040; AA062700.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR InterPro; IPR001611; IRR.
DR InterPro; IPR000483; IRR_Cterm.
DR InterPro; IPR003885; IRR_Cyst.
DR InterPro; IPR003591; IRR_Cyp.
DR InterPro; IPR00157; TIR.
DR Pfam; PF01463; LRCT; 1.
DR Pfam; PF00560; LRR_1; 12.
DR Pfam; PF01582; TIR_1.
DR PRINTS; PR00019; LEURICRPT.
DR SMART; SM00082; LRCT; 1.
DR SMART; SM00365; LRR_SD2; 6.
DR SMART; SM00369; LRR_TYR; 13.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PSS0104; TIR; 1.
KW Receptor.
SQ
SEQUENCE 841 AA; 96014 MW; 603936A17B834735 CRC64;

Alignment Scores:
Pred. No.: 7.83e-180 Length: 841
Score: 2573.00 Matches: 519
Percent Similarity: 71.91% Conservative: 103
Best Local Similarity: 60.00% Mismatches: 189
Query Match: 2.96% Indels: 54
DB: Gaps: 8

US-09-396-985b-48 (1-50000) x 06WCDS (1-841)
QY 37400 TGAAGAAATGCAATAATTAATCTAAGACTACATATCACTGCTTATATGATCCCA 37459
Db 26 TrpAspProCysValGlnValAlaProAsnIleSerTyrGln----- 39
QY 37460 GTTATGATCTTGAATGATATTTTCTAATGATTTTGCTGCTGACATAGTGTATGTT 37519
Db 40 CysMetGlnLeuAsnLeuTyrLysIleProAsnIlePro----- 53
QY 37520 ATCATCACTGTACCAAGTGAAGAAATGACAAATCTGACAGATTCCTCTGCTACACC 37579
Db 54 -----IleSerThrLysMetLeuAspLeuSerPheAsnTyrLeuAlaGHis--- 68
QY 37580 ATCATCACTGTTTGTCTGTACAGTTCCTTTTACAAATTAACAGGTATATCATATCT 37639
Db 69 -----LeuGlySerHisAsnPheSer----- 75
QY 37640 GTTTGATCATATGATATGATGAGAGCTGTATATGATTAAGAAAGGTTTTTTTTCAGCA 37699
Db 76 -----SerPheProGln 79
QY 37700 AATATCATATGATATCTCTTTTGCCCATAGGTGAGAAATGAAACAATTAAGAGCAG 37759

```

Dh	80	LeuGIInValIeuAspIeuSer-----ArgCysGluIleuysIleIleGluIuAsp	96
Qy	37760	GCATGGCATGCTTTACACCACTCTCCAACTGTATGTACAGAAACCCTTATCCAGAGT	37819
Dh	97	ThrheGIngluIeuAsnIleuSerThrIleuIleuThrGluysnProIleGInSer	116
Qy	37820	TTTTCCCAAGAGATTCTCTGGACCTACACAGTTTACAGAAATCGTGCGCTGTGAGACA	37879
Dh	117	LeuIaIrrpGlyIaIlePheSerGlyIeuSerSerIeuGInIleuysValaIaValGluThr	136
Qy	37880	AAATTTGGCGCTCTCAGAAAGCTTCCCATTTGACAGCTTATATACCTTAAGAAGCACTAT	37939
Dh	137	AsnIeuValSerIeuAsnAspPheProIleGlyIleuIleuysAsnIeuysGluIeuysn	156
Qy	37940	GTGGCTACCAATTTTATACATTCCTGTAAAGTTTACCTGCATATTTTCCATCTGACGAAC	37999
Dh	157	ValaIaIleAsnPheIleIleIleSerPheIuysIeuProGluIuThrPheSerIleuProAsn	176
Qy	38000	CTAGTACATGTGATCTTTCTTTATACATATATTCAAACTATTACTGTCAACGACTTACAG	38059
Dh	177	LeuGluIleuysIleuAspIeuSerIeAsnAsnIleIleGInAsnIleuTyTrGluAspValIuys	196
Qy	38060	TTTTACGTGAAATCCACAAGTCAATCTCTTTTACACATGCTTTTGAACCCATATGAC	38119
Dh	197	ValIeuIleGInIuMetProIleuIleAsnIleuSerIeuAspIeuSerIeuAsnProIeuAsp	216
Qy	38120	TTTCATTAAGACCAAGCGCTTTACAGGAAATTAACTCCATCAATGACTCTTAAGAGGTAT	38179
Dh	217	PheIleGluProGlyIuThrPheIuysGluIleuIleuAsnIuIleuThrIeuAspIeAsn	236
Qy	38180	TTTAATAGCTCAAAATATATATGAAGAACTTGCGCTTCAAAACCTGGCTGTTTACACGTCCAT	38239
Dh	237	PheAsnSerSerIleValIeIuysIuThrCysIleGInGlyIeuIaIleuysIuThrAsn	256
Qy	38240	CGGTGATCTTTGGAGAAATTAAAGAAAGAAAGCAATCTGAAATTTTGAACCCCTATAC	38299
Dh	257	ArgIeuValIeuGlyGluPheIuysAsnGluIaIuysIeuGInIuAspIeAspIeSerIePhe	276
Qy	38300	ATGGAGAAGCATATGTGATGTGACCACTATGAGAGTTCAGGTTTACATATCAATATGATTTT	38359
Dh	277	LeuGluIuGlyIeuCysAsnIeuIuThrIleGInGInPheArgIleIaIaIuIleuAspIuysPhe	296
Qy	38360	TCA--GATGATATGTGTAAGTTCCATGCTTGTCGCGCAATGTTTCTGCAATGTCTGTGCA	38416
Dh	297	SerGluysAspIeIuThrAspIeuPheAsnCysIeuIaIeAsnIaIeSerValIleSerIeuIeu	316
Qy	38417	GGTGTATCTATAAAATATCTAGAAAGATGTTCTTAAACATTTCAAAATGGCAATCTTATCA	38476
Dh	317	SerIleSerIeuGlySerIeuGInIaIeIleuIleuysAspPheArgIrrpGInIaIeIuGIn	336
Qy	38477	ATCATTTAGATGTCAACTTAAGAGGTTTCCAACTGTGATGTATCCCTTCTTAAAGTTTG	38536
Dh	337	IleIleAsnCysAspIeAspIeAspIuysPheProIaIeIuIleuysIeuSerIeuIuysIuysPhe	356
Qy	38537	ACTTTAATCTAGAACAAAGGCTTATCATGATTTTAAAAAAGTGGCCCTTACCAAGTCTCACG	38596
Dh	357	ValPheIuThrAspAsnIuysAspIleIeSerThrPheIuGluIuPheGInIeuProSerIeuGIn	376
Qy	38597	TATCTAGATCTTATGTAATAATGACATGAGCTTTTATAGTGGTTCGTGTTCTTATTTCTGATTTG	38656
Dh	377	TyrIeuAspIeuIuysArgAsnIaIeIleuSerPheIuysGlyCysSerIeIaIeIuThrAspPhe	396
Qy	38657	GGAAACAAGCCCTGACGACCTTACAGCTGACGCTTCAATGCGTCCCAATTTAGATGCGC	38716
Dh	397	GlyIuThrIuAsnIeuIuysIleuAspIeuSerPheAsnAspValIleIuThrIeuGlySer	416
Qy	38717	AATTTCAATGGGTCTAGAGAGCTGACACATGAGATTTTTCAGACATCTTAAAAAAG	38776
Dh	417	AsnIleIuIeGluIleuGInIleuGInIleuAspIheIuIleIleSerIuIleuysGIn	436
Qy	38777	GTCAAGAAATTCAGGGTCTTATCCCTTGAAGAAAGCTATTTACCTTGAACATCTTAT	38836
	:::		

[illegible]

Oy	39914	TTGATGTGAAGAAAGCCTGGAAATCCCTGACCAAAACGCAGAGAAGAAA-----CAAGAA	39964
Dd	817	LeuAatgLyIsP-ProGInserProGIUGLYThralAspaIacLuthrAnProGINGLN	836
Oy	39965	ACGCCAACCTTGACC 39979	
Dd	837	AlathrThrSerThr 841	
RESULT 13			
ID	Q6WCDA	PREDIMINARY;	PRT; 841 AA.
AC	Q6WCDA4		
DT	05-JUL-2004	(TREMBLrel. 27, Created)	
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)	
DE	Toll-like receptor 4.		
GN	Name=TLR4;		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovinae; Bos		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=2283971; PubMed=12915733; DOI=10.1073/pnas.1333957100;		
RA	White S.N., Taylor K.H., Abbey C.A., Gill C.A., Womack J.E.;		
RT	"Haplotype variation in bovine Toll-like receptor 4 and computational		
RL	prediction of a positively selected ligand-binding domain.";		
DR	Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).		
DR	EMBL; AY297043; AAC62701.1; JOINED.		
DR	EMBL; AY297042; AAC62701.1; JOINED.		
DR	GO; GO:0016020; C:membrane; IEA.		
DR	GO; GO:0004888; F:transmembrane receptor activity; IEA.		
DR	InterPro; IPR001611; LRR.		
DR	InterPro; IPR000483; LRR_Cterm.		
DR	InterPro; IPR003885; LRR_cyst.		
DR	InterPro; IPR003591; LRR_typ.		
DR	InterPro; IPR000157; TIR.		
DR	Pfam; PF01463; LRCT; 1.		
DR	Pfam; PF00560; LRR_1; 12.		
DR	Pfam; PF01582; TIR; 1.		
DR	PRINTS; PRO0019; LEUICHRPT.		
DR	SMART; SMO0082; LRCT; 1.		
DR	SMART; SMO0365; LRR_SD22; 6.		
DR	SMART; SMO0369; LRR_TYP; 13.		
DR	SMART; SMO0255; TIR; 1.		
DR	PROSITE; PS0104; TIR; 1.		
KW	Receptor.		
SQ	SEQUENCE 841 AA; 95954 MW; AD6D06ACEF44CG91 CRC64;		
Alignment Scores:			
Fred. NO.:	1.le-179	Length:	841.
Score:	2571.00	Matches:	519
Percent Similarity:	71.91%	Conservative:	103
Best local Similarity:	60.00%	Mismatches:	189
Query Match:	2.96%	Indels:	54
Dd:	2	Gaps:	8
US-09-396-985B-48 (1-50000) x Q6WCDA (1-841)			
Oy	37400	TGCAAAAAATGATTAATTATCTTAAGACTACATCATCACTGCTTATGTATACCCA	37459
Dd	26	TTPasprProCySvalGlnValAlProAsnIlleSerTyrlh-----	39
Oy	37460	GTATVGAATCTTGAATGATTTTTCTTAATGATTTCTGCTGCATCACTAGTGATGATT	37519
Dd	40	CysmetGluleuAenleuTyrlYlsIleProAspAmIlePro-----	53
Oy	37520	ATCATCACTGACGAATGTGAAAATGACAATACTGCAAGATTCCTCTCTGTCACACC	37579
Dd	54	-----IlleSerThrLySMetLeuAspLeuSerPheAsnTryleuArgHis---	68

QY	37380	ATCATACCCGTTTGGCTCGTACAGATTTTCTCTTACATAACATGATATCATATCT	37639
Ds	69	-----LeuGlySerHisAsnProSer-----	75
QY	37640	GTTTGTATCATGATATGGTATGGAGCATGTATGTCATTAAAGAGGTTTTTTTTTCAGCAA	37699
Ds	76	-----SerHisProGlu79	
QY	37700	AAATACATTAATGGTATCTCTTTTGCCCATAGGTGTGAATTTGAAACAAATTGAACAAG	37759
Ds	80	LeuGlnValLeuAspLeuSer-----ArgCysGluIleIysIleIleGlnAspAsp	96
QY	37760	GCAATGATGCTTATACACCACTCTTGAACCTTATATCTACACAGAAACCCCTATCCAGAT	37819
Ds	97	ThrPheGlnIleuLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSer	116
QY	37820	TTTTCCCAAGAAATTTCTCTGACCTTACAAAGTTTGAACAATCTGGTGGCTGTGGAGACA	37879
Ds	117	LeuAlaTrpGlyAlaPheSerGlyLeuSerSerIleGlnIleValAlaValGluThr	136
QY	37880	AAATGGCCCTCTGTAGAAACCTTCCCTATTTGACACAGCTTATTAACCTTAAAGAACTCAAT	37939
Ds	137	AsnLeuValSerLeuAsnAspPheProIleGlnHisLeuIleAsnLeuIleGluLeuAsn	156
QY	37940	GTGGCTACCAATTTTATACATTTCTGTAAAGTTACCTGCATATTTTCCATCTGACGAC	37999
Ds	157	ValAlaHisAsnPheIleHisSerPheIleuPro****PheSerAsnLeuProAsn	176
QY	38000	CTATGATACATGGATCTTTCTTATCATATTTCAATTTCAACATTAACGTACAGCATTTACG	38059
Ds	177	LeuGlnHisLeuAspLeuSerAsnAsnIleGlnAsnIleTyrlGluAspValIys	196
QY	38060	TTTTCTACGTGAAATCCACAGATCATCTCTCTTATAGACATCTTTGAACCCATATGAC	38119
Ds	197	ValLeuHisIleGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAsp	216
QY	38120	TTCAATTCAGACCAACGCTTTTACAGGAATTAAGCTTCATGAATCTGTAAGAGGTAT	38179
Ds	217	PheIleGluProGlyThrPheIleuGluIleIleIleValLeuThrLeuArgSerAsn	236
QY	38180	TTTAAATGCTCAATATATATGAATAATTTGCCCTTCAAAACCTGGCTGTATACGTCAT	38239
Ds	237	PheAsnSerSerHisValMetCysTrpCysIleGlnGlyLeuAlaGlyLeuIleuSerThrAsn	256
QY	38240	CGGTGATCTTTGGGAGAAATTTAAAGATGAAGAAATCTGGAATTTTGAACCTCTATC	38299
Ds	257	ArgLeuValLeuGlyIleuPheIleuAsnGluAsnGlyIleuGlnArgPheAspArgSerPhe	276
QY	38300	ATGAAAGACTATGTGATGACCATTTGATGAGTTGAGTTGAGTTAACAATATACAATGATTT	38359
Ds	277	LeuGlnGlyLeuCysAsnLeuThrIleGlnGlnPheArgIleAlaIleTyLeuAspPhe	296
QY	38360	TCA---GATGATATTTGTAAGTTCCATTTGCTTGGGCAATGTTTTCGCAATGCTCTGGCA	38416
Ds	297	SerGlyAspAspHisAspLeuPheAsnCysLeuAlaAsnValSerValIleSerLeuLeu	316
QY	38417	GGGTATCTATAAANAATCTAGCAAGATGTTCTGTAACATTTCAAAATGGCAATCCCTATCA	38476
Ds	317	SerIleSerIleuIleSerIleuGlnAlaLeuLeuIleuAspPheArgTrpIleHisLeuGlu	336
QY	38477	ATCATTAAGATGTCACTTAAAGCATTTCCACTTCGATCTACACCTTTCTTAAAGTTTG	38536
Ds	337	IleIleAsnCysAspPheAspIleuPheProAlaLeuIleuSerSerIleuIleuIleAspPhe	356
QY	38537	ACTTTACTATGAACAAAGGCTCTACAGTTTAAAAAAGTGCCCTACCAAGTTCTCAGC	38596
Ds	357	ValPheThrAspAsnIleuAspIleSerThrPheTrpGlnPheGlnLeuProSerLeuGln	376
QY	38597	TATCTGATCTTATAGTGAATGCAATGCACTTATAGGTTGGTGTCTTATATCGATTTG	38656
Ds	377	TyLeuAspLeuIleuArgAsnHisLeuSerSerPheIleuGlyCysCysSerHisThrAspPhe	396

```

QY 38657 GGAACAAAGCCTGAGACCTTACAGCTTCAATGGTGCCTATGAGGCC 38716
D 397 G|YThrThrAsnLeuYshISLeuAspSerPheAsnAspValIleThrLeuGlySer 416
QY 38717 AATTGACATGGCTAGAGAGCTGACAGACCTGAGATTTTTCAGACCTTATTAAGG 38776
D 417 AsnPheMetGlyLeuGlnGlnLeuGlnIshIleuAspPheGlnIshSerThrLeuGln 436
QY 38777 GTCCAGAAATCTGAGGCTTATTCCTGAAAAGCTACTTTTACCTTGACATCTTAT 38836
D 437 ILeAsnAlaPheSerAlaPheLeuSerLeuArgAsnLeuArgIYLeuAspIleSerTyr 456
QY 38837 ACTTACACCAAAATGATCTTGATGATATTTCTTGCTGACAGCTTCAACACATTA 38896
D 457 ThrAsnIleArgIleValPheIshGlyIlePheThrGlyLeuValSerLeuGlnThrLeu 476
QY 38897 AAAATGGCTGGCAATTTCTTCAAAAGACACACCTTTCAAAATGCTTTGCAACACACA 38956
D 477 LyMetAlaGlyAsnSerPheGlnAsnAsnLeuProAspIlePheThrGlyLeuThr 496
QY 38957 AACTTGACATTCCTGAGATCTTCAAAATGCAATTTGCAAAATATCTGGGGGTATTT 39016
D 497 AsnLeuThrValLeuAspLeuSerLeuGlySerGlnLeuGlnValAlaGlnThrAlaPhe 516
QY 39017 GACACCTCCATAGACCTTCAATTAATATGATGACACACATCTTATTTTGGAT 39076
D 517 HiserLeuSerSerLeuGlnValLeuAsnMetSerIshAsnIYLeuLeuSerLeuAsp 536
QY 39077 TCATCCCATTTAAACAGCTGTATTCCTCAGACCTTTGATGACAGTTTCATGCAATA 39136
D 537 ThrPheLeuTyrGlnProLeuHiserLeuArgIleLeuAspGlySerPheAsnArgIle 556
QY 39137 GAGACATCTAA---GGAATCTGCAACATTTTCCAAAGATCTGACCTTCAATCTT 39193
D 557 MetAlaSerIYshGlnGlnGlnLeuGlnAsnLeuProAspSerLeuThrTyrLeuAsnLeu 576
QY 39194 ACTTACATTTCTGTGCTTGTATATGTCACATGAAATCTGACAGTGGTCAAGGAA 39253
D 577 ThrGlnAsnAlaPheAlaCysValCysGlnIshGlnSerPheLeuGlnThrValIYAsp 596
QY 39254 CAGAGACGTTCTGTGTAATGTTGAACAAATGACATGTGCAACACCTGTAGAGATGAT 39313
D 597 GlnArgGlnLeuLeuValGlyAlaGlnGlnMetCysAlaGlnProLeuAspMetGln 616
QY 39314 ACCCTTCAAGTGGATTTTAAATATCTGACCTTATATGTCACAGACATTCATCAGT 39373
D 617 AspMetProValLeuSerPheArgAsnAlaThrCysGlnLeuSerIYshIleIshSer 636
QY 39374 GTGTCAAGTGTCAGTGTGATTTGGTATCCATGTAGACATTTCTGATATACACTTCTAT 39433
D 637 ValSerValValThrValLeuLeuValSerValValGlyValLeuValIYLeuPheTyr 656
QY 39434 TTTGACCTGATCTTATTTCTGCTGTAAAGTACAGACAGAGAGAAAGCATCTATGAT 39493
D 657 PheHisLeuMetLeuLeuAlaGlyCysValYshIYshTyrGlyArgGlyGlnSerIleTyrAsp 676
QY 39494 GCATTTGATCTCTGAGTCAAGATGAGACCTGGGTGAGAAATGAGCTGTAAAGAT 39553
D 677 AlaPheValIleTyrSerSerGlnAspGlnAspIYshPyrValAlaGlnGlnLeuValIYAsn 696
QY 39554 TTAGAAGAGAGAGTCCCGCTTTCACCTCTGCTTCACTACAGAGACTTTATTCCTGCT 39613
D 697 LeuGlnGlnGlyValProProPheGlnLeuYshIshIYshTyrArgAspPheIleProGly 716
QY 39614 GTAGCCATTTGCTCCACATCATCCAGAGAGCTTTCACAGAGAGCCGAGAGCTTATGCTG 39673
D 717 ValAlaIleAlaAlaAsnIleIleGlnGlnGlyPheHisIYshSerArgIYValIleVal 736
QY 39674 GTAGGTGTAGACCTTATTCAGAGCCGCTGTATCTTGAATATAGATTCCTCAA 39733
D 737 ValValSerGlnHisPheIleGlnSerArgIYshTyrCysIlePheGlnIYshIleAlaGln 756
QY 39734 ACATGGCAGTTTCTGAGAGCCGCTGTGACATTCATCTTCAATTGCTTGAAGAGTTGAG 39793

```

```

D 757 ThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIYshLeuGln 776
QY 39794 AAGTCCCTGTGAGGACAGAGCTGGAATGTATGCTCTTTCAGAGAAACACTTACCTG 39853
D 777 LysSerLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeu 796
QY 39854 GAATGGAGAGCAATCTCTGGGAGAGACATCTTCTGAGAGACTTAAATGACCTTA 39913
D 797 GlnTrpGlnAspSerValLeuGlnIYshIshValPheThrArgIYshLeuArgIYshAlaLeu 816
QY 39914 TTGATGAAAAGCCTCGAATCTTGAACAAACAGACAGAGAGAA-----CAGAA 39964
D 817 LeuAlaGlyIYshProGlnSerProGlnGlyThrAlaAspAlaGlnThrAsnProGlnGln 836
QY 39965 ACAGCACTTGAGCC 39979
D 837 AlaThrThrSerThr 841

RESULT 14
TLR4_HORSE STANDARD; PRT; 843 AA.
ID TLR4_HORSE
AC Q9WTM3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Vandeplass M.L., McNeill B.W., Barton M.H., Moore J.N.;
RT "Cloning and sequencing of equine Toll-like receptor 4 (TLR4).";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via their respective TIR domains (by similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via their respective TIR domains (by similarity).
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 1 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements or send an email to license@ebi.ac.uk).

```

Accession	Protein	Length	Score	Similarity	Local Similarity	Match	Conservative	Mismatch	Indel	Gap
DR	CO: 0042088; P-T-helper 1 type immune response; ISS.									
DR	InterPro; IPR001611; LRR.									
DR	InterPro; IPR000483; LRR_Cterm.									
DR	InterPro; IPR003591; LRR_Typ.									
DR	InterPro; IPR000157; TIR.									
DR	Pfam; PF00560; LRR; 13.									
DR	Pfam; PF01582; TIR; 1.									
DR	PRINTS; PRO0019; LEORICHRPT.									
DR	SMART; SM00369; LRR_Typ; 1.									
DR	SMART; SM00082; LRCT; 1.									
DR	SMART; SM00255; TIR; 1.									
DR	PROSITE; PS50104; TIR; 1.									
KM	Glycoprotein; Immune response; Inflammatory response;									
KW	Leucine-rich repeat; Receptor; Signal; Transmembrane.									
FT	SIGNAL	1	23							
FT	CHAIN	24	843							
FT	DOMAIN	24	633							
FT	TRANSMEM	634	654							
FT	DOMAIN	655	843							
FT	REPEAT	53	76							
FT	REPEAT	77	100							
FT	REPEAT	101	124							
FT	REPEAT	128	149							
FT	REPEAT	150	173							
FT	REPEAT	174	197							
FT	REPEAT	203	225							
FT	REPEAT	277	300							
FT	REPEAT	311	334							
FT	REPEAT	351	373							
FT	REPEAT	374	399							
FT	REPEAT	401	422							
FT	REPEAT	423	446							
FT	REPEAT	447	470							
FT	REPEAT	471	495							
FT	REPEAT	496	519							
FT	REPEAT	521	544							
FT	REPEAT	545	566							
FT	REPEAT	569	593							
FT	DOMAIN	674	820							
FT	CARBOHYD	35	35							
FT	CARBOHYD	189	189							
FT	CARBOHYD	205	205							
FT	CARBOHYD	282	282							
FT	CARBOHYD	295	295							
FT	CARBOHYD	498	498							
FT	CARBOHYD	527	527							
FT	CARBOHYD	576	576							
FT	CARBOHYD	626	626							
FT	SEQUENCE	843 AA;	96495 MW;	B597689AD6F7A69	CR64;					
Alignment Scores:										
Pred. No.:	2,17e-179	Length:	843							
Score:	2567.00	Matches:	519							
Percent Similarity:	72.32%	Conservative:	108							
Best Local Similarity:	59.86%	Mismatch:	182							
Query Match:	2.35%	Indels:	58							
DB:	1	Gaps:	9							
US-09-396-985B-48 (1-50000) x TLR4_HORSE (1-843)										
QY	37400 TGGAAAAATGCAATTAATATCTAAGACTACATATCACTGCTTTATGTAACCCA	37459								
Db	26 TTPspProcysValGlnValValProAsnThrThyGln-----	39								

[illegible]

```

Db      397 LeuylsThrThrArgLeuLyShiLeuAspLeuSerPheAsnAspValIleSerMetSer 416
Qy      38714 GCSAAATTCATGGGTCTAGAGAGCTGACGACCTGGATTTTTCAGCTCTACTTAA 38773
Db      417 SerAsnMetGlyLeuGlnGlnMetGlnIshLeuAspPheGlnIshSerThrLeuLys 436
Qy      38774 AGGGTCAAGAAATTCGAGCGCTTATCCCTTGAAAAAGTACTTTTACCTTGACATCTCT 38833
Db      437 GlnIshSerAspPheProValPheLeuSerLeuLysAsnLeuArgTyrLeuAspIleSer 456
Qy      38834 TATPCTAACCAAAATTCAGTCTGATGATATTTCTGGCTTGACCAGTCTCAACA 38893
Db      457 TyrThrAsnThrArgValPheHisGlyTyrPheAspArgLeuValIleSerLeuGlnVal 476
Qy      38894 TTTAAATGGCTGGCAATTCCTTCAAGAACAACCCCTTGCAATGCTTGGCAACA 38953
Db      477 LeuLysPheCysAlaGlyAsnSerPheLysAspAsnPheLeuProAsnIlePheAspGluMet 496
Qy      38954 ACAAACTGACATTCCTGATCTTTCTAAATGTCATTCGAAACAATATCTTGGGGGTA 39013
Db      497 ThrAsnMetThrThrLeuAspLeuSerLysCysAsnLeuGlnValIshSerGlnLysAla 516
Qy      39014 TTGACACCTTCATAGACTTCAATTAATAATGATGCAACAATCTATGTTTGG 39073
Db      517 PheCysLeuLeuProArgLeuArgValLeuAsnMetSerHisAsnAsnLeuLeuPheLeu 536
Qy      39074 GATTCATCCCATTTAATACAGCTGATTCCTCGACGACCTGTTGATGCAATTCG 39133
Db      537 AspMetLeuProTyrLysProLeuHisSerLeuGlnIleLeuAspCysSerPheAsnArg 556
Qy      39134 ATAGACATCTAA---GGAAATCTGCACATTTTCCAAAGATCTAGCCCTTCTCAAT 39190
Db      557 IleValIshPheLysTrpGlnGlnLeuGlnHisPheProSerSerIshLeuAsn 576
Qy      39191 CTTACTAACAAATTCCTGCTTGTATATGTAATCAACATCAAAATTCCTGCACTGGCTCAG 39250
Db      577 LeuThrGlnAsnAspPheHisCysValCysGlnTyrGlnSerPheLeuGlnTrpValLys 596
Qy      39251 GAAACAGACAGCTCTTGTAATGTTGAACAATGATGATGCAACCTGAGAGATG 39310
Db      597 AspGlnAspGlnLeuLeuValGlnValGlnHisValCysValIshLeuValIshLeuGlnMet 616
Qy      39311 AATACCTCTAGTGGTGGATTTTAATATATCTACTGTTATATGTCACAGACATCATC 39370
Db      617 ArgGlyMetProValLeuGlnPheAsnAsnIshThrCysGlnIshSerLysThrIleVal 636
Qy      39371 AGTGTGACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 39430
Db      637 GlyLysSerValPheSerIleLeuMetValSerValIshLeuValIshLeuValIshPhe 656
Qy      39431 TATTTTACCTGATTAATGCTGGCTGTAATAAGTACACAGAGAGAGAGATCAT 39490
Db      657 TyrPheHisLeuMetLeuLeuHisGlyCysLysLysTyrGlnArgGlnSerIshLys 676
Qy      39491 GATGCAATTCGATCTACTGAGTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39550
Db      677 AspAlaPheValIshLysSerSerClnAspLeuAspTrpValIshGlnLeuValLys 696
Qy      39551 AATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39610
Db      697 AsnLeuGlnGlnGlnValProProPheGlnLeuCysLeuHisTyrArgAspPheIshPro 716
Qy      39611 GGTGTAGCATTCGTCGCAATCATCATCATCATCATCATCATCATCATCATCATCATCAT 39670
Db      717 GlyValAlaIshLeuAlaAsnIshLeuGlnGlnGlnPheHisLysSerArgLysValIsh 736
Qy      39671 GTGTAGTGTCTGACATTTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39730
Db      737 ValValValSerGlnHisPheHisLeuGlnSerArgTyrCysIshPheGlnTyrGlnIshAla 756
Qy      39731 CAACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39790
Db      757 GlnThrTrpGlnPheLeuSerSerArgLysGlnIshLysIshPheIshValIshLeuHisLysLeu 776

```

```

Qy      39791 GAGAGTCCCTGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39850
Db      777 GlnLysSerLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuAsnArgAsnTrpTyr 796
Qy      39851 CTGGAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39910
Db      797 LeuGlnTrpGlnAspPheValLeuGlnArgHisIshPheThrPArgArgLeuArgLysAla 816
Qy      39911 CTATGGATGGAGAAAGCCTCGAATCCTGAGCAAGAGCA-----GAG 39952
Db      817 LeuLeuAspLysProTrpSerProAlaGlyThrAlaAspAlaIshGlnSerArgGln 836
Qy      39953 GAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 39973
Db      837 HisAspAlaGlnThrSerThr 843

RESULT 15
ID      TLR4_FELCA STANDARD; PRT; 833 AA.
AC      P58727;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Toll-like receptor 4 precursor.
GN      Name=TLR4;
OS      Felis silvestris catus (Cat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX      NCBI_TaxID=9685;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Yoshiooka N., Kano R.;
RT      "Felis catus Toll like receptor 4";
RL      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Cooperates with Ly96 and CD14 to mediate the innate
CC      immune response to bacterial lipopolysaccharide (LPS). Acts via
CC      MYD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC      secretion and the inflammatory response (By similarity).
CC      -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC      multi-protein complex containing at least CD14, Ly96 and TLR4.
CC      Binds Ly96 via the extracellular domain. Binds MYD88 and TIRAP via
CC      their respective TIR domains (By similarity).
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC      -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC      -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC      -1- SIMILARITY: Contains 1 TIR domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AB060687; BAB43947.1; -.
DR      HSPB; O60603; IFTX.
DR      GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
DR      GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR      GO; GO:0004888; F:transmembrane receptor activity; ISS.
DR      GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR      GO; GO:0016046; P:detection of fungi; ISS.
DR      GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR      GO; GO:0042116; P:macrophage activation; ISS.
DR      GO; GO:0045576; P:macrophage activation; ISS.
DR      GO; GO:0045671; P:negative regulation of osteoclast different. . .; ISS.
DR      GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . .; ISS.
DR      GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . .; ISS.
DR      GO; GO:0045368; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR      GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . .; ISS.
DR      GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR      InterPro; IPR001611; LRR.

```

DR InterPro; IPR000483; LRR Cterm.
 DR InterPro; IPR003591; LRR_Typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR; 12.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_Typ; 1.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS0104; TIR; 1.
 DR Glycoprotein; Immune response; Inflammatory response;
 KW Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT DOMAIN 24 632 Toll-like receptor 4.
 FT TRANSMEM 633 653 Extracellular (Potential).
 FT DOMAIN 654 833 Cytoplasmic (Potential).
 FT REPEAT 53 76 LRR 1.
 FT REPEAT 77 100 LRR 2.
 FT REPEAT 101 124 LRR 3.
 FT REPEAT 128 149 LRR 4.
 FT REPEAT 150 173 LRR 5.
 FT REPEAT 174 197 LRR 6.
 FT REPEAT 203 225 LRR 7.
 FT REPEAT 228 252 LRR 8.
 FT REPEAT 310 334 LRR 9.
 FT REPEAT 350 372 LRR 10.
 FT REPEAT 373 398 LRR 11.
 FT REPEAT 399 421 LRR 12.
 FT REPEAT 422 445 LRR 13.
 FT REPEAT 447 469 LRR 14.
 FT REPEAT 470 494 LRR 15.
 FT REPEAT 495 518 LRR 16.
 FT REPEAT 520 542 LRR 17.
 FT REPEAT 544 566 LRR 18.
 FT REPEAT 568 592 LRR 19.
 FT DOMAIN 673 819 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 238 238 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 570 570 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 625 625 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 833 AA; 95592 MW; 383A84F2B8BA55EA CRC64;

Alignment Scores:
 Pred. No.: 4.08e-176 Length: 833
 Score: 2522.50 Matches: 490
 Percent Similarity: 78.76% Conservative: 107
 Best Local Similarity: 64.64% Mismatches: 156
 Query Match: 2.90% Indels: 5
 DB: 1 Gaps: 3

US-09-396-985b-48 (1-50000) x TIR4_FELICA (1-833)

QY 37691 TTTCAGCAAAATCATATATGATATCTTTTCCCATAGGTGGAATTAACAAT 37750
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 77 PheProGluLeuGlnValLeuAspLeuSer-----ArgCysGlnIleGlnIleLe 93
 QY 37751 GAAAGCAAGGATGATGCTTACACCACTTCAAACTTGATATGACGAAACCT 37810
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 94 GluAspAspAlaTyrGlnGlyLeuAsnHisLeuSerIleLeuIleThrGlyAsnPro 113
 QY 37811 ATCCAGATTTTCCCGCAGAGTTCTCTGACATTAACAATTATAGAGAATCTGTGCT 37870
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 114 IleGlnIleArgLeuPheProGlyAlaPheSerIleLeuSerIleGlnIleValAla 133
 QY 37871 GTGAGACAAAAATTTGGCTCTCTAGAAAAGCTTCCCTATTGACAGCTTAACTTAAG 37930

Db 134 ValGluThrAsnIleLeuSerLeuGluAspPheProIleGlyHisLeuIleThrLeuLys 153
 QY 37931 AAATCAATGGGCTGACAAATTTATATACATTCCTGTAGTACCTGCAATTTTCCAT 37990
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 154 GluLeuAsnValAlaHisAsnLeuIleHisSerPheLysLeuProGluTyrPheSerAsn 173
 QY 37991 CTGACGAAACCAAGTACATGATGCTTTTATATAGTATATTAACATGATACGTCAAC 38050
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 174 MetSerAsnLeuGluTyrLeuAspLeuSerAsnLysIleGlnAsnIleTyrHisLys 193
 QY 38051 GACTTACAGTTTCTACGTGAAATATCAAGTCAATCTCTTTAGACATGCTTTGAAAC 38110
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 194 AspLeuGlnValLeuHisGlnIlePheProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsn 213
 QY 38111 CCATTTGATCTTCAAGACCAAGCTTTGAGGAAATTAAGCTTCATGAATGATCTGA 38170
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 214 ProLeuAspPheIleGlnProGlyAlaPheLysGlnValIleLysLeuArgGluLeuThrLeu 233
 QY 38171 AGAGTAATTTTATAGCTCAAAATATATAGAAACTTGCCCTGAAACCTGGCTGTTTA 38230
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 234 ArgSerAsnPheAsnSerThrAspValMetLysAlaSerIleGlnGlyLeuAlaGlyLeu 253
 QY 38231 CACCTCCATCGGTGATCTTGGAGAAATTTAAGATGAAGAAATCTGAATTTTGA 38290
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 254 GlnIleHisGlnLeuValLeuGlyGluPheLysAsnGlnIleArgAsnLeuGlyArgPheAsp 273
 QY 38291 CCCTCTATCATGAGGACTATGTGATGATGACCATTTGATGAGTTAAGCTTATACA 38350
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 274 LysSerIleLeuGlnGlyLeuCysAsnLeuIleIleGlnLysPheArgIleAlaTyrPhe 293
 QY 38351 AATGATTTTTCAGATGATATGTT--AAGTCCATGCTTGGGAATGTTTCGAATG 38407
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 294 AspLysPheSerGluAspAlaIleAspSerPheAsnLysLeuAlaAsnValSerThrIle 313
 QY 38407 TCTTCGACAGGTGATATATATATATATATATAGATGCTCTTAACATTAATGGCAA 38467
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 314 SerLeuValHisLeuIleTyrPheLysGlyLeuLysGlnLeuProLysAsnLeuGlyTyrGln 333
 QY 38467 TCTTATCAATCATTAAGTCAACTTAAGCACTTCAAGCTTCAAGCTTCAAGCTTCT 38527
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 334 ArgLeuIleValValLeuValAsnCysGluPheGlnIlePheProThrTyrLysLeuAspProLeu 353
 QY 38527 AAAAGTTGACTTAACTATGACCAAGAGGCTATGCTTTTAAAGAGGCGCTTACA 38587
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 354 LysGluLeuValPheSerAlaAsnGluValArgAsnAlaPheThrGlnValLysLeuGlu 373
 QY 38587 AGTCTCAGCTATGATCTTATGATGAAATGCACTGAGCTTATGCTGCTGTTCTTAT 38647
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 374 SerLeuGluPheLeuAspLeuSerArgAsnAspPheSerLeuLysSerCysSerGlu 393
 QY 38647 TCTGATTTGGAAACAAACAGCTGACACTTACAGCTTCAAGCTTCAAGCTTCAAGCT 38707
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 394 ArgAspLeuIleThrThrArgLeuLysValLeuAspLeuSerPheAsnAlaIleThr 413
 QY 38708 ATGAGTCCCAATTAAGGGCTGTAAGAGCTGACAGCTTATTTGAGCTTCACT 38767
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 414 IleSerSerAsnPheLeuGluLeuGlnIleGlnIleTyrLeuAspPheGlnHisSerSer 433
 QY 38768 TTAAGAGGTCAAGAAATCTGACGCTTATCCCTGAAAGCACTTATTAAGCTTGAAC 38827
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 434 LeuLysGlnValSerAspPheSerValPheLeuProLeuLysAsnLeuAlaGlyTyrLeuAsp 453
 QY 38828 ATCTCTTATATCAACCAAAATTAAGCTTGAATGATATTTCTGGCTTGAACAGCTTC 38887
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 454 IleSerTyrThrHisThrGlnValAlaPheHisGlyLysPheAsnGlnIleLeuIleSerLeu 473
 QY 38888 AACACATTAATAATGGCTGCAATTTCTTCAAGAGCAACACCTTTCAATGCTTTGCA 38947
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 474 GlnIleLeuLysMetAlaGlyAsnSerPheGlnAspAsnLeuProAsnIlePheMet 493
 QY 38948 AACACAAAAATTTGACATTCCTGATCTTTCAATATGCAATTTGCAAAATATCTTGG 39007
 ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 Db 39007

Db 494 GlutenthreonineleucineasparagineleuvalineSerGln 513
QY 39008 GGGGTAATTGACACCCCTCCATAGACTTCAATTATAATGATGACACACAATCTATTG 39067
Db 514 ValAlaPheAsnSerLeuProlyleuGlnleuAsnMetSerHisAsnHisleuLeu 533
QY 39068 TTTTGGATTATCCCATTTATTAACGAGCTGATTCCTCAGACACTCTTGATTGCACTTTC 39127
Db 534 SerleuAspThrleuProtyrGluProleuHisSerleuGlnThrleuAspCysSerPhe 553
QY 39128 AATGCATAGAGACATCTAA--GGAATCTGCACATTTTCCAAAGACTTAGCCTTC 39184
Db 554 AsnArgIleValAlaSerlyeGluGlnleuArgHisPheProSerAsnleuSerSer 573
QY 39185 TTCAATCTTACTAACAATTCCTGTTGCTTGTATATGACATCAAAATTCCTGCACTGG 39244
Db 574 LeuAsnleuThrArgAsnAspPheAlaCysvalCysGluHisGlnSerPheleuGlnTrp 593
QY 39245 GTCAGGAACAGAGACAGTTCCTGATGATGTTGAACAAATGATGATGCAACACTGTA 39304
Db 594 ValIysAspGlnArgGlnleuLeuValGluValGluGlnMetValCysAlaIysProleu 613
QY 39305 GAGATGAATACCTCTTAGTGTGATTTAATAATCTTACCTGTTATATGATACAGACA 39364
Db 614 AspmetGlnIlyMetProMetleuAsnPhaArgAsnAlaThrCysGlnValArgIysThr 633
QY 39365 ATCATCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39424
Db 634 IleIleThrGlySerValPheThrValleuLeuValPheleuValValleuValIlyr 653
QY 39425 CACTTCTATTTTCACTGATCTTAATGCTGCTGTAATAAGTACAGAGAGAGAAAAGC 39484
Db 654 LysPheTyrPheHisleuMetleuLeuAlaGlyCysIlySerIlySerArgGlyGlnSer 673
QY 39485 ATCTATGATGATTTGTGATGATCTGATGATGATGATGATGATGATGATGATGATGAT 39544
Db 674 ThrTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTrpValArgAsnGlnleu 693
QY 39545 GTAAAGAAATTGAGAAAGAGAGTGGCCGCTTTCACCTTGCTGCTTACACTACAGAGACTT 39604
Db 694 ValIysAsnleuGluGluValProProPheGlnleuCysleuHisTyrArgAspPhe 713
QY 39605 ATTCCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 39664
Db 714 IleProGlyValAlaIleAlaIleAsnIleIleGlnGluGlyPheHisIysSerArgIys 733
QY 39665 GTTATGTGTAGTGTCTAGACATTTATTCAGAGCCGTTGCTGATCTTTGAATATGAG 39724
Db 734 ValIleValValIleSerGlnHisPheIleGlnSerArgTrpCysIlePheGluTyrGly 753
QY 39725 ATTGCTCAACATGCGATTTTCTGAGCAGCGCTGCGATCATCTTCAATGCTGCTTGAAG 39784
Db 754 IleAlaGlnTrpGlnPheleuSerSerArgAlaGlyIleIlePheIleValleuGln 773
QY 39785 AAGGTTGAGAGTCCCTGCTGAGCAGCAGGATGATGATGATGATGATGATGATGATGAT 39844
Db 774 LysleuGluIlySerleuLeuArgGlnIleValGluIleuTyrArgleuLeuAsnArgAsn 793
QY 39845 AACTTACTGGAATGAGAGACATCTCTGAGAGGACATCTTCTGAGAAAGACTTAA 39904
Db 794 ThrTyrleuGluTrpGluAspSerValleuGlyArgHisIlePheTrpArgArgleuArg 813
QY 39905 AATGCCCTATTGATGAGAAAAGCCTGAACTCTGAGCAAAACAGCAGAGAAAGAA 39958
Db 814 LysAlaLeuLeuAspGlyLysProArgCysProGluGlyMetAlaAspAlaGln 831

Search completed: March 30, 2005, 03:04:45
Job time : 5482 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_n2p model

Run on: March 29, 2005, 09:56:53 ; Search time 145.403 Seconds
(without alignments)
18060.838 Million cell updates/sec

Title: US-09-396-985B-5
Perfect score: 5943
Sequence: 1 tcgagcgccgcccgcggcgag.....aaaaaaaaaaaaaaaa 3395

Scoring table: BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09396985/funat_28032005_155742_21135/app_query.fasta_1.85098
-DB-A=Geneseq_16Dec04 -QMT=faetan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09396985 @CGN_1_1_4007 @funat_28032005_155742_21135 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:
1: geneseqp1980s:
2: geneseqp1990s:
3: geneseqp2000s:
4: geneseqp2001s:
5: geneseqp2002s:
6: geneseqp2003as:
7: geneseqp2003bs:
8: geneseqp2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2860.5	48.1	839	6	ABU04773 Human exp
2	2860.5	48.1	839	6	ABU04774 Human exp
3	2860.5	48.1	839	6	ABU04775 Human exp
4	2860.5	48.1	839	7	ADCT78785 Human PRO
5	2860.5	48.1	839	7	ADCT48826 Human PRO
6	2844	47.9	837	2	AAW86361 Human DNA
7	2844	47.9	837	2	AAE16102 Human DNA
8	2844	47.9	837	6	ABU04776 Human exp
9	2837	47.7	837	5	AAE16116 Human DNA
10	2796.5	47.1	801	8	AD057797 Squirrel

11	2782.5	46.8	795	8	AD057791 Rheus mo
12	2781.5	46.8	795	8	AD057800 Hamadryas
13	2777	46.7	808	8	AD057803 Chimpanze
14	2773	46.7	808	8	AD057782 Chimpanze
15	2761	46.5	808	8	AD057785 Gorilla t
16	2751.5	46.3	801	8	AD057788 Gibbon to
17	2726	45.9	799	2	AAW86352 Human DNA
18	2726	45.9	799	5	AAE16093 Human DNA
19	2726	45.9	799	5	ABH83162 Human Tol
20	2726	45.9	799	6	ABR42963 Human Tol
21	2726	45.9	799	7	ADB39121 Human Tol
22	2726	45.9	799	8	ADP56566 Human Tol
23	2726	45.9	799	8	ADP48597 Human Tol
24	2558.5	43.1	745	8	AD057794 White-fac
25	2528.5	42.5	738	8	ADP29455 Human sec
26	898.5	15.1	208	3	AAW88059 Human Tol
27	883	14.9	179	7	ADC42707 Murine To
28	761.5	12.8	178	8	ADN12270 IL-1R/TLR
29	609	10.2	661	2	AAW28510 Product o
30	609	10.2	661	2	AAW87556 B cell su
31	609	10.2	661	7	ADC38652 Human sec
32	609	10.2	661	7	ADF68098 Human MP5
33	601.5	10.1	650	3	AAW82527 Human RPI
34	595	10.0	661	2	AAW47274 Human B-c
35	575	9.7	1032	5	AAO21588 Murine To
36	575	9.7	1032	7	ADE85953 Mouse Tol
37	575	9.7	1032	7	ABW01559 Murine To
38	559	9.4	1050	5	AAO21579 Murine To
39	559	9.4	1050	7	ADE85947 Mouse Tol
40	559	9.4	1050	7	ABW01556 Murine To
41	548	9.2	1059	5	AAO21587 Murine To
42	548	9.2	1059	7	ADE85951 Human Tol
43	548	9.2	1059	8	ADQ88188 Human 122
44	541.5	9.1	859	6	AAE33341 Mouse tol
45	541	9.1	1041	2	AAW41768 Human PRO

ALIGNMENTS

RESULT 1	ABU04773 standard; protein; 839 AA.
ID	ABU04773
AC	ABU04773;
XX	
XX	29-JAN-2003 (first entry)
XX	
DE	Human expressed protein tag (EPT) #1439.
XX	
KW	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW	protease; protease inhibitor; transporter; cytoskeletal protein;
KW	receptor; transcription factor; cancer; MHC;
KW	major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX	
OS	Homo sapiens.
XX	
FN	W0200278524-A2.
XX	
PD	10-OCT-2002.
XX	
PF	28-MAR-2002; 2002MO-US009671.
XX	
XX	28-MAR-2001; 2001US-0279495P.
PR	21-MAY-2001; 2001US-0292544P.
PR	08-AUG-2001; 2001US-0310801P.
PR	01-OCT-2001; 2001US-0326370P.
PR	04-DEC-2001; 2001US-0336780P.
PR	20-FEB-2002; 2002US-0358985P.
XX	
XX	(ZYCO-) ZYCOs INC.
PA	
XX	Chicz RM, Tomlinson AJ, Urban RG;
PI	

XX WP1; 2003-040607/03.

DR New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.

XX Example 2; SEQ ID NO 1439; 134pp; English.

PS The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX
XX
SQ Sequence 839 AA;

Alignment Scores:
Pred. No.: 2,67e-280 Length: 839
Score: 2860.50 Matches: 559
Percent Similarity: 80.24% Conservative: 115
Best Local Similarity: 66.55% Mismatches: 159
Query Match: 48.13% Indels: 7
DB: Gaps: 5

US-09-396-985B-5 (1-3395) x ABU04773 (1-839)

QY 260 ATGATGCTCTTGGCATCTGGCTGGAGCTGTGATCATGCGATG--TTCCTTTCTGTC 316
DB 1 MetMetSerAlaSerArgLeuAlaGlyThrIleuIleProAlaMetAlaPheLeuSerCys 20
QY 317 CTGAGACGAGAGAGTGAATCCCTGCGATAGAGGACTCTTATATATACCTACCATGC 376
DB 21 ValArgProGluSerTyrPgluProCysValGluValAlaProAlaIleThrTyrGlnCys 40
QY 377 ATGATCATGAGATCTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGACCTAGAT 436
DB 41 MetGluLeuAsnPheTyrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 60
QY 437 CTGAGCTTCAACCCCTGAGAGATCTTAAAGAGCTATAGCTTCACCAATTTCTCAACAT 496
DB 61 LeuSerPheAsnProLeuAlaArgHileuGlySerTyrSerPhePheSerPheProGluLeu 80
QY 497 CAGTGGCTGAGTTTATCCAGGTGGAATTTGAGACAAATTTGAAAGACAGGATGGCATGGC 556
DB 81 GluValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 100
QY 557 TTAACACGACTCTCAACCTTGTAAGTACAGAGAACTTATCAAGAGTTTCCACAGAG 616
DB 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
QY 617 AGTTTTCGTGAGCTTAAATTTAGAGATCTGTGGCTGTGAGAGCAAAATGACCTCT 676
DB 121 AlaPheSerGlyLeuSerSerLeuGlnIlyLeuValAlaValGluThrAsnLeuAlaSer 140
QY 677 CTAGAGGGTTTCGATTTGAGACAGCTTATATCTTAAAGAACTTAAAGTGGCTCATAT 736
DB 141 LeuGluAsnPheProIleGlyHisIleuLysThrLeuLysGluLeuAsnValAlaHisAsn 160
QY 737 CTTATACATTCCTTAAAGTGGCTGATATATTTTCTATATCGACAAACCTTGAACATGTG 796

DB 161 LeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGlnIleLeu 180
QY 797 GATCTTCTTATATACCTATATTCAAACTATTTCTGTCAAAAGACTTACAGTTTCTACGTGA 856
DB 181 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGln 200
QY 857 AATCCCAAGTCAATCTCTTATAGACCTGTCTTAAACCAATGATGATCCATTCAGGCC 916
DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerIleLeuAsnProMetAsnPheIleGlnPro 220
QY 917 CAAGCTTTCAAGAAATTTAGCTCCATGATTAAGTCTTAAAGTAATTTTAATAGCTCA 976
DB 221 GlyAlaPheLysGluIleArgLeuHisIlyLeuThrLeuArgAsnPheAspSerLeu 240
QY 977 AATGACTGAAATATGCTTCAAAACATGACTGTTTACATGCTCCATCGGTGATCTTG 1036
DB 241 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisIArgLeuValLeu 260
QY 1037 GGAGAAATTTAAATGAAGAGATCTGAAAGTTTGAACCGTCTGTGATGAGAGACTA 1096
DB 261 GlyGluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGluGlyLeu 280
QY 1097 TGCATGTGAGCATTTGATGAGTTCAGGTTAAACATATATAATCATTTTTCAGATGATAT 1156
DB 281 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 300
QY 1157 TATATATCTC--AATGCTTGGCAATATTTCTGCATATGCTTTTCACAGGTGATCATTA 1213
DB 301 IleAspLeuPheAsnCysIleLeuThrAsnValSerSerPheSerLeuValSerAlaThrIle 320
QY 1214 AACACATAGACAGATGTTCTTAGCATTTCAATGAGCAATCTTATCATCATTTAGATGT 1273
DB 321 GluArgValLysAspPheSerTyrAsnPheGlyTyrPgluHisIleuGluLeuValAsnCys 340
QY 1274 CATCTTAAGCTTTCCAAAGCTGAGCTTACCTTTTCTTAAAGTGAAGCTTTAATAC 1333
DB 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
QY 1334 AACAGAGAGATATACAGCTTTGGTCAAGTGGCTCTGCCAAGTCTCAGATATCTAGATCTT 1393
DB 361 AsnLysGlyLysAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
QY 1394 AGTAGAATGCTCAAGAGCTTTAGAGGTGCTGTCTTATTCGATTTTGAACAAACAC 1453
DB 381 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
QY 1454 CTGAAGTACTTAAAGCTCAGCTTCAATGTGTGATCTGTATGATGATGCCAATTCATGGGT 1513
DB 401 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1514 CTGAAGAGCTGGAATACCTGAGACTTTCAGACATCCACTTTAAAGGTCACAGAAATTC 1573
DB 421 LeuGlnGluLeuGluHisIleAsnAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 440
QY 1574 TCAGTGTCTTATCTCTTGAAGAACTTCTTACCTTGAACATCTCTTACATTAATCAACAA 1633
DB 441 SerValPheLeuSerLeuAsnLeuIleTyrLeuAspIleSerHisThrHisThrArg 460
QY 1634 ATTGACTTGTGATGATATTTCTTGCTGTGATGATGATCTCAACATTTAAAGTGGCTGC 1693
DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 480
QY 1694 AATTCCTTCAAGACCAACCCCTTCAATGCTCTTTTCAACAAACACACAACTTAACTTC 1753
DB 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuAsnValLeuThrPhe 500
QY 1754 CTGATCTTCTTAAATGCAACCTGGAACAGATATCTAGGGGGATTTGACACACTTAC 1813
DB 501 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 520
QY 1814 AGACTCCAGTTATTAACATGATGATCAACAACTACTGTTTCTGATTCATCCATTAAT 1873

```

Db      521 SerLeuGlnValIleuAsnMetSerHisAsnAsnPheserLeuAspThrPheProTyr 540
Qy      1874 AAACAGCTGTACTCCCTCAGGACTTGAATGCACTTTCATTCGATCAGACATCC-- 1930
Db      541 LysCysLeuAsnSerLeuGlnValIleuAspTyrSerLeuAsnHisIleMetThrSerLys 560
Qy      1931 AAAGAAATACCTGCAACATTTTCCAAAGAGTACCGCTTCCTCAATCTGATTAATATTCT 1990
Db      561 LysGlnGlnIleuGlnHisPheProSerSerLeuHisPheLeuAsnIleThrGlnAsnAsp 580
Qy      1991 GTTGCTGTATATGTAATATCATGAAATTTCTTGCAAGTGGTCAAGAGACCAAGAAATGTC 2050
Db      581 PheAlaCysThrCysGlnHisIleGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu 600
Qy      2051 TTGGTGAATGTGAAACAAATGAATGTGATCACCCTAATAGACATGAAAGCCCTCCCTGGTG 2110
Db      601 LeuValGlnValGlnValGlnValGlnValGlnValGlnValGlnValGlnValGlnVal 620
Qy      2111 TTGGATTTTTCAGAAATTCACCTGTTATATATATCAAGATCATCATCAGTATCGGTGTC 2170
Db      621 LeuSerLeu---AsnIleThrCysGlnMetAsnIleThrIleIleGlyValSerValLeu 639
Qy      2171 AGTGTCTGTGTGAGCACTGTAGACATTTCTGATATACCATTTCTATTTTCACTGATA 2230
Db      640 SerValIleuValIleValSerValIleValIleValIleValIleValIleValIle 659
Qy      2231 CTATTGTGCTGCTGTAAATAATACAGCAAGAGAAACATCTTGTATGATGCTTGTGATC 2290
Db      660 LeuLeuAlaGlyCysIleLysTyrGlyArgGlnValIleTyrAspAlaPheValIle 679
Qy      2291 TACTCGAGCCAGAAATGAGAGCTGGGTGAGAAACAGCTGTAAAGAAATTTGAAAGAGA 2350
Db      680 TyrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValIleValIleValIleVal 699
Qy      2351 GTGCCCGCTTTCAGCTTGTGCTTCATTAACAGGACCTTATCTCTGTGATCCATGCT 2410
Db      700 ValProProPheGlnLeuCysLeuHisIleTyrArgAspPheIleProGlyValAlaIle 719
Qy      2411 GCCAAACATCATCCAGAAAGCTTCCACAGAGCCGGAAGTATTTGGTGGTGTCTAGA 2470
Db      720 AlaAsnIleIleHisGlnGlyPheHisIleLysSerTrpValIleValValIleValIle 739
Qy      2471 CACTTTATCCAGAGCCGCTGTGATCTTGAATATGATGATGCTCAGACATGCGAGTTT 2530
Db      740 HisPheIleGlnSerArgTrpCysIlePheGlnIleValIleGlnIleThrGlnPhe 759
Qy      2531 CTGAGTACCGCTCTGCGATCATCTTCATTTGCTTGAAGAAAGTGGAGAACTCTGCTG 2590
Db      760 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnIleValIleGlnIleThrLeu 779
Qy      2591 AGGACAGAGCTGCAATGTATTCGCTTTTTCAGCAAAACACCTTACCTGAGTGGAGAGAC 2650
Db      780 ArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnTrpTyrLeuGlnTrpGlnAsp 799
Qy      2651 AATCTCTGGGAGAGACATCTTCTGAGAGAGACTCAAAAAGCCCTGTGATGAGAAA 2710
Db      800 SerValLeuGlnValArgHisIlePheTrpArgTrpLeuArgValAlaLeuLeuAspLys 819
Qy      2711 GCCTTGAATCCAGAT-----GAAACATCAAGAGAAAGCAAGAAACAACTTGG 2761
Db      820 SerTrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle 839

```

```

RESULT 2
ABU04774
ID      ABU04774 standard; protein; 839 AA.
XX      AC      ABU04774;
XX      DT      29-JAN-2003 (first entry)
XX      DE      Human expressed protein tag (EPT) #1440.
XX      KW      Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

```

```

KW      protease; protease inhibitor; transporter; cytoskeletal protein;
KW      receptor; transcription factor; cancer; MHC;
KW      major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW      adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
OS      Homo sapiens.
PN      WO200278524-A2.
PD      10-OCT-2002.
PP      28-MAR-2002; 2002WO-US009671.
PR      28-MAR-2001; 2001US-0279495P.
PR      21-MAY-2001; 2001US-0292544P.
PR      08-AUG-2001; 2001US-0310801P.
PR      01-OCT-2001; 2001US-0326370P.
PR      04-DEC-2001; 2001US-0336780P.
PR      20-FEB-2002; 2002US-0358985P.
PA      (ZYCO-) ZYCO INC.
XX      Chicx RM, Tomlinson AJ, Urban RG;
XX      WPI; 2003-040607/03.
PT      New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT      cytoskeletal proteins, receptors or transcription factors), useful for
PT      treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT      leukaemia.
PS      Example 2; SEQ ID NO 1440; 134pp; English.
XX      The invention describes a purified polypeptide, which comprises a
XX      fragment of a kinase, phosphatase, protease, protease inhibitor,
XX      transporter, cytoskeletal protein, receptor or transcription factor. The
XX      polypeptide is useful as an immunogenic composition for eliciting in a
XX      mammal an immunogenic response directed against any of the purified
XX      polypeptide. The purified polypeptide, or the antibody that binds to this
XX      polypeptide, is useful for treating cancer. The polypeptide is also
XX      useful for identifying compounds that binds to a naturally processed
XX      class I or class II MHC-binding polypeptide. The polypeptides and
XX      polynucleotides are particularly useful for treating or preventing
XX      myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX      lymphoma or leukaemia. These are also useful for screening agents for
XX      treating the above mentioned diseases. This sequence represents an
XX      expressed protein tag (EPT) isolated from human tissue for translational
XX      profiling. Note: This sequence does not appear in the printed
XX      specification but was obtained in electronic format directly from WIPO at
XX      ftp.wipo.int/pub/published_pct_sequences
XX      Sequence 839 AA;

```

```

Alignment Scores:
Score: 2.67e-280 Length: 839
Percent Similarity: 2860.50 Matches: 559
Best Local Similarity: 80.24% Conservative: 115
Query Match: 66.55% Mismatches: 159
DB: 48.13% Indels: 7
Gaps: 5
US-09-396-985b-5 (1-3395) x ABU04774 (1-839)

```

```

Qy      260 ATGATGCTCTCTTTCGATCTGCGTGGAGCTCTGATCATGCGATG---TTCTTTCCTGC 316
Db      1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
Qy      317 CTGAGACAGAGAGCTTGAATCCCTGATGAGAGTACTTCTCTAATATATACCTACCAATGC 376
Db      21 ValArgProGlnSerTrpGlnProCysValGlnValValProAsnIleTrpGlnCys 40
Qy      377 ATGATCAGATCTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGAACTAGAT 436

```

Dh 41 MetGluLeuAsnPhenylTyrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 60
Qy 437 CTGAGCTTCAACCCCTGAGAGATCTTAAAGATATAGCTTACCAATTCTCAAACTT 496
Dh 61 LeuSerPheAsnProLeuArgHileuGlySerTyrSerPhePheSerPheProGluLeu 80
Qy 497 CAGGGCGGATTTATCCAGGTGGAATTTGACCAATTGGAAGACAAAGCATGGCATGGC 556
Dh 81 GluValLeuAsnLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 100
Qy 557 TTAACACAGCTCTCAACCTTGGATGACAGAGAAACCTTATCAAGATTTTCCCAAGA 616
Dh 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
Qy 617 AGTTTCTGACCTAACAAATTTAGAGAAATGGTGGCTGGAGACAAAATGACCTCT 676
Dh 121 AlahSerGlyLeuSerSerLeuGlnLysLeuValAlaValGluThrAsnLeuAlaSer 140
Qy 677 CTAGAGGCTTCCCAATTTGACAGCTTATATCTTAAAGAACTAAATGGCTCATAT 736
Dh 141 LeuGluAsnProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisIasn 160
Qy 737 CTATACATTCCTTAAAGTGCCTGAATATTTTCTATCTGACAAACCTAGAACATGTG 796
Dh 161 LeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeu 180
Qy 797 GATCTTTCTTAACTATATTCACAACTATTTCTGTCAAGACCTTACAGTTCTACGTA 856
Dh 181 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGln 200
Qy 857 AATCCCAAGTCAATCTCTTTAGACCTGTCTTAAACCAATGACCTTCAAGACC 916
Dh 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnProIleGlnPro 220
Qy 917 CAACCTTTCAAGGATTTAGGCTCCATGATTTGACTTAAAGAAATTTTATATAGCTCA 976
Dh 221 GlyAlaPheLysGluIleArgLeuHisIleLysLeuThrLeuArgAsnAsnPheAspSerLeu 240
Qy 977 AATGATCTGAAGAATGTGCTTCAAAACATGACTGTGTTTACATGTCCATCGTGTATCTG 1036
Dh 241 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisAspGlyLeuValLeu 260
Qy 1037 GGAGAAATTTAAATAATGAAGAATCTGGAAGATTTTGGACCTTCTGTCATGAGAAGACTA 1096
Dh 261 GlyIleuPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGlnGlyLeu 280
Qy 1097 TGCATGTGACATTTGATGAGTTCAGTTTAACATATATTAATCAATTTTTCAGATGATTT 1156
Dh 281 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 300
Qy 1157 TATATATCTC--AATTGCTTGGCAAAATTTTCTGCAATGTCTTTCACAGGTGTCATATA 1213
Dh 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
Qy 1214 AAACACATGAGAGATGTTCTCAGGCAATTTCAAAATGCAATCTTATCAATCATAGATGT 1273
Dh 321 GluArgValLysAspPheSerTyrAsnPheGlyTyrGlnHisLeuGluLeuValAsnCys 340
Qy 1274 CATCTTAAGCTTTTCCAAAGCTGATCTACCTTTTCTTAAAGTTGAGCTTAACTACC 1333
Dh 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
Qy 1334 AACGAGAGGATACGCTTTGGTCAAGTTGGCTGTGCCAAGTCTCAGATATCTAGATTTT 1393
Dh 361 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
Qy 1394 AGTGAATATGCATGCTTTAGAGGTGCTGTTCTTATCTGATTTTGAACAAACAC 1453
Dh 381 SerArgAsnGlyLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrThrSer 400
Qy 1454 CTGAAGTACTTAAAGCTCAGCTTCAATGTGTCTCATCTGATGAGTGCACAACTTCAAGGT 1513
Dh 401 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420

Qy 1514 CTAGAGAGCTGGATATACCTGACCTTTCAGACTCCACTTAAAGGTCACAGAAATTC 1573
Dh 421 LeuGlnGluLeuGluIleLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 440
Qy 1574 TCAGTGTCTTATCTGTGAAAACTTCTTATCTTACATCTCTTACACTTAATACCAA 1633
Dh 441 SerValPheLeuSerLeuAsnArgAsnLeuIleTyrLeuAspIleSerHisThrHisArg 460
Qy 1634 ATTGACTTTGATGGCATATTTCTTGGCTTGATCAGTCTCAACACTTTAAATAATGGCTGGC 1693
Dh 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 480
Qy 1694 AATTTCTTGAACAGAACACCCCTTGAATGTCTTAAACAAACAACTTAACATTC 1753
Dh 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
Qy 1754 CTGATCTTTTAAATGCCAACTGGAACAGATATCTTAGGGGGTATTTTGAACACTCTAC 1813
Dh 501 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 520
Qy 1814 AGACTCCAGTTATTAACATGAGTCAACACAACTTACTGTTTGGATCCATCCATTA 1873
Dh 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 540
Qy 1874 AAACAGCTGATCCCTCCAGACCTTTGATGAGTTTCAATGCAATGACATGACATCC-- 1930
Dh 541 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 560
Qy 1931 AAAGAAATATGCAACATTTTCCAAAGAGCTAGCCGTCTTCAATCTGACTTAATATCT 1990
Dh 561 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
Qy 1991 GTTGCTTGATATGTGAATATCAGAATTTTTCGAGTGGCTCAAGACCAAGAAATGCTTC 2050
Dh 581 PheAlaCysThrCysGluHisGlnSerPheLeuGlnTyrIleLysAspGlnArgGlnLeu 600
Qy 2051 TTGGTGAATGTGAACAAATGAATGGATCGATCACTATACATGACAAAGCCCTCCGTGT 2110
Dh 601 LeuValGluValGluTyrMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 620
Qy 2111 TTGATTTTACGAATTTCCACCTGTATATATACAAAGCTATCATCATGATGATCGGTGTC 2170
Dh 621 LeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 639
Qy 2171 AGTGTGTTGTGGTACCTGTAGCAATTTCTGATATACCACTTCAATTTTCACTGATA 2230
Dh 640 SerValLeuValAlaSerValAlaAlaValLeuValTyrAspPheTyrPheHisLeuMet 659
Qy 2231 CTATATGCTGGCTGTAATAAAGTACAGCAGAGAGAAAGCATCTATGATGATTTGTGATC 2290
Dh 660 LeuLeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnIleTyrAspAlaPheValIle 679
Qy 2291 TACTCGAGCCAGATGAGACTGGGTGAGAAACAGAGCTGTGTAAGATTTTGAAGAAAGA 2350
Dh 680 TyrSerSerGlnAspGluAspTyrValArgAsnGluLeuValLysAsnLeuGluGluGly 699
Qy 2351 GTGCCCCGCTTACGCTTTGCTTTCATTAACAGGACTTATTTCTGTGTAGCATTGCT 2410
Dh 700 ValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 719
Qy 2411 GCCAATCATATCCAGAAAGGCTTCCAAAGCCGAGAAAGCTTATTTGGTGGTGTCTAGA 2470
Dh 720 AlaAsnIleIleHisGluGlyPheHisLysSerArgLysValIleValAlaValSerGln 739
Qy 2471 CACTTATTCAGAGCCCTTGGTGTATCTTGAATATAGATGTCAGATGGCAGTTT 2530
Dh 740 HisPheIleGlnSerArgTyrPyrHisPheGluTyrGluIleAlaGlnThrTrpGlnPhe 759
Qy 2531 CTGAGTAGCCGCTTGGCATATCTTCAATGTCTTGTGAAGAAAGTGAAGAACTCTTCTG 2590
Dh 760 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluTyrThrLeuLeu 779

QY 2591 AGGCGAGGCTGGAATGATTCGCTTCTTACGAGAAACACCTACCTGAGTGGAGGAC 2650
 Db ArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnUtrpLubsp 799
 QY 2651 AATGCTCTGGGAGGACATCTTCTGGAGAACTCAAAAAAGCCCTGTGGATGGAAA 2710
 Db SerValLeuGlyArgHisIlePheThrArgArgLeuArgValAlaLeuLeuSpGlyLys 819
 QY 2711 GCCCTGAATCCAGAT-----GAAACATCAGAGAGAAACAGAGCAACACTTTG 2761
 Db 820 SerTrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnIleThrSerIle 839
 RESULT 3
 ABU04775
 ID ABU04775 standard; protein; 839 AA.
 AC ABU04775;
 XX 29-JAN-2003 (first entry)
 DE Human expressed protein tag (EPT) #1441.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PE 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicx RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 PT
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1441; 134bp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide, the purified polypeptide, or the antibody that binds to this
 CC polypeptide. The useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 839 AA;
 Alignment Scores:
 Prod. No.: 2,676-280
 Score: 2860.50
 Percent Similarity: 80.24%
 Best Local Similarity: 66.55%
 Query Match: 48.13%
 DB: 6 Gaps: 5
 US-09-396-985B-5 (1-3395) x ABU04775 (1-839)
 QY 260 ATGATGCTCTCTTGCATCTGGCTGGAGACTGTGATCAGCATG---TTCCTTCTCTGC 316
 Db 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerYs 20
 QY 317 CTGAGACCGAGGAGCTTGAATCCCTGCATGAGGTACTTCTTAATATTACTTACCAATGC 376
 Db 21 ValArgProGlnSerTrpGlnProCysValGlnValAlaProAsnIleThrTyrGlnCys 40
 QY 377 ATGATCAGAAATCTCAGCAAAAATCCCTCATGACATCCCTTATTGACCAAGAACTGAT 436
 Db 41 MetGlnLeuAsnPheTyrLysIleProAsnLeuProPheSerThrLysAsnLeuAsp 60
 QY 437 CTGAGCTTCAACCCCTGAGATCTTAAGAGCTATAGCTTCACCAATTTCTCACAACTT 496
 Db 61 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGlnLeu 80
 QY 497 CAGTGGCTGATTTATTCAGGTGTGAATTGAGCAATTGAGCAAGGACATGCGCATGCG 556
 Db 81 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaTyrGlnSer 100
 QY 557 TTAACCAAGCTCTCAACTTGTGTCTGACAGAAACCTTCAAGAGTTTTCCTCCAGGA 616
 Db 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
 QY 617 AGTTTCTTGGACCAACAAATTTAGAGATCTGTGCTGGAGACAAATGACCTCT 676
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGlnThrAsnLeuAlaSer 140
 QY 677 CTAGAGGGTTTCCATTTATGACAGCTTATATCTTAAAGAACTAAATGTGGCTCATAT 736
 Db 141 LeuGlnAsnPheProIleGlnIleLeuIleThrLeuIleGlnLeuAsnValAlaHisAsn 160
 QY 737 CTATACATTCCTTAAAGTGGCTGATATTTTCTATCTGACAAACCTTGAACATGTG 796
 Db 161 LeuIleGlnSerPheLysLeuProGlnIleTyrPheSerAsnLeuThrAsnLeuGlnHisLeu 180
 QY 797 GATCTTCTTATTAACCTAATTTCAACTATTTCTGCAAGAGTTTCTACGGTAA 856
 Db 181 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuValGlnHisGln 200
 QY 857 AATCCCAAGTCATCTCTCTTAGACCTGTCTTAAACCAATGACCTCATTCAGGCC 916
 Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 917 CAAGCTTTCAAGGAATTTAGGCTCCATGAATTGACTTGAAGAAATTTTAAAGCTCA 976
 Db 221 GlyAlaPheLysGlnIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu 240
 QY 977 AATGATGAGAAATGTGCTTCAAAAACATGCTGTTTAAATGCTTCAATGCTGATGCTG 1036
 Db 241 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeu 260
 QY 1037 GGAAGATTTAAATGAAGAAATCTGGAAGATTTCAGCGTTCTGTATGAGAGACTA 1096
 Db 261 GlyGlnPheArgAsnGlnGlyLysAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 280
 QY 1097 TGCAATGTGACATGTATGAGTTTCAAGTTTAACATATTAATCATTTTTCAGATGATATT 1156
 Db 281 CysAsnLeuThrIleGlnGlnPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 300

QY 1157 TATATCTC--AATGCTGGCAATATTTCTGCAATGTCCTTTACAGGTGTAACATA 1213
 Db 301 ILeasrpeuhencyleuThrAsnValSerSerleuValSerValThrIle 320
 QY 1214 AAACACATCAGCAATGTTCTCAGCAATTTCAATGGCAATCCTTATCATCATTAAGTGT 1273
 Db 321 GluArgValIlyAspPheSerTyRAsnPhedLyTrpGlnHsleuGluLeuValAsnCys 340
 QY 1274 CATCTTAAGCTTTCCAAAGCTGAGTCTTACCTTTCTTAAAGAGTGCATTTAACTACC 1333
 Db 341 LyePheGlyGlnPheProthleuLysleuLysSerleuYAspGlyLeuThrPheThrSer 360
 QY 1334 AACAGAGAGATATACAGCTTGGTCAAGTGGCTGCCAAATCTCAGATATCTAGATCTT 1393
 Db 361 AsnIlyGlyGlnAlaPheSerGluValAspLeuProSerleuGluPheLeuAspLeu 380
 QY 1394 AGTGAATGCCATGAGCTTTAGAGTTCGTCGTTCTTATTTCTGATTTTGGACAAACAC 1453
 Db 381 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1454 CTGAAGATCTTAGACCTCAGCTTCAATGGTGTCAATCCGATGAGTGCACATTCAGGGT 1513
 Db 401 LeuLysTyRleuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPhelGly 420
 QY 1514 CTAGAAGAGCTGAATACCTGACTTTCAGCACTCACTTAAATAAAGTCAAGAAATTC 1573
 Db 421 LeuGluGlnleuGlnHsleuAspPheGlnHsSerAsnleuYAspGlnMetSerGluPhe 440
 QY 1574 TCAGTGTCTTATCTTTGAAAACTTCTTACCTTGAACATCTTTACATTAATACCAA 1633
 Db 441 SerValIleLeuSerLeuArgAsnleuIleTyRleuAspIleSerHsIleThrHsArg 460
 QY 1634 ATTACTTGTGATGGCATATTTCTGGCTGTGATGCTCAACACTTTAAAAAGGCTGGC 1693
 Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerleuGluValleuLysMetAlaGly 480
 QY 1694 AATTCCTTCAAGACAACACCTTCAATGCTTTCAACACACAACTTAACATTC 1753
 Db 481 AsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGluLeuArgAsnleuThrPhe 500
 QY 1754 CTGATCTTTTAAATGCAACTGGAACAGATATCTAGGGGGGTATTTGACACCTCTAC 1813
 Db 501 LeuAspLeuSerGlnCysGlnleuGluGlnleuSerProThrAlaPheAsnSerleuSer 520
 QY 1814 AGACTCCAGTATTAACATGAGTCAACAACACTGCTTTCGATCCATCCATTAAT 1873
 Db 521 SerleuGlnValleuAsnMetSerHsIAsnAsnPhelSerleuAspThrPheProTyR 540
 QY 1874 AAACAGCTGTACTCCCTCAGACTCTGATTCGATTCGATTCGATTCGATTCGATTC 1930
 Db 541 LysCysleuAsnSerleuGlnValleuAspTyRSerleuAsnHsIleMetThrSerLys 560
 QY 1931 AAAGCAATCTGCAACATTTTCCAAAGAGTGTAGCCGCTTCAATCTGACATTAATCTT 1990
 Db 561 LysGlnGluLeuGlnHsPheProSerSerleuAlaPheLeuAsnleuThrGlnAsnAsp 580
 QY 1991 GTTGCTGTATATGATGATCAGAAATTTCTGAGAGTGGTCAAGAGCAGAAATATGTC 2050
 Db 581 PheAlaCysThrCysGlnHsGlnSerPheleuGlnTrpIleYAspGlnArgGlnleu 600
 QY 2051 TTGGTGAATGTGAACAATGAATGTGCATCAGTATGACATGAAGGCTCCCTGGTG 2110
 Db 601 LeuValIgluValIgluArgMetGluCysAlaThrProSerAspTyRAsnGlyMetProVal 620
 QY 2111 TTGCAATTTACGAATTCCTGTTATATATACAAAGATATCAAGTATCGGTGTC 2170
 Db 621 LeuSerleu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValleu 639
 QY 2171 AGTGGCTTGTGATGACATCTGATTCGATTCGATTCGATTCGATTCGATTCGATTC 2230
 Db 640 SerValleuValSerValValAlaValleuValTyRlyPheTyRPhelIleuMet 659
 QY 2231 CTATTCGTGCTGTAAAGTACAGCAGAGAGAAAGCATCTATGATTCATTTGTGATC 2290

Db 660 LeuLeuAlaGlyCysIleLysTyRglYArgGlyGluAsnIleTyRAspAlaPheValIle 679
 QY 2291 TACTGAGCCAGAAATAGAGCTGGGTGAGAAACAGACTGGTAAAGATTTAGAAAGGA 2350
 Db 680 TyRSerSerIAspGlnAspTrpValArgAsnGlnleuValIlyAsnleuGluGly 699
 QY 2351 GTGCCCCGCTTTCAGCTTGGCTTCATTAACAGGAATTTATTCCTGGTGTAGCCATTC 2410
 Db 700 ValProPheGlnleuGlnCysleuHsIleTyRArgAspPheIleProGlyValAlaIleAla 719
 QY 2411 GCCAACATCATCCAGAAAGGCTTCACAAAGACCCGAAAGTTATTTGGTGGTCTACA 2470
 Db 720 AlaAsnIleIleHsIleGluGlyPheHsIlySerArgLysValIleValValIleSerGln 739
 QY 2471 CACTTTATCCAGACCCGCTGGTGTATCTTGAATATGAGATTCGACATGGCAGTTT 2530
 Db 740 HisPheIleGlnSerArgTrpCysIlePheGlyTrpIleAlaGlnThrTrpGlnPhe 759
 QY 2531 CTGAGTAGCCGCTCTGGCATCATCTTCATTTGCTTGAAGAAAGTGAAGATCTTGTCTG 2590
 Db 760 LeuSerSerArgAlaGlyIleIlePheIleValleuGlnLysValIgluYsThrleuLeu 779
 QY 2591 AGGCAGCAGGTGCAATTTGATCGCTTTCTTAGCAAAACCTTACCTCGAGTGGAGAC 2650
 Db 780 ArgGlnGlnValIgluLeuTyRArgLeuLeuSerArgAsnThrTyRleuGluTrpGluAsp 799
 QY 2651 AATGCTCTGGGGAGGACATCTTCTGAGAAGACTCAAAAAGCCCTGTGATGGAGAA 2710
 Db 800 SerValleuIlyArgHsIlePheThrPArgLysleuArgValAlaLeuLeuAspGlyLys 819
 QY 2711 GCCTGTGATCCAGAT-----GAAACATCAGAGAAAGMACAAGACCAACTTGTG 2761
 Db 820 SerTrpAsnProGluGlnThrValGlyThrGlyCysAsnTrpGlnGluAlaThrSerIle 839
 RESULT 4
 ADCT8785
 ID ADCT8785 standard; protein; 839 AA.
 AC ADCT8785;
 XX 01-JAN-2004 (first entry)
 DT XX
 XX Human PRO protein #7.
 DE XX
 KW human, PRO; cancer; inflammatory bowel disease; ulcerative colitis;
 KW Crohn's disease.
 XX
 OS Homo sapiens.
 PN W02003034984-A2.
 XX
 PD 01-MAY-2003.
 XX
 PF 15-OCT-2002; 2002W0-US033070.
 XX
 PR 19-OCT-2001; 2001US-0340083P.
 XX
 PA (GERTH) GENENTECH INC.
 PI Goddard A, Gurney AL;
 XX
 DR WPI; 2003-461990/45.
 DR N-PSDB; ADCT8784.
 XX
 PT New PRO polynucleotide and polypeptide, useful for the manufacture of a
 PT medicament for diagnosing or treating cancer or inflammatory bowel
 PT disorder e.g., ulcerative colitis or Crohn's disease.
 PS
 PS Claim 12; SEQ ID NO 14; 327bp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of human PRO
 CC proteins. The DNA and protein sequences of the invention are useful for

CC the diagnosis and treatment of cancer and inflammatory bowel disease
 CC (e.g. ulcerative colitis or Crohn's disease). The present amino acid
 CC sequence represents a human PRO protein of the invention.

SO Sequence 839 AA:

Alignment Scores:

Pred. No.:	2,67e-280	Length:	839
Score:	2860.50	Matches:	559
Percent Similarity:	80.24%	Conservative:	115
Best Local Similarity:	66.55%	Mismatches:	159
Query Match:	48.13%	Indels:	7
		Gaps:	5

US-09-396-985B-5 (1-3395) x ADCT8785 (1-839)

```

QY 260 ATGATGCTCTCTGATCTGGCTGGAGCTGATCATGCAATG--TTCTTTCTCTGC 316
DB 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
QY 317 CTGAGACGAGGAGGATGATCCCTGACATAGAGGACTCCTAATATTACCTACCAATGC 376
DB 21 ValArgProGluSerThrPgluProCysValGluValAlaProAsnIleThrTyGlnCys 40
QY 377 ATGATCAGAACTCAGCAAAATCCCTCATGACATCCCTTATTCAACCAAGACCTAGAT 436
DB 41 MetGluLeuAsnPheTyLeuIleProAsnLeuProPheSerThrTyLeuAsnLeuAsp 60
QY 437 CTGAGCTTCAACCCCTGAAAGATCTTAAGAGCTTACCTTACCAATTTCTCAACTT 496
DB 61 LeuSerPheAsnProLeuArgHisLeuGlySerTySerPhePheSerPheProGluLeu 80
QY 497 CAGTGGCTGATTTATCCAGGCTGAATTAAGACAATTGAAGACAAGGATGATGCG 556
DB 81 GlnValLeuAspLeuSerArgCysGluIleGlnThrIleGlnAspGlyAlaTyGlnSer 100
QY 557 TTAACACGACTCTCAACCTTGATCTGAACAGAAACCTTACAGAGTTTTCACAGCA 616
DB 101 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaIleGly 120
QY 617 AGTTTCTGACATTAACAATTGATGAGATCTGGTGGCTGGAGACAAAAATGACCTCT 676
DB 121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValAlaGluThrAsnLeuAlaSer 140
QY 677 CTAGAGGGTCTTCATATTGACAGCTTATATCTTAAAGAACTAAATGGGCTCATAT 736
DB 141 LeuGluAsnProIleGlyHisLeuGlySerThrLeuGlyLeuValAlaHisIleAsn 160
QY 737 CTATACATTCCTTAAGTGCCTGAATATTTCTATCTGACAAACCTAGAACATGTG 796
DB 161 LeuIleGlnSerPheLeuLeuProGluIlePheSerAsnLeuThrAsnLeuGlnHisLeu 180
QY 797 GATCTTCTTAACTATATTAACAATTTCTGCTCAAGACTTACAGTTTCTACGTGA 856
DB 181 AspLeuSerSerAsnIleGlnSerIleTyCysThrAspLeuAspValIleHisGln 200
QY 857 AATCCCAAGCAATCTCTTTAGACCTGCTTAAACCAATTCATCCATCAAGCC 916
DB 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
QY 917 CAAGCCTTTCAGGAAATTAGCTCCATGATTAATGACTTAAGAGTAATTTTAATAGCTCA 976
DB 221 GlnAlaPheLeuGlyIleArgLeuHisIleLeuThrIleuArgAsnAsnPheAspSerLeu 240
QY 977 AATGTCAGAAATGCTCTTCAAAACATGACTGCTTATACATGTCATCGGTGATCTTG 1036
DB 241 AsnValMetCysIleGlnGlyLeuAlaGlyLeuGlnIleValHisIleArgLeuValLeu 260
QY 1037 GGAGAAATTTAAATGAAGAATCTGGAAGATTTCAGCTTGCATGCAAGAGACTA 1096
DB 261 GlnValPheArgAsnGlnGlyAsnLeuGlnIleAspLeuSerAlaIleGlnGlyLeu 280
QY 1097 TGAATGTGACATTTGATGAGTTAAACATATTAATCAATTTTTCAGATGATATT 1156

```

```

DB 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaIleTyLeuAspIle 300
QY 1157 TATATCTC--AATTCCTGGCAATATTTCCGATGCTTTCACAGGTGTCATATA 1213
DB 301 IleAspLeuPheAsnCysLeuThrAsnValSerSerLeuValSerValThrIle 320
QY 1214 AATCAGATGAGAGATGTTCTTAGAGCTTTCAAATGCAATCTTATCAATCATTAGATGT 1273
DB 321 GlnArgValIleAspPheSerTyLeuAsnPheGlyTyrPgluHisIleGluLeuValAsnCys 340
QY 1274 CATCTTAAGCCTTTTCCAAAGCTGATCTACCTTTTCTTAAAGTGGACTTAACTAC 1333
DB 341 LysPheGlnPheProThrLeuTyLeuIleLeuSerLeuTyAspArgLeuThrPheThrSer 360
QY 1334 AATCAGAGAGATATACACTTGTGATGCTGCTGCAAGTCCAGATCATATCTGATCTT 1393
DB 361 AsnIleGlyAlaAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
QY 1394 AGTAGAATGCGCATGAGCTTTCAGAGTGGCTGTTCTTATCTGATTTTGAACAAACAC 1453
DB 381 SerArgAsnGlyLeuSerPheIleGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
QY 1454 CTGAAGTACTTAAAGCTTCAAGCTTCAATGCTGTCATCCTGATGATGAGTCAACTGATG 1513
DB 401 LeuTyThrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 420
QY 1514 CTGAAGACGCTGAATACCTGAGACTTTCAGACCTCCACTTAAAAAAGTCACAGAAATTC 1573
DB 421 LeuGlnGlnLeuGlnIleAsnAspPheGlnHisSerAsnLeuTyGlnMetSerGluPhe 440
QY 1574 TCAGTGTCTTATCTCTTGAAGAACTCTTACCTTACATCTCTTACATCAATATACAAA 1633
DB 441 SerValIleLeuSerLeuAsnGlnLeuIleTyLeuAspIleSerHisIleThrArg 460
QY 1634 ATTGACTTGAATGAGCATATTTCTTGCTGATCAGTCTCAACACTTAAATAGCTGCGC 1693
DB 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuIleMetAlaGly 480
QY 1694 AATCTTTCAGAAACACACACCTTTCAAATGCTCTTTCAGAAACACACAACTTAACTTC 1753
DB 481 AsnSerPheGlnGlnLeuAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
QY 1754 CTGATCTTCTTAATGCAATGCAAGTGAACAGATATCTAGGGGGGATTTGACACACTTAC 1813
DB 501 LeuAspLeuSerGlnCysGlnLeuGlnIleLeuSerProThrAlaPheAsnSerLeuSer 520
QY 1814 AGACTCCAGTTATTAACATGAGTCAACAACCTACTGTGTTCTGATCCATCCATAT 1873
DB 521 SerLeuGlnValIleAsnMetSerHisAsnAsnPheSerLeuAspThrPheProTyr 540
QY 1874 AATCAGCTGATCTCCCTCAGAGACTTGTGATGCAATGCAATGCAATGCAATCC-- 1930
DB 541 LysCysLeuAsnSerLeuGlnValIleAsnAspTySerLeuAsnHisIleMetThrSerLys 560
QY 1931 AATGGAATCTGCAACATTTTCCAAAGAGCTGAGCTGCTTCAATGCAATTAATTTCT 1990
DB 561 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
QY 1991 GTTGCTTGATATGATGATATGCAATTTCTGCAAGTGGTCAAGACAGAAATGCTC 2050
DB 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnIlePheLysAspGlnArgGlnLeu 600
QY 2051 TTGGTGAATGTTGAACAAATGAATGTCATCCTTATAGACATGAAGGCTCCCTGTG 2110
DB 601 LeuValGlnValIleGlnArgMetGlnCysAlaThrProSerAspIleGlyMetProVal 620
QY 2111 TTGATTTTGAATTCACCTGTTATATATACAAAGCTATCATCATGATGATGCTGCTG 2170
DB 621 LeuSerLeu--AsnIleThrCysGlnMetAsnIleThrIleIleGlyValSerValLeu 639
QY 2171 AGTGTGCTTGATGAGCACTGATGATTTCTGATATACCACTTATTTTTCAGCTGATA 2230

```



```

Db      640 SerValIeuValIaSerValIaIaValIeuValTyrIlysPheTyrPheHisIleuMet 659
Qy      2231 CTTATTCCTGGCTCTGTAATAAATACAGAGAGAGAAAGCATCTATGATGCTTTGTGATC 2230
Db      660 LeuIeuValIeuCysIleIeuSerGlyArgGlyIuIeuSnIleTyrAraPheValIle 679
Qy      2291 TACTGAGCCAGAAATGAGAACTGGGTGAGAAACAGCTGTGTAAGAAATTTGAGAAAGGA 2350
Db      680 TyrIeuSerGlnAraPheGluAspTyrValIaArgSnIleuValIuSaaIeuGluGly 699
Qy      2351 GTGCCCCGCTTTGAGCTTGGCTTCATTAACAGGACCTTATTCCTGGTGAGCCATTGCT 2410
Db      700 ValIProPheGlnIeuCysIleuHisIeuTyrArgAraPheIleProGlyValIaIleAla 719
Qy      2411 GCGAATCATCCAGAAAGCTTCACAAAGCCGAGAAAGTATTCGTGGTGTCTACGA 2470
Db      720 AlaSnIleIleHisGluGlyPheHisIeuSerArgIuValIleValIaValSerGln 739
Qy      2471 CACTTTATCCAGAGCCGTTGGTGTATCTTTGAATATGAGATTGCTCAGACATGGCAGTTT 2530
Db      740 HisPheIleGlnSerArgIuTyrCysIleIlePheGluTyrGluIleAlaGlnThrIlePhe 759
Qy      2531 CTGAGTACGCGCTCTGGCATATCTTCATTGCTCTTGAGAAAGTGAGAAAGTCTTGCTG 2590
Db      760 LeuSerSerArgIaGlyIleIleIlePheIleValIeuGlnIuSValIuGlyuThrIleu 779
Qy      2591 AGGACAGAGCTGCAATGTATGCGCTTCTTGAGAAACACCTACCTCGAGTGGAGAGAC 2650
Db      780 ArgGlnGlnValIaGluIeuTyrArgIeuIeuSerArgSnIleTyrIleuGluTyrGluAsp 799
Qy      2651 AATGCTCTGGAGAGCAGCATCTTCTGAGAGAACTCAAAAAAGCCCTGTTGATGAGAAA 2710
Db      800 SerValIeuGlyArgHisIleIlePheTyrArgIeuArgIeuArgIuSValIeIleuAspGlyIuS 819
Qy      2711 GCCTTGAATCCAGAT-----GAAACATCAGAGAGAAACAAAGCAACATTTG 2761
Db      820 SerIProPheGlnIeuGlyThrValIaGlyThrGlyCysAenIProGlnIuIaThrSerIle 839

RESULT 5
ADD48826
ID      ADD48826 standard; protein, 839 AA.
XX      AC      ADD48826;
XX      DT      02-DEC-2004 (revised)
XX      DT      29-JAN-2004 (first entry)
XX      DE      Human Protein AAF05316, SEQ ID NO 14536.
XX      KM      Human; pain; neuronal tissue; gene therapy;
XX      KM      spinal segmental nerve injury; chronic constriction injury; CCI;
XX      KM      spared nerve injury; SNI; Chung.
XX      OS      Homo sapiens.
XX      OS      Unidentified.
XX      PN      MO2003016475-A2.
XX      PD      27-FEB-2003.
XX      PF      14-AUG-2002; 2002WO-US025765.
XX      PR      14-AUG-2001; 2001US-0312147P.
XX      PR      01-NOV-2001; 2001US-0346382P.
XX      PR      26-NOV-2001; 2001US-0333347P.
XX      PA      (GENO ) GEN HOSPITAL CORP.
XX      PA      (FARB ) BAYER AG.
XX      PI      Woolf C, D'urso D, Befort K, Costigan M;
XX      WP1; 2003-268312/26.
XX      DR      GENBANK; AAF05316.

```

```

XX      PT      New composition comprising two or more isolated polypeptides, useful for
XX      PT      preparing a medicament for treating pain in an animal.
XX      PS      Example 1; Page; 1017pp; English.
XX      SS      The invention discloses a composition comprising two or more isolated rat
XX      CC      or human polynucleotides or a polynucleotide which represents a fragment,
XX      CC      derivative or allelic variation of the nucleic acid sequence. Also
XX      CC      claimed are a vector comprising the novel polynucleotide, a host cell
XX      CC      comprising the vector, a method for identifying a nucleotide sequence
XX      CC      which is differentially regulated in an animal subjected to pain and a
XX      CC      kit to perform the method, an array, a method for identifying an agent
XX      CC      that increases or decreases the expression of the polynucleotide sequence
XX      CC      that is differentially expressed in neuronal tissue of a first animal
XX      CC      subjected to pain, a method for identifying a compound which regulates
XX      CC      the expression of a polynucleotide sequence which is differentially
XX      CC      expressed in an animal subjected to pain, a method for identifying a
XX      CC      compound that regulates the activity of one or more of the
XX      CC      polynucleotides, a method for producing a pharmaceutical composition, a
XX      CC      method for identifying a compound or small molecule that regulates the
XX      CC      activity in an animal of one or more of the polypeptides given in the
XX      CC      specification, a method for identifying a compound useful in treating
XX      CC      pain and a pharmaceutical composition comprising the one or more
XX      CC      polypeptides or their antibodies. The polynucleotide or the compound that
XX      CC      modulates its activity is useful for preparing a medicament for treating
XX      CC      pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX      CC      injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX      CC      therapy). The sequence presented is a human protein (described in Table 3
XX      CC      of the specification) which is differentially expressed during pain.
XX      CC      Note: The sequence data for this patent did not form part of the printed
XX      CC      specification, but was obtained in electronic form directly from WIPO at
XX      CC      ftp.wipo.int/pub/published_pcr_sequences.
XX      SQ      Sequence 839 AA:

Alignment Scores:
Pred. No.:      2,676-280      Length:      839
Score:          2860.50      Matches:      559
Percent Similarity: 80.24%      Conservative: 115
Best Local Similarity: 66.55%      Mismatches: 159
Query Match:    48.13%      Indels:      7
DB:             7      Gaps:      5

US-09-396-985b-5 (1-3395) x ADD48826 (1-839)
Qy      260 ATGATGCTCTCTGTCATCTGGCTGGAGCTCTGATCATGGCATG--TTCTTTCTCTGC 316
Db      1 MetMetSerAlaSerArgIeuAlaGlyThrIleuIleProAlaMetAlaPheLeuSerCys 20
Qy      317 CTGAGACCAAGGAGCTTGAATCCCTGCATGAGAGTACTTCTTAATTTACTTCCCATGCG 376
Db      21 ValArgProGluSerTyrGluProCysValGluValProAsnIleThrTyrGlnCys 40
Qy      377 ATGATCAGAACTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGACCTTAGAT 436
Db      41 MetGluIeuAsnIleuTyrIleIleProAsnIleuProPheSerThrIuSaaIeuAsp 60
Qy      437 CTGAGCTTCAACCCCTGAAAGATCTTAAGAAGCTTATAGCTTCAACAAATTTCTCAAACTT 496
Db      61 LeuSerPheAsnProIeuArgHisIleuGlySerTyrSerPheSerPheProGluIeu 80
Qy      497 CAGTGGCTGATTTATTCAGGTGTGAATTTGAGACAAATTGAACAAAGCATGGCATGGC 556
Db      81 GlnValIeuAspIeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 100
Qy      557 TTAACAGCTCTCAACCTTGACTGACAGAAACCTTCAAGATTTCCCGCAGA 616
Db      101 LeuSerHisIeuSerThrIleuIleuThrGlyAsnProIleGlnSerIleuAlaIeuGly 120
Qy      617 AGTTTTCGTGACTAACAAATTTAGAGAACTGTGGTGGCTGTGAGACAAAAATGACCTCT 676
Db      121 AlaPheSerGlyIeuSerSerIeuGlnIuIeuValIaValIaGluThrAsnIleuAlaSer 140

```


QY 677 CTAGAGGGTTTCCATATTGGACAGCTTATCTTAAAGAACTAAATGGCTCATAT 736
 Db 141 LeuGluAsnProIleGlyHisLeuYsthrLeuYsgluLeuAsnValAlaHisAsn 160
 QY 737 CTTATACATCTCTTAAAGTGGCTGAATTTTCTAATCTGACAAACCTAGACATGTG 796
 Db 161 LeuIleGlnSerPheLysLeuProGluYrPheSerAsnLeuThrAsnLeuGlnHisLeu 180
 QY 797 GATCTTCTTATACATATTCATCAACCTATTTCTGCAAGACTTACGTTCTAGTAA 856
 Db 161 AsnLeuSerSerAsnLysIleGlnSerIleYrCysThrAspLeuArgValLeuHisGln 200
 QY 857 AATCCCAAGTCATCTCTTAAAGCTGCTTAAACCCAAATGACCTCCATCAAGCC 916
 Db 201 MetProLeuAsnLeuSerLeuAsnSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 917 CAGGCTTTCAGGGAATTAGGCTCCATGATTAAGCTTACAGAAAGTAAATTAATAGCTCA 976
 Db 221 GlyAlaPheLysGluIleArgLeuHisIleYsLeuThrLeuArgAsnAsnPheAspSerLeu 240
 QY 977 AATGACGAAATGCTGCTTCAAAACATGACTGGTTTACATGCTCATCGGTGATCTTG 1036
 Db 241 AsnValMetLysThrCysIleGlnIleGluLeuAlaGlyLeuGluValHisArgLeuValLeu 260
 QY 1037 GGAGAAATTTAAATAAGAAAGATCTGGAAGATTTTGAACCGTCTGTCATGAGAAAGACTA 1096
 Db 261 GlyIlePheArgAsnGluGlyAsnLeuGluYsPheAspLysSerAlaLeuGlnGlyLeu 280
 QY 1097 TGCATGTGACATGATGATGAGTTCAGGTTAAATATATATATATATATATATATATAT 1156
 Db 281 CysAsnLeuThrIleGluGluPheArgLeuAlaYrLeuAspYrYrLeuAspAspIle 300
 QY 1157 TATATATCTC--AATTGCTTGCAAAATATTTCTGCAATGCTTTTACACGGGTACATATA 1213
 Db 301 IleAspLeuPheAsnCysLeuHisThrAsnValSerSerPheSerLeuValSerValThrIle 320
 QY 1214 AAACATACAGACAGATGTTCTTAGGCAATTCATTAAGCTTATCAATCATTAAGATGT 1273
 Db 321 GluArgValLysAspPheSerLysAsnPheGlyTrpGlnHisIleLeuValAsnCys 340
 QY 1274 CATCTTAAGCCTTTCCAAAGCTGATGCTTCTTAAAGTGGACTTAACTAAC 1333
 Db 341 LysPheGlyGlnPheProThrLeuYsLeuYsSerLeuYsArgLeuThrPheThrSer 360
 QY 1334 AACAGAGAGATATGACTTGTGCAAGTGGCTGCCAATCTCAGATATCTGATATCTT 1393
 Db 361 AsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGluPheLeuAspLeu 380
 QY 1394 AGTAGAATGCCATGAGCTTAAAGTGTGCTGTTCTTATTTCTGAATTTGGAACAAC 1453
 Db 381 SerArgAsnGlyLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1454 CTGAAGTATCTTAAGCTCAGCTTCAATGATGCTCATCTGATAGTGCACACTTATGGGT 1513
 Db 401 LeuYsYrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnAspPheLeuGly 420
 QY 1514 CTAAGAGCTGGAATACCTGGACTTTAGACACTCCACTTAAAAAAGTACAGCAATTC 1573
 Db 421 LeuGlnGlnLeuGlnHisIleAspPheGlnHisSerAsnLeuYsGlnMetSerGlnPhe 440
 QY 1574 TCAGTGTCTTATCTCTGAAAAAACCTTCTTAACCTGACATCTCTTCACTAATACAAA 1633
 Db 441 SerAlaPheLeuSerLeuArgAsnLeuIleYrLeuAspIleSerHisIleThrArg 460
 QY 1634 ATTGACTTTGATGCAATTTCTTGCTGCTGATCAAGTCAACACTTAAATAAGCTGCGC 1693
 Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuYsMetAlaGly 480
 QY 1694 AATTCTTTCAAGACACACCTTTCAATGCTTTTCAAAACAACAACAACTTAACTATTC 1753
 Db 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500

QY 1754 CTGATCTTTTAAATGCAACCTGAACACAGATATCTAGGGGGGTATTGACACACTTAC 1813
 Db 501 LeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSer 520
 QY 1814 AGACTCCAGTATTAAACATGAGTGCACAAACCTACTGTTCTTGATTCATCCCAATTAT 1873
 Db 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProYr 540
 QY 1874 AAACAGGCTGATCCCTCAGACCTTGATTCAGGTTTCAATGCCATAGACATCC-- 1930
 Db 541 LysCysLeuAsnSerLeuGlnValLeuAspYrSerLeuAsnHisIleMetThrSerLys 560
 QY 1931 AAAGAAATCTGCAACATTTTCCAAAGAGTCTAGCCCTCTTCAATCTGACATTAATAATCT 1990
 Db 561 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
 QY 1991 GTTCTGTATATGTAATATCAGAAATTTCTTGACGTGGCTGACAGAACCAAAATGCTC 2050
 Db 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleThrIleYsAspGlnArgGlnLeu 600
 QY 2051 TTGGTGAATGTTGAACAAATGAAATGTCATCACTTACATCAATGAAGGCTCCCTGTG 2110
 Db 601 LeuValGlnValGluArgMetGluCysAlaThrProSerAspYsGlnGlyMetProVal 620
 QY 2111 TTGGATTTTCAATTCACCTGTTATATATACAAAGACTTATCAATGATGATGGTGTG 2170
 Db 621 LeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 639
 QY 2171 AGTGTGCTGTGATGACCTGATGACATTTCTGATATACAACTTATTTTCACTGATA 2230
 Db 640 SerValLeuValValSerValValAlaValLeuValYrLysPheYrPheHisLeuMet 659
 QY 2231 CTTATTCCTGCTGTAAATAAGTACAGACAGAGAAAGCATCTATGATGATTTGATC 2290
 Db 660 LeuLeuAlaGlyCysIleLysYrGlyArgGlyGluAsnIleYrAspAlaPheValIle 679
 QY 2291 TACTCAGACAGATGAGTACGAGTGTGAGAAACAGCTGTGAAAGATTTAGAAAGAGA 2350
 Db 680 TyrSerSerGlnAspGlnAspTrpValArgAsnGluLeuValLysAsnLeuGlnGly 699
 QY 2351 GTGCGCGCTTTCAGCTTTCCTTCAATTAACAGGACTTATTCCTGCTGATGCCATTTGCT 2410
 Db 700 ValProProPheGlnLeuCysLeuHisIleYrArgAspPheIleProGlyValAlaIleAla 719
 QY 2411 GCCAATCATCAAGAAAGGCTTCCAAAGCCGGAAGAAATTTATGCTGCTGCTTACA 2470
 Db 720 AlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValSerGln 739
 QY 2471 CACTTATCAGAGCCGTGGTATCTTGAATATGAGATGCTCAGATGACGACTTT 2530
 Db 740 HisPheIleGlnMetArgTrpCysIlePheGlnYrGlnIleAlaGlnHisTrpGlnPhe 759
 QY 2531 CTGAGTAGCCGCTGTGACATCATTTGCTTGTCTGAGAAAGTGAAGAGTCTGCTG 2590
 Db 760 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnYsThrLeuLeu 779
 QY 2591 AGGCAAGAGTGCATTTGATGCTCTTCTTGAAGAAACCTTACAGTGGAGAGAC 2650
 Db 780 ArgGlnGlnValGluLeuYrArgLeuLeuSerArgAsnThrYrLeuGlnIleTrpGluAsp 799
 QY 2651 AATGCTCTGGAGGAGCAGCATCTTCTGAGAGAACTCAAAAAGCCGTGTGATGGAGAAA 2710
 Db 800 SerValLeuGlnYrGlnHisIlePheThrArgValLeuArgLysAlaLeuLeuAspGlyLys 819
 QY 2711 GCCTGAATTCAGAT-----GAAACATCAGAGAAAGAACAGAAAGCAACACTTTG 2761
 Db 820 SerTrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnIleAlaThrSerIle 839

RESULT 6

AAW86361 ID AAW86361 standard; protein; 837 AA.

AC AAW86361;

XX 15-MAR-1999 (first entry)
DT
XX Human DNAX toll-1-like receptor DTLR4.
DE
XX DNAX toll-1-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor;
KW interleukin 1 receptor; phosphate metabolism; innate immunity response;
KW modulate inflammatory function; morphological effect;
KW immunological disorder.
XX
XX Homo sapiens.
OS
XX W09850547-A2.
FN
XX 12-NOV-1998.
PD
XX
XX 07-MAY-1998; 98WO-US008979.
PE
XX 07-MAY-1997; 97US-0044293P.
PR 22-JAN-1998; 98US-0072212P.
PR 05-MAR-1998; 98US-0076947P.
PR
XX (SCHE) SCHERING CORP.
PA
XX
XX Hardiman GT, Rock FL, Bazan JF, Kastelein RA;
PI WPI, 1999-059670/05.
DR N-PSDB; AAV80675.
DR
XX Human DNAX toll-1-like receptor, DTLR 2-10 - used to, e.g. alter phosphate
PT metabolism, modulate inflammatory function or innate immunity responses.
PT
XX
XX Claim 3; Page 147-149; 171pp; English.
PS
XX
XX The present invention specifically describes human DNAX toll-1-like
CC receptors 2 to 10 (DTLR2-10). The present sequence is human DTLR4 given
CC in the present invention. Also described are: (1) a fusion protein
CC comprising a DTLR protein or peptide; (2) a binding compound, preferably
CC an antibody or antibody fragment which specifically binds to a DTLR
CC protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide
CC; (4) an expression vector comprising the nucleic acid of (3); and (5) a
CC host cell comprising the vector of (4). The host cell of (5) can be used
CC to produce the DTLR proteins. The DTLR proteins can be used to alter
CC phosphate metabolism, to modulate inflammatory function, innate immunity
CC responses or morphological effects. The DTLR proteins can be used in the
CC treatment of conditions exhibiting abnormal expression of the receptors
CC of their ligands. These abnormalities are typically manifested by
CC immunological disorders
CC
XX
SQ Sequence 837 AA;

Alignment Scores:
Pred. No.: 1.26e-278 Length: 837
Score: 2844.00 Matches: 558
Percent Similarity: 80.10% Conservative: 114
Best Local Similarity: 66.51% Mismatches: 159
Query Match: 47.85% Indels: 8
DB: 2 Gaps: 6

US-09-396-985B-5 (1-3395) x AAW86361 (1-837)
QY 263 ATGCTCTTCGATCGTGGAGCTGATCATGCGATG--TTGCTTTCTGCTG 319
DB 1 MetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCysVal 20
QY 320 AGACCAAGAGCTTGAATCCCTGATAGAGTACTTCTTAATATTACTTACCAATGATG 379
DB 21 ArgProGluSerTrpGluProCysValGluVal---ProAlaIleThrTyGlnGlyMet 39
QY 380 GATCAGAAATTCGACAAATCCCTGATGACATCCCTTATTACCAAGAAAGCTAGATCTG 439
DB 40 GluLeuAsnPheTyrLeuIleProAspAsnLeuProPheSerThrLeuAsnLeuAspLeu 59

QY 440 AGCTCAACCCCTGAGAGATCTTAAGAGCTATAGCTCAGCAATTTCTCAGACTTCAG 499
DB SerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeuGln 79
QY 500 TGGCTGATTTATTCAGGTGTGAAATTGAGCAATTTGAAGACAAAGCAGTGCCTTA 559
DB 80 ValLeuAspLeuSerArgCysGluIleGlnTrpIleGluAspGlyValTyrGlnSerLeu 99
QY 560 AACCACTCTCAACCTTGATGATGACAGAAACCCATGACAGGTTTCCCGAGAGT 619
DB 100 SerHisLeuSerThrLeuIleLeuTrpGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
QY 620 TTTTCTGACTAATTTAGAAATCTGTGCTGTGTGAGACAAATAATGACCTCTTA 679
DB 120 PheSerGlyLeuSerSerLeuGlnIleValAlaValGluThrAsnLeuAlaSerLeu 139
QY 680 GAGGTTTCANATTTGACAGCTTATATCTTAAGAAATCTAAATGTGCTCAATCTT 739
DB 140 GluAsnPheProIleGlyHisLeuIleGlyThrLeuIleGlyValAlaHisAsnLeu 159
QY 740 ATACATTTCTTTAAGTTCCTGAAATTTTCTTAATCTGACAAACCTAGAACATGAGAT 799
DB 160 IleGlnSerPheLeuProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeuAsp 179
QY 800 CTTTCTTATACATATATTCAAACTATTCTGTCAAGACTTACAGTTTCTACGTCGAAAT 859
DB 180 LeuSerSerAsnIleGlnIleSerIleTyrCysThrAspLeuArgValLeuHisGlnMet 199
QY 860 CCCCAAGTCATCTCTTTTGAACCTGTCTTTAAACCAATGATTCATTCAGCCCA 919
DB 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnProGly 219
QY 920 GCCTTCAGGAATTTGGCTCCATGAAATGACCTTAAGAACTTAATTTATAGCTCAAT 979
DB 220 AlaPheLeuGluIleArgLeuHisIleLeuThrLeuArgAsnHisPheSerLeuAsn 239
QY 980 GATCTGAAATATGCTCTTCAAAACATGACTGTATTATCATGTCATCGTTGATCTTGGGA 1039
DB 240 ValMetLeuThrCysIleGlnIleGlyLeuAlaGlyLeuGluValHisArgLeuValLeuGly 259
QY 1040 GAATTTAAATGAAAGAAATCTGAAAGATTTTGACCGTCTGTCAATGGAAGAACTATGC 1099
DB 260 GluPheArgAsnGluGlyAsnLeuGluIlePheAspIleSerAlaLeuGluGlyLeuCys 279
QY 1100 AATGTAGCATTTAGATGATTCAGTTAACAATATTAATATTTTCAGATGATATTAT 1159
DB 280 AsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIleIle 299
QY 1160 AATCTC--AATTGCTTGCGAAATATTTCTGCAATGCTTTCAAGGTGTACATATAAA 1216
DB 300 AspLeuPheAsnIleCysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGlu 319
QY 1217 CACATGACAGATGTTCTTAGGCAATTTCAATGCGAATCTTATCATCATTAATGATGTCAT 1276
DB 320 ArgValIleAspPheSerTyrAsnPheGlyTrpGlnHisLeuLeuValAsnCysIle 339
QY 1277 CTTAAGCTTTTCCAAAGCTGAGTCACTTTTCTTAAGAGTGAACCTTAACCTAACAC 1336
DB 340 PheGlyGlnPheProThrLeuIleLeuIleValSerLeuIleValArgLeuThrPheThrSerAsn 359
QY 1337 AGAGAGATATCAGCTTTGGTCAAGTGGCTGCTGCGCAAGTCCAGATATCTTAGTCTTAGT 1396
DB 360 LysGlyIleValAsnAlaPheSerGluValAspLeuProSerLeuGluIlePheLeuAspLeuSer 379
QY 1397 AGAAATGCCATGAGCTTTAAGAGTGTGCTGTCTTATTCTGATTTTGGAAACAAACCTG 1456
DB 380 ArgAsnIleLeuSerPheIleGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu 399
QY 1457 AAGTACTTAAAGCTCAGCTCAATGAGTGCATCTGATGAGTGCACAACTTCAAGGCTA 1516
DB 400 LysTyrLeuAspLeuSerPheAsnGlyValIleThrPheSerSerAsnPheLeuGlyLeu 419
QY 1517 GAAGAGCTGGAATATCTGAGACTTTCAGACATTCACCTTAATAAAGTCACAGAAATCTCA 1576

```

Db      420  GlnGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPheSer 439
Qy      1577  GTGTTCTATCTCTGAAAAAATCTTTACCTTGACATCTCTTACCAATATCCAAAT 1636
Db      440  ValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisIleThrIleThrVal 459
Qy      1637  GACTTTGATGCGATATTTCTTGAGTCAGTCCACACTTAAATGAGCTGGCAAT 1696
Db      460  AlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGlyAsn 479
Qy      1697  TCTTTCAAGACACACACCTTTCAATGTCTTTACAAACACAAACAACTTAACTTCGTG 1756
Db      480  SerPheGlnGlnAsnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPheLeu 499
Qy      1757  GATCTTTTAAATGCGCACTGGAACAGATATCTAGGGGGGATTTGACACACTCTACAGA 1816
Db      500  AspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSerSer 519
Qy      1817  CTCCAGTATTTAAACATGATGACAAACAACTACTGTTCTTGATCCATCCATTAATAA 1876
Db      520  LeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyrLys 539
Qy      1877  CAGCTGTACTCCCTCAGACCTTTGATTGACAGTTTCAATCGCATAGACATCC--AAA 1933
Db      540  CysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLysLys 559
Qy      1934  GGAATATCTGCAACATTTTCCAAAGCTAGCCGCTTCATCTGACATTAATATCTCTGT 1993
Db      560  GlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
Qy      1994  GCTTGATATGATGATATCAGAAATTTCTTGACAGTGGTCAAGAGACCAAGAAATGTTCTG 2053
Db      580  AlaCysThrCysGlnHisGlnSerPheLeuGlnTrrIleLysAspGlnArgGlnLeuLeu 599
Qy      2054  GTGAATGTTGAACAATGAATGTGCATCACCATTATGACATGAGAGCCTCCCTGGTGTG 2113
Db      600  ValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProValLeu 619
Qy      2114  GATTTTGAATTCACCTGTTATATATCAAGATATCATCATCAGTATCGGTGTCGT 2173
Db      620  SerLeu--AsnIleThrCysGlnMetAsnIleThrIleGlyValSerValLeuSer 638
Qy      2174  GTGCTTGATGAGCCTGATGATCTGATATTCACACTTATTTTCACTGATATCTT 2233
Db      639  ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeu 658
Qy      2234  ATTGCTGCTGTAAAGATACAGACAGAGAGAAAGCATCTATGATGCAATTTGTGATTCAC 2293
Db      659  LeuAlaGlyCysIleTyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIleTyr 678
Qy      2294  TCGAGCCGAATGAGACTGGGTGAGAAACAGACCTGTAAAGATTTTGAAGAGAGATG 2353
Db      679  SerSerGlnAspGlnAspTrrValArgAsnGlnLeuValLysAsnLeuGlnGlnGlyVal 698
Qy      2354  CCCGCTTGAGCTTGCTTCATATACAGAGGACTTATTCGGGTGAGCATTTGCTGTCGC 2413
Db      699  ProProPheGlnLeuCysLeuHisIleTyrArgAspPheIleProGlyValAlaIleAla 718
Qy      2414  AACATCATCAGAGAGCTTCCACAAAGCCGGAAGTTATTTGGTGGTGTCTAGACAC 2473
Db      719  AsnIleIleHisGlnGlyPheHisIleLysSerArgLysValIleValValSerGlnHis 738
Qy      2474  TTTATTCAGAGCCGTGGTGTATCTTTAAATATGAGATGTCTCAGACATGCGCATTTCTG 2533
Db      739  PheIleGlnSerArgTrrCysIlePheHisIleTyrGlnIleAlaGlnThrIleGlnPheLeu 758
Qy      2534  AGTAGCCCTCTGGCATCATCTTCTCTGAGAAAGTGAAGTGAAGTCTGCTGAGG 2593
Db      759  SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg 778
Qy      2594  CAGCAGGTGCAATTTGATCGCTTTTGAAGAAACACTTACTGAGTGGAGAGACAT 2653

```

```

Db      779  GlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTrrGlnAspSer 798
Qy      2654  GCTCTGGGGAGAGCATCTTCTGAGAGAACTCAAAAAGCCGTGGAGAGAAAGCC 2713
Db      799  ValLeuGlyArgHisIlePheTrrArgArgLeuArgLysAlaLeuAspGlyLysSer 818
Qy      2714  TTGATCCAGAT-----GAAACATCAGAGAGAGAAACAAAGAAACAACTTTG 2761
Db      819  TrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrrGlnIleAlaThrSerIle 837

RESULT 7
AAE16102
ID  AAE16102 standard; protein; 837 AA.
AC  AAE16102;
DT  26-MAR-2002 (first entry)
DE  Human DNAX Toll like receptor (DTLR) 4 #2.
KW  Human; DNAX Toll like receptor; DTLR; therapy; immunological disorder;
OS  Interleukin 1; IL-1; screening; immunomodulator; chromosome 9q32-33.
XX  Homo sapiens.
XX  MO2001.90151-A2.
XX  29-NOV-2001.
XX  23-MAY-2001; 2001WO-US016766.
XX  25-MAY-2000; 2000US-0207558P.
XX  (SCHE ) SCHERING CORP.
XX  Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SWK, Liu Y,
XX  WPI; 2002-083085/11.
XX  DR  N-PSDB; AAD26292.
XX  PT  New DNAX Toll like receptor (DTLR) proteins, useful for treating
XX  conditions exhibiting abnormal expression of the receptors of their
XX  ligands, particularly abnormalities manifested by immunological
XX  disorders.
XX  Claim 3; Page 41; 297bp; English.
XX  PS
XX  CC  The invention relates to mammalian receptor proteins, e.g., primate,
XX  human DNAX Toll like receptor (DTLR) protein and their corresponding
XX  nucleic acids. The DTLR is useful for treating conditions exhibiting
XX  abnormal expression of the receptors of their ligands. Such abnormality
XX  is manifested by immunological disorders. In particular, the DTLR is
XX  useful for treating various disease or disorders associated with abnormal
XX  expression or abnormal triggering of response to a ligand. The DTLR is
XX  also useful as an immunogen for the production of antisera or antibodies
XX  specific, e.g. capable of distinguishing between other interleukin (IL)-1
XX  receptor family members, for the DTLR or its various fragments. The
XX  purified DTLR can be used to screen monoclonal antibodies or antigen-
XX  binding fragments. The antibodies are useful for screening expression
XX  libraries for particular expression products. These are useful for
XX  detecting or diagnosing various immunological conditions related to
XX  expression of DTLR or cells that express it. The present sequence is
XX  human DTLR4 protein. The DTLR4 gene is located on chromosome 9q32-33.
XX  Note: The present sequence SEQ ID NO 26 is stated to be similar to the
XX  sequence shown in page 240-243 (AAE16116). However these sequences differ
XX  at several locations
XX  XX
XX  Sequence 837 AA:
XX
XX  Alignment Scores:
XX  Pred. No.: 1,26e-278 Length: 837
XX  Score: 2844.00 Matches: 558
XX  Percent Similarity: 80.10% Conservative: 114

```


QY 2354 CCGCGCTTTCAGCTTGGCTTCATTCAGGAGCATTTATTCCTGGTGTAGCCATGCTGCC 2413
D 699 PropioninleuCyLeuHieTyArgAspPheileProGlyValAlaileHala 718
QY 2414 AACATCATCCAGGAAGGCTTCCACAAAGCCGGAAGTTATTTGGTGTCTTACAC 2473
D 719 AsnIleileHsGluGlyPheHieLysSerArgValileValValSerGlnHs 738
QY 2474 TTATTCAGAGCCGCTGGTGTATCTTTGATATGATGATGCTCAGACATGGCAGTTCTG 2533
D 739 PheileGlnSerArgTTPCyAliePheGlnTyGlnileAlaGlnHTrTPGlnPheleu 758
QY 2534 AGTACCGCTGTGGCATCATCTTCATTCCTTGAAGAAAGTGAAGTCTTGTGTAGG 2593
D 759 SerSerArgAlaGlyIleilePheileValleuGlnValGlnTyThreleuArg 778
QY 2594 CAGCAGGTTCGAATGTATGCTGCTTTTGAGCAAAACACTTACCTGAGTGGAGGACAT 2653
D 779 GlnGlnValGlnleuTyArgleuLeuSerArgAsnHTrTyLeuGlnTrpGlnAspSer 798
QY 2654 GCTCTGGGAGGACATCTTCTGAGAGAGCTCAAAAAGCCCTTGGATGAAAGCC 2713
D 799 ValleuGlyArgHsilePheHTrpArgArgleuArglyAlaLeuAspGlyLysSer 818
QY 2714 TTGAATCCAGAT-----GAAACATCAGAGGAACAAGCAACACTTGG 2761
D 819 TrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerile 837
RESULT 8
ABU04776 :
ID ABU04776 standard; protein; 837 AA.
XX ABU04776;
AC
XX
DT 29-JAN-2003 (first entry)
DE Human expressed protein tag (EPT) #1442.
XX
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukemia.
XX
OS Homo sapiens.
XX
XX W0200278524-A2.
FN
XX
PD 10-OCT-2002.
XX
PF 28-MAR-2002; 2002WO-US009671.
XX
XX 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
XX
XX (ZYCO-) ZYCOs INC.
PA
XX
PI Chicx RM, Tomlinson AJ, Urban RG;
XX
XX WPI; 2003-040607/03.
XX
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 1442; 134pp; English.
XX
XX The invention describes a purified polypeptide, which comprises a

CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_sequences
XX
SQ Sequence 837 AA;
Alignment Scores:
Pred. No.: 1,266-278 Length: 837
Score: 2844.00 Matches: 558
Percent Similarity: 80.10% Conservative: 114
Best Local Similarity: 66.51% Mismatches: 159
Query Match: 47.85% Indels: 8
DB: 6 Gaps: 6
US-09-396-985B-5 (1-3395) x ABU04776 (1-837)
QY 263 ATGCTCTCTTGCATCTGCTGGACCTGTGATCAGCATG--TTCTTCTTCTGCTG 319
D 1 MetSerAlaSerArgleuAlaGlyThreleuLeuProHlaMetAlaPheleuSerCysVal 20
QY 320 AGACGAGAAAGCTTGAATCCCTGCATAGAGGACTTCTTATTTACTTACCAATGCATG 379
D 21 ArgProGlnSerTrpGlnProCysValGlnVal--ProAsnIleHTrTyGlnCysMet 39
QY 380 GATCAGATCTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGAACTGATCTG 439
D 40 GlnleuAsnPheTyRlySileProAspAsnleuProPheSerHTrTySAsnleuAspLeu 59
QY 440 AGCTTCAACCCCTGAGATCTTGAAGGATAGTACTTCAACCAATTTCTGCAACCTTCA 499
D 60 SerPheAsnProleuArgHsileuGlySerTySerPheSerPheProGlnleuGln 79
QY 500 TGGCTGATTTATTCAGGTGTGAATTAAGACAAATTGAAGCAAGCATGGCATGGCTTA 559
D 80 ValleuAspLeuSerArgCysGlnIleGlnHTrIleGlnAspGlyAlaTyArgGlnSerleu 99
QY 560 AACAGCTCAACCTTGGTGTAGCAGAAACCTTCAAGAGTTTCCCGCAGAACT 619
D 100 SerHsleuSerHTrleuIleleuThrglyAsnProIleGlnSerleuAlaLeuGlyAla 119
QY 620 TTTTCTGAGTAAACAATTTTGAAGATCTGTGGCTGTGAGCAAAATGACCTCTCTA 679
D 120 PheSerIlyleuSerSerleuGlnlyleuValAlaValGlnHTrAsnleuAlaSerleu 139
QY 680 GAGGTTTCATATTTGACAGCTTATATCTTAAAGAACTAAATGGTGCATATATCTT 739
D 140 GlnAsnPheProIleGlyHsileuTyThreleuGlnleuAsnValAlaHsAsnleu 159
QY 740 ATACATTCCTTTAAGTGGCTGAAATATTTTCTTAAATGACAAACCTTGAACATGTGAT 799
D 160 IleGlnSerPheTySileuProGlnTyPheSerAsnleuHTrAsnleuGlnHsleuAsp 179
QY 800 CTTTCTTATATATATTTCAAACTATTTCTGTCAAAAGCTTACAGTTCTTACGTAAT 859
D 180 LeuSerSerAsnlySileGlnSerIleTyCyThrAspLeuArgValleuHsleuMet 199
QY 860 CCCCAAGTCAATCTCTTTAGACCTGTCTTAAACCAATGACATTCATCAAGCCAA 919
D 200 ProleuAsnleuSerleuAspLeuSerleuAsnProMetAsnPheIleGlnProGly 219

QY	920	ACCTTTCAGGGAAATTAAGGCTCCAGAAATTAAGTCTGTAACAAATAATATTTTAATTAAGCTCAAT	972
Db	220	AlaPheIlySGuIIleArgLeuNIleValSerThrLeuAlaGlyAsnAlaPheAspSerLeuAsn	239
QY	980	GTACTGAAAAATGTGGCTTCAAAACACATGACTGGTTTACATGTCCATCGGTTGATCTTGGGA	1039
Db	240	ValMetIyStrCyIIleGlnGlyLeuAlaGlyLeuGluValIleIleValGlyLeuValLeuGly	259
QY	1040	GAATTTAAAAATGAAAGGAATCTGGAAAGTTTGAACGCTTGTCTGACGAAGAAGCTATGC	1099
Db	260	GIuPheArgAsnGluGlyAsnLeuGluIlySerPheAspIySerAlaLeuGluGlyLeuGly	279
QY	1100	AATGAGACATTTAGATTCAGGTTACATATATTAATTCATTTTCAGATGATTTAT	1155
Db	280	AsnLeuThrIIleGluGluPheArgLeuAlaTyrlLeuAspTyrlTyrlLeuAspAspIIle	299
QY	1160	AATCTC---AATGTGCTGGCAAAATTTCTGCAAGTCTTTCACAGGTGTCATATATAA	1216
Db	300	AspLeuPheAsnCySleuThrAsnValSerSerPheSerLeuValSerValThrIIleGlu	319
QY	1217	CACATGACAGATGTTCTTAGGATCTTCAATATGCAATCCTTATCATCATTAATGTCAT	1276
Db	320	ArgValIyAspPheSerTyrlAsnPheGlyTyrlGlnIleSleuGluLeuValAsnCySly	339
QY	1277	CTTAAGCCTTTTCCAAAGCTAGTCTACCTTTCTTAAAAAGTTAGACTTTAACTCAAC	1336
Db	340	PheGlyGlnPheProThrLeuIlySleuIySerLeuIyAsuGlyLeuThrPheThrSerAsn	359
QY	1337	AGAGAGATATCAGCTTGTGTCAGTGGCTGCGCAAGTCCAGATATCTAGATCTTGT	1396
Db	360	IySGIyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeuSer	379
QY	1397	AGAAATGCCATGACGCTTTAGAAGTGTCTGTTCTTATTTGATTTTGGAAACAACCTG	1456
Db	380	ArgAsnGlyLeuSerPheIyGlyIyCySerGlnSerAspPheGlyThrThrSerIeu	399
QY	1457	AAGTACTTAAGACTTACGCTTCAATGCTGTCACTCGATGAGTGGCACTTATGAGGTGA	1516
Db	400	IyStrTyrlLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu	419
QY	1517	GAGAGCTGGAATATCTGAGACTTTGACAGATCCACTTTAAAAAGGTGACAGAAATTTCA	1576
Db	420	GIuGlnLeuGluIleAsnAspPheGlnIleSleAsnLeuIySGIleMetSerGluPheSer	439
QY	1577	GTGTCTTATCTCTTGGAAAACTTGTTCATCTTGAACATCTGTGATCACTTAATACCAAAAT	1636
Db	440	ValPheLeuSerLeuAspAsnLeuIeTyrlLeuAspIleSerIleThrIleThrArgVal	459
QY	1637	GACTTGTATGGCAATTTCTTGCTGTATCACTGTCAACACTTTAAAAATGAGTGGCAAT	1696
Db	460	AlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuIyMetAlaGlyAsn	479
QY	1697	TCTTTCAAGACAAACACCTTTCAAAATGCTTTAAACACACAAACCTTAAACATTCCTG	1756
Db	480	SerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuAspAsnLeuThrPheLeu	499
QY	1757	GATCTTTTAAATGCGCAACTGGAAACAGATATAGAGGGGATATTGACAACTTACAGAA	1816
Db	500	AspLeuSerGlnCyGlnLeuGluIleuSerProThrAlaPheAsnSerLeuSerSer	519
QY	1817	CTCCAGTTATTAACATGATGACAAACACTTACTGTTTCTGGATTCATCCCATTAATAA	1876
Db	520	LeuGlnValIleuAsnMetSerIleAsnAsnPhePheSerLeuAspThrPheProTyrlIy	539
QY	1877	CAGCTGTACTCCCTGAGACCTTGTATGCACTTTCATTCGATAGACATCC---AAA	1933
Db	540	CysLeuAsnSerLeuGlnValIleuAspTyrlSerLeuAsnIleIleMetThrSerIyIyAs	559
QY	1934	GGAAATCTGCAACATTTTCCAAAGAGCTAGACCGCTTCAATCTGACATTAATCTGTG	1993
Db	560	GIuGluLeuGlnIleIlePheProSerSerIleuAlaPheLeuAsnLeuThrGlnAsnAspPhe	579
QY	1994	GCTTGTATATGTGAATATCAGAAATTTCTTGACAGTGGGTCAAGGACAGAAAAATGTTCTTG	2053

[illegible]

PD 29-NOV-2001.
 XX 23-MAY-2001; 2001WO-US016766.
 XX 25-MAY-2000; 2000US-0207558P.
 XX (SCHE) SCHERING CORP.
 XX Hardiman GT, Rock FL, Bazan JF, Kastelein RA, Ho SMK, Liu Y,
 PI WPI: 2002-083085/11.
 DR N-PSDB; AAD26306.
 XX New DNAX Toll like receptor (DTRL) proteins, useful for treating
 PT conditions exhibiting abnormal expression of the receptors of their
 PT ligands, particularly abnormalities manifested by immunological
 PT disorders.
 XX Claim 3; Page 240-243; 297pp; English.
 PS The invention relates to mammalian receptor proteins, e.g., primate,
 CC human DNAX Toll like receptor (DTRL) protein and their corresponding
 CC nucleic acids. The DTRL is useful for treating conditions exhibiting
 CC abnormal expression of the receptors of their ligands. Such abnormality
 CC is manifested by immunological disorders. In particular, the DTRL is
 CC useful for treating various disease or disorders associated with abnormal
 CC expression or abnormal triggering of response to a ligand. The DTRL is
 CC also useful as an immunogen for the production of antisera or antibodies
 CC specific, e.g., capable of distinguishing between other interleukin (IL)-1
 CC receptor family members, for the DTRL or its various fragments. The
 CC purified DTRL can be used to screen monoclonal antibodies or antigen-
 CC binding fragments. The antibodies are useful for screening expression
 CC libraries for particular expression products. These are useful for
 CC detecting or diagnosing various immunological conditions related to
 CC expression of DTRL or cells that express it. The present sequence is
 CC human DTRL4 protein, alternative version. The DTRL4 gene is located on
 CC chromosome 9q32-33. Note: The present sequence SEQ ID NO 26 is stated to
 CC be similar to the sequence shown in page 41 (AAE16102). However these
 CC sequences differ at several locations
 XX
 SO Sequence 837 AA;
 Alignment Scores:
 Pred. No.: 6,47e-278 Length: 837
 Score: 2837.00 Matches: 557
 Percent Similarity: 79.98% Conservative: 114
 Best Local Similarity: 66.39% Mismatches: 160
 Query Match: 47.74% Indels: 8
 Gaps: 6
 US-09-396-985B-5 (1-3395) x AAE16116 (1-837)
 QY 263 ATGCTCTTGGATCTGGCTGGAGCTGTGATCATGCGATTG--TTCCTTTCTGCTG 319
 Db 1 MetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCysVal 20
 QY 320 AGACGAGGAGACTGGAATCCCTGCATAGAGTACTCTTAATTAATTAATTAATTAATG 379
 Db 21 ArgProGluSerTrpGluProCysValGluVal--ProAsnIleThrTyrGlnCysMet 39
 QY 380 GATCAGATCTCAGCAAAATCCCTCATAGCATCCCTTAATTAACCAAGCAAGCTGATCTG 439
 Db 40 GluLeuSerPheTyrGlyIleProAspAsnLeuProPheSerThrIleAsnLeuAspLeu 59
 QY 440 AGCTTCAACCCCTGGAAGATCTTAAGAGCTTATGCTTACCAATTTTCAAACTTGA 499
 Db 60 SerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeuGln 79
 QY 500 TGGCTGATTTATTCAGGCTGTGAATTAAGCAATTAAGCAAGGCAATGCGATGCTTA 559
 Db 80 ValLeuAspLeuSerLeuArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSerIle 99
 QY 560 AACGAGCTCTCAACCTTGATCTGACAGAGAAACCTTATCAAGAGTTTTCACAGAGAGT 619

Db 100 SerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
 QY 620 TTTTCTGAGTAACAATTTTGAATCTGGTGGCTGGAGAGCAAAAATGACCTCTGTA 679
 Db 120 PheSerGlyLeuSerSerLeuGlnLeuValAlaValGluThrAsnLeuAlaSerIle 139
 QY 680 GAGGCTTTCATATTTGACAGCTTATATCCCTTAAGAAATTAATGCTCATATCTT 739
 Db 140 GluAsnPheProIleGlyHisLeuLeuThrLeuLeuGluLeuAsnValAlaHisAsnLeu 159
 QY 740 ATACATCTTTAAGTGGCTGAAATATTTTCTTAATGACAAACCTTAAGATGATGAT 799
 Db 160 IleGlnSerPheLeuProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeuAsp 179
 QY 800 CTTTCTTATATCTATATTAACAATTTTCTGTCACAACTTACAGTTCTTACGTAAT 859
 Db 180 LeuSerSerAsnLeuValIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGlnMet 199
 QY 860 CCCCAAGTCATCTCTTGTAGACCTGTCTTAACCAATTAAGCTCATGACCCCA 919
 Db 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeu--PrometAsnPheIleGlnProGly 219
 QY 920 GCCTTTCAGGAAATTAAGCTTCATGAATTAAGCTTAAGAAATTAATTAATGCTCAAT 979
 Db 220 AlaPheLeuGluIleArgLeuHisIleLeuThrLeuArgAsnAsnPheAspSerLeuAsn 239
 QY 980 GTACTGAAAATNGTCCCTTCAAAAACATGACGCTTATACATGCTCCATGCTGATCTGGA 1039
 Db 240 ValMetLeuThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeuGly 259
 QY 1040 GAATTTTAAATGAAGAATCTGGAAGTTTGAACGCTTCTGCATGAGAGACTATGC 1099
 Db 260 GluPheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeuCys 279
 QY 1100 AATGTAGCATGTAGTGAATGAGTTAATCATATTAATATCAATTTTTCAGATGATTTAT 1159
 Db 280 AsnLeuThrIleGlnGluProArgLeuAlaTyrLeuAspLysTyrTyrLeuAspAspIleIle 299
 QY 1160 AATCTC---AATGCTTGGCAAAATATTTTCGATGCTTTCACAGGCTCATATTA 1216
 Db 300 AspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGln 319
 QY 1217 CACATGACAGATGTCTTACGATTTTCAATTAAGCAATCCCTTATCATCATTAATGTCAT 1276
 Db 320 ArgValIysAspPheSerTyrAsnPheGlyTyrPheIleHisLeuGluLeuValAsnCysLys 339
 QY 1277 CTTAAGCCTTTCCAAAGCTGAGTCTACCTTTTCTTAAGAGTTGACCTTAATCAAC 1336
 Db 340 PheGlyGlnPheProThrLeuLeuLysLeuSerLeuLysArgLeuThrPheThrSerAsn 359
 QY 1337 AGAGAGATATCAGCTTGGTCACTGCTGCTGCAAGTCTGCAATATCTATGATCTTAT 1396
 Db 360 LysGlyIleAsnAlaPheSerGluValAspLeuProSerLeuGlnPheLeuAspLeuSer 379
 QY 1397 AGAAATGCAATGAGCTTATAGAGTGTGCTGTTCTTAATCTGATTTTGAACCAACCTG 1456
 Db 380 ArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu 399
 QY 1457 AAGTACTTAAGACCTCAGCTTCAATGATGTCATCTGATGATGCAACCTTATGAGTCTA 1516
 Db 400 LysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419
 QY 1517 GAAGAGCTGAATATCCTGAGCTTACACATCCCACTTAAAGGTCACAGATTTCTCA 1576
 Db 420 GluGlnLeuGlnHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPheSer 439
 QY 1577 GTGTTCTTATCTCTTGA AAAATCTTCTTACCTTGAACATCTTCACTTAATCAAAAT 1636
 Db 440 ValPheLeuSerLeuAlaGlnLeuIleTyrLeuAspIleSerHisThrHisArgVal 459
 QY 1637 GACTTGAAGCATATTTCTTGGCTTGATGATCTCAACCTTAAATGCTGCGCAAT 1696


```

Db      460 AlaPheAenglyIlePheAenglyLeuSerSerLeuGluValLeuIysMetAlaGlyAsn 479
Qy      1697 TCCTTCAAAAGACACACCCTTTCAAAATGCTTTCAAAACACAAACCTTAACCTTCTG 1756
Db      480 SerPheGlnGluAenPheLeuProAspIlePheThrGluLeuArgAenLeuThrPheLeu 499
Qy      1757 GATCTTCTTAATGCTCAAACTGGAACAGATATCTAGGGGGGATTTGACACACTCTACAGA 1816
Db      500 AspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAenSerLeuSerSer 519
Qy      1817 CTCAGTATTATTAACATGAGTACACAAACCTACTGTTCTTGATCCATCCATTATPAA 1876
Db      520 LeuGlnValLeuAenMetSerHisAsnAenPheSerLeuAenProThrPheProTyrLys 539
Qy      1877 CAGGTGATCCGCCAGAGCTTGAATTCAGTTTCATGCGCATAGAGACATCC--AAA 1933
Db      540 CysLeuAenSerLeuGlnValLeuAenPyrSerLeuAenHisIleMetThrSerLysLys 559
Qy      1934 GGAATTAATCAACATTTTCCAAAGAGTACCGCTTTCATCTGACTAATATATCTGTT 1993
Db      560 GlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAenLeuThrGlnAenAspPhe 579
Qy      1994 GCTTGATATGTAATATCAGAAATTTCTTGACGTGGGTCAAGAGACCAAAATGTTCTTG 2053
Db      580 AlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeuLeu 599
Qy      2054 GTGAATGTTGAACAAATGAATGTGCATCACCCTATAGACATGAAGGCTCCCTGCTGTG 2113
Db      600 ValGluValGluArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProValLeu 619
Qy      2114 GATTTTACGAATTCACCTGTTATATATACAAAGACTATCATCTAGTTCGGTGGTCACT 2173
Db      620 SerLeu---AenIleThrCysGlnMetCasnLysThrIleIleGlyValSerValLeuSer 638
Qy      2174 GTGCTTGAGTACGACCTGATGACATTTCTGATATACCACTTCTATTTTCACTGATACTT 2233
Db      639 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMetLeu 658
Qy      2234 ATTCGCTGCTGTAAATAATACAGACAGAGAAAGCACTTATGATGCACTTGTGATCTAC 2293
Db      659 LeuAlaGlyCysIleLysTyrGlyArgGlyGlnAenIleTyrAspAlaPheValIleTyr 678
Qy      2294 TCGAGCCAGATGAGGACTGGGGTGAAGAACAGCTGTAAAGAAATTTAGAAAGAGATG 2353
Db      679 SerSerGlnAspGluAspTrpValArgAsnGlnLeuValValAenLeuGlnGlyVal 698
Qy      2354 CCCGCTTTCAGCTTGTGCTTCATTAACAGGACCTTATCTGCTGTGACCATGCTGCC 2413
Db      699 ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaAla 718
Qy      2414 AACATCAATCCAGAAAGCTTCCAAAGACCGGAAAGTTATGGGTGGGTCTTACAGAC 2473
Db      719 AsnIleIleHisGlyGlyPheHisIleLysSerArgLysValIleValValValSerGlnHis 738
Qy      2474 TTATTCAGAGCCGCTGCTGATCTTGAATATGAGATTGCTCAGACATGCGAGTTTCTG 2533
Db      739 PheIleGlnSerArgTrpCysIlePheGluTyrGlnIleAlaGlnThrTrpGlnPheLeu 758
Qy      2534 AGTAGCCGCTGTGCATCATCTTCTTCTTGAGAAAGTGAGAGACTCTTGCTGAGG 2593
Db      759 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLeuArg 778
Qy      2594 CAGCAGGTGCAATGTATCGCTTCTTACAGAAACACTTACCTCGAATGGAGAGACAT 2653
Db      779 GlnGlnValGlnLeuTyrArgLeuLeuSerArgAenThrTyrLeuGlnTrpGlnAspSer 798
Qy      2654 GCTCTGGGAGGACATCTTCTGAGAGAGACTCAAAAGCCCTTGATGAGAAAGCC 2713
Db      799 ValLeuGlyArgHisIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 818
Qy      2714 TTGAATTCAGAT-----GAAACATCAGAGAGAAACAAGACCAACTTGG 2761
Db      819 TrpAenProGlnGlyThrValGlyThrGlyCysAenTrpGlnGlnAlaThrSerIle 837

```

```

RESULT 10
AD057797
ID AD057797 standard; protein; 801 AA.
XX
AC AD057797;
XX
DT 12-AUG-2004 (first entry)
XX
DE Squirrel monkey toll-like receptor 4 SEQ ID NO:18.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
XX immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
XX sepsis; severe sepsis; septic shock; asthma; squirrel monkey.
XX
OS Saimiri sciureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 14
FT /label= Leu, Phe
XX
XX W02004042365-A2.
XX
XX 21-MAY-2004.
XX
XX 03-NOV-2003; 2003WO-US036247.
XX
XX 01-NOV-2002; 2002US-0423113P.
XX
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
XX Messier W;
XX
XX WPI; 2004-400726/37.
XX
XX N-PSDB; AD057795; AD057796.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX sequence of the Old World monkey with that of a human.
XX
XX Disclosure; SEQ ID NO 18; 11pp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey
XX comprising comparing the TLR4 polynucleotide sequence of the Old World
XX monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX method of the invention has antibacterial, immunosuppressive, and
XX antiasthmatic activity. The method is useful in identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an Old World monkey where the
XX bacterial infection. The methods, agents and composition are useful in
XX treating sepsis, severe sepsis or septic shock and asthma. The present
XX sequence represents squirrel monkey TLR4.
XX
SQ Sequence 801 AA;
XX
Alignment Scores:
Pred. No.: 8.16e-274 Length: 801
Score: 2796.50 Matches: 539
Percent Similarity: 80.90% Conservative: 105
Best Local Similarity: 67.71% Mismatches: 149
Query Match: 47.06% Indels: 3
DB: 8 Gaps: 3
US-09-396-985b-5 (1-3395) x AD057797 (1-801)
Qy      350 GTACTTCTTAATATTACTTCAATGATGATGATCTCAGAAATCCCTCATGAC 409
Db      1 ValValProAenValThrTyrGlnCysMetGlnLeuAen***TyrLysIleProAspAsn 20
Qy      410 ATCCCTTATTCACCAAGAACTTGATCTGAGCTTCAACCCCTGAAAGATCTTAAAGAC 469
Db      21 IleProPheSerThrLysAsnLeuAspLeuSerPheAsnProLeuArgHisLeuGlySer 40

```


470 TATAGCTTCAAAATTTCTCAAACTGAGTGGATTTATCCAGGTGGAATTAG 529
 41 HisSerPhePheAsnPheProGluLeuGlnValLeuAspLeuSerArgCysAspIleGln 60
 530 ACAATTGAAGCAAGGATGCGATGCTTAAACAGCTCTCAACCTTGGTATGACAGA 589
 61 ThrIleGluAspGlyAlaTyrGlnSerLeuSerHisIleuSerThrIleuThrGly 80
 590 AACCTATCAAGAGTTTCCCAAGAGTTTCTGAGCTATCAAAATTTAGAGAAATG 649
 81 AsnProIleGlnAsnLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnValSer 100
 650 GTGGCTGGAGACAAAATGACCTCTAGAGGGTTTCCATATGACACCTTATATCC 709
 101 ValAlaValGluThrHisIleuLeuSerLeuGlnAsnPheProIleGlyHisIleuLeuSer 120
 710 TTAAGAACTAATATGCTCATATATCTTATACATTCCTTAAAGTTGCTGAATATTT 769
 121 LeuIysAspLeuAsnValAlaHisIleAsnLeuIleGlnSerPheIysLeuProGluTyrPhe 140
 770 TCTATCTGACAACTGATGATCTGATCTTTCTTATATCTATATCAATATTTCT 829
 141 SerAsnLeuThrAsnLeuGlnHisIleuAspLeuSerSerAsnAsnIleGlnAsnIleTyr 160
 830 GTCAAGACTTACAGTTTCTACGTGAATAATCCCAAGCTCATCTCTTATAGACCTGCT 889
 161 CysIysAspLeuGlnValLeuHisIleGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
 890 TTAACCCCAATGATCTCCATTCAGCCCAAGCCCTTTCAGGGAATTAGGCTCATGAATTG 949
 181 LeuAsnProIleAsnPheIleGlnProGlyAlaPheIysGluIleArgLeuHisIleuLeu 200
 950 ACTGTAAGAGTAATTTTATAGCTCAATATGATCTGAATAATGCTTCAAAACATGACT 1009
 201 ThrLeuArgAsnAsnPheAspSerLeuAsnAlaMetCysThrCysIleGlnGlyLeuAla 220
 1010 GATTACATGTCATCGGTGATCTTGGAGAGATTAAAGATTTAAAGAAAGATCTGGAAAGT 1069
 221 GlyLeuGlnValHisArgLeuValLeuGlyIlePheArgAsnGlnAlaArgAsnIleGlnAsp 240
 1070 TTGAACGCTTGTGATGGAAGACTATGATCAATGATGACATGATGATGATGATGATGATCA 1129
 241 PheAspIysSerAlaIleuGlnGlyLeuCysAsnLeuThrIleAsnGluPheArgLeuAla 260
 1130 TATATAATCATTTTTCAGATGATTTTATATATCTC--AATGCTTGGCAAAATTTCT 1186
 261 TyrLeuAspAspPheLeuAspAspIleIleAspLeuPheAsnCysLeuAlaAsnValSer 280
 1187 GCAATGCTTTCACAGGTGATCATATTAACAACATAGACAGATGTTCTTCAAGGATTTTCAA 1246
 281 SerPheSerLeuValAsnValHisIleIleuArgValGluAspPheSerTyrAsnPheArg 300
 1247 TGGCAATCTTATCATCATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1306
 301 TrpGlnHisIleuGlnLeuValAsnCysValAlaPheGlnGlnPheProPheIleuLeuLys 320
 1307 TTTCTTAAAGTTGACCTTAACTACCAACAGAGATATCAGCTTGGTCACTGAGTGCCT 1366
 321 SerLeuIysArgLeuThrPheThrAlaAsnIysGlyArgAsnHisPheSerGlnValAsp 340
 1367 CTGCAAGCTTCAGATATCTAGATCTTATAGAAATGCAAGAGCTTATAGAGTTGCTGCT 1426
 341 LeuProSerLeuGlnPheLeuAspLeuSerArgAsnGlyLeuSerPheIysGlyCysArg 360
 1427 TCTTATCTGATTTTGAACAACAACCTGGAAGTATGACCTTCAAGCTTCAATGATGCTC 1486
 361 SerGlnSerAspPheGlyThrThrSerLeuIysTyrIleuAspLeuSerPheAsnAspVal 380
 1487 ATCTGATGAGTGCACATTCATGGGCTTAAAGAGCTGGAATACCTGACCTTCAAGAC 1546
 381 IleThrMetGlySerAsnPheLeuGlyLeuGlnGlnIleuGlnHisIleuAspPheGlnHis 400

1547 TCCACTTAAAGATGACAGAAATCTCAGTGTCTTATCTCTTGAAGAAATCTTTTAC 1606
 401 SerAsnLeuIysGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTyr 420
 1607 CTGACATCTCTTACATTAATACCAAAATGACTTTGATGAGCATATTTCTTGGCTGATC 1666
 421 LeuAspIleSerHisThrHisIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuPhe 440
 1667 AGCTTCAACCTTAAAGATGCTGCAATTTCTTGAAGCAACACCTTCAATGATGC 1726
 441 SerLeuIysValLeuIysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuGluAspIle 460
 1727 TTTCAAAACAACAACCTTAACTTACATTCCTGATCTTTCTAATGCCAATGGAACAGATA 1786
 461 PheThrAspLeuAsnLeuIlePheLeuAspLeuSerGlyCysGlnLeuGlnLeu 480
 1787 TCTAGGGGGGATTTGACACACTTACAGACTCCAGTTATTTAAACATGAGTCAACAAC 1846
 481 SerProThrAlaPheAspSerLeuProArgLeuArgIleLeuAsnMetSerHisAsnAsn 500
 1847 CTACTGTTTCTGATCCATCCCATTAATAACAGCTGACCTCCAGAGACTCTGATGTC 1906
 501 PhePheAlaLeuAspThrPheProTyrLysHisIleuTyrSerLeuGlnValLeuAspTyr 520
 1907 AGTTCAATGCAATGAGACATCCAAAGA--ATATGCAACAATTTTCCAAAGACTTA 1963
 521 SerLeuAsnHisIleGlyThrSerLysAsnGlnGlnLeuGlnHisPheProSerSerLeu 540
 1964 GCCGCTTCAATCTGACTTAATATTTCTGTTGCTTGATATGTAATATCAGAAATTTCTTG 2023
 541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
 2024 CAGGGGTCAACAGACCAAGAAATCTTGTGTGAATCTTGAACAAAGAAATGTCATCA 2083
 561 GlnTrpIleuAspGlnArgLeuValGlnValGlnGlnMetGlyCysAlaThr 580
 2084 CCTATGACATGAAGGCTCCTGCTGTGATTTTCAATTCACCTGTTATATATAC 2143
 581 ProLeuAsnArgIysGlyIleProValLeuSerLeu--AsnIleThrCysGlnMetSer 599
 2144 AAGACTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2203
 600 LysThrIleIleGlyValSerValLeuSerValLeuValAlaSerValAlaValAlaValLeu 619
 2204 AATACCACTTATTTTACCTGATCATCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2263
 620 ValTyrLysPheTyrPheHisIleuMetLeuLeuAlaCysIleTyrGlyArgGly 639
 2264 GAAAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2323
 640 GluAsnThrTyrAspAlaPheValIleTyrSerSerGlnAspGluAspTrpValArgAsn 659
 2324 GAGCTGTAAGAAATTTAAAGAAAGAGTCCCGCTTTCAGCTTGGCTTCACTTATTAACG 2383
 660 GluLeuValIysAsnLeuGlnGlnGlyValIleProProPheGlnLeuCysLeuHisTyrArg 679
 2384 GACTTATCTGCTGATGACCATTCCTGCAACATCATCCAGAGAGCTTCCCAAGAGC 2443
 680 AspPheIleProGlyValAlaIleAlaAlaAsnIleHisGlnGlyPheHisIleuSer 699
 2444 CGAAAGTATATGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2503
 700 ArgLysValIleValValIleValSerGlnHisPheIleGlnSerArgTrpCysIlePheGln 719
 2504 TATGAGATGCTCAGACATGCACTTCTGATGAGCGCTCTGACATCATCTTCAATGCTC 2563
 720 TyrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgIleGlyIleIlePheIleVal 739
 2564 CTGGAAGAAATGAGAGAGCTCTTGTGATGAGAGAGCTGCAATGATGATGATGATGATGATGAT 2623
 740 LeuGlnIysValGlnLysSerLeuArgGlnGlnValGlnLeuIysTyrArgLeuLeuSer 759
 2624 AGAAACCTTACCTCGATGGAGAGCAATGCTCTGGGAGAGGCACATCTTCTGAGAGAGA 2683

Db 760 ArgensthrlyrleuGluTrpGluAspSerValIeuGlyArgHisIlePheTrpArg 779
Qy 2684 CTCAAAAAGCCCTGTGGATGAGAAAACCTTGAATCCAGATGAACA 2731
Db 780 LeuArgysAlaLeuLeuAspGlyArgProTrpAsnProGluGlyThr 795
RESULT 11
AD057791
ID AD057791 standard; protein, 795 AA.
XX
AC AD057791;
XX
DT 12-AUG-2004 (first entry)
XX
DE Rhesus monkey toll-like receptor 4 SEQ ID NO:12.
XX
XX toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW sepsis; severe sepsis; septic shock; asthma; rhesus monkey.
XX
OS Macaca mulatta.
XX
FH Key Location/Qualifiers
FT Misc-difference 635
FT /label= lys, Asn
XX
XX MO2004042365-A2.
XX
XX 21-MAY-2004.
XX
XX 03-NOV-2003; 2003WO-US036247.
XX
XX 01-NOV-2002; 2002US-0423113P.
XX
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX
XX Messier W;
XX
XX WPI: 2004-400726/37.
XX
XX N-PSDB: AD057789, AD057790.
XX
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
PT in treating sepsis and asthma, by comparing the TLR4 polynucleotide
PT sequence of the Old World monkey with that of a human.
XX
XX Disclosure; SEQ ID NO 12; 11bp; English.
XX
XX The invention relates to a novel method for identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an old world monkey
CC comprising comparing the TLR4 polynucleotide sequence of the Old World
CC monkey with corresponding TLR4 polynucleotide sequence of a human. The
CC method of the invention has antibacterial, immunosuppressive, and
CC antiasthmatic activity. The method is useful in identifying a nucleotide
CC change in a TLR4 polynucleotide sequence of an Old World monkey where the
CC change may be associated with reduced sensitivity to Gram-negative
CC bacterial infection. The methods, agents and composition are useful in
CC treating sepsis, severe sepsis or septic shock and asthma. The present
CC sequence represents rhesus monkey TLR4.
XX
XX Sequence 795 AA;
SQ
Alignment Scores:
Pred. No.: 2,14e-272 Length: 795
Score: 2782.50 Matches: 537
Percent Similarity: 81.26% Conservative: 109
Best Local Similarity: 67.55% Mismatches: 146
Query Match: 46.82% Indels: 3
DB: 8 Gaps: 3
US-09-396-985B-5 (1-3395) x AD057791 (1-795)
Qy 350 GTACTTCTAATATATTAACCAATGATGATCAGATCTCAGCAAAATCCCTCATGAC 409

Db 1 ValValProksnIleThrTyrgInCySmetGluLeuAsnPhenTyryIlePheProAsn 20
Qy 410 ATCCCTATTCAACCAAGAACTTAGATCTGAGCTTCAACCCCTGAAAGATCTTAAGAAC 469
Db 21 LeuProPheSerThrIySasnLeuAspLeuSerPheAsnProIeuArgHisIleGlySer 40
Qy 470 TATAGCTTACCAATTTCTCAGACTGAGCTGATTTATTCAGAGTGTGAATTGAG 529
Db 41 TyrSerPhePheSerPheProGluLeuValIeuAspLeuSerTrgysGluIleGln 60
Qy 530 ACAATTGAGACAGGAGCGATGCGCTTAACAGCTCTCAACCTTGATCTGACAGCA 589
Db 61 ThrIleGluAspGlyAlaTyrgInSerLeuSerHisIleSerThrIleuThrGly 80
Qy 590 AACCTTATCAGAGCTTTTCCCAAGAACTTTTCTGAGACTAACAAATTTAGAAATCG 649
Db 81 AsnProIleGlnSerIleuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnTySleu 100
Qy 650 GTGGCTGTGAGACAAAAATGACCTCTAGAGGTTTCCATTTGAGACCTTATATCC 709
Db 101 ValAlaValGluThrAsnLeuAlaSerLeuGluAsnProIleGlyHisLeuTyThr 120
Qy 710 TTAAGAACTTAATGTGGCTCATTAATCTTAATCATTTCTTAAAGTTGCTGAATATTT 769
Db 121 LeuysGluLeuAsnValAlaHisIleAsnLeuIleGlnSerPheTySleuProGluTyPhe 140
Qy 770 TCTAATCTGACCAACCTGAAACATGTGAGATCTTTCTTAATCATTAATTTCAACTATTTCT 829
Db 141 SerAsnLeuThrAsnLeuGluHisIleuAspLeuSerSerAsnTySleuGlnAsnIleTyS 160
Qy 830 GTCMAAGACTTACAGTTTCTACGTTGAAATCCCAAGTCAATGCTCTTATGACCTGTCT 889
Db 161 CyelysAspLeuGlnValIleuHisIleGlnMetProLeuSerAsnLeuSerLeuAspLeuSer 180
Qy 890 TTAACCCCAATGATCTCCATTCAGGCCCAAGCTTTCAAGGAAATGAGCTTCATGATTG 949
Db 181 LeuAsnProIleAsnPheIleGlnProGlyAlaPheTySleuIleArgLeuHisTySleu 200
Qy 950 ACTCTAAGAAATTAATTTAATAGCTCAATGTACTGAAATGTGCGCTTCAAAACATGACT 1009
Db 201 ThrIeuArgSerAsnPheAspLeuAsnValMetTySleuThrCySleuGlnTySleuAla 220
Qy 1010 GGTTACATGCTCATGGCTGATCTTGAGAGATTTTAAATGAATGAAGATCTGAAAGT 1069
Db 221 GlyLeuGluValHisArgLeuValIleuGlyGlnPheArgHisGlnArgHisGluGlu 240
Qy 1070 TTGACCGTTCTGTGATGAGAGGACTATGCAATGTGAGCATTTAGATGCTCAGGTTTACA 1129
Db 241 PheAspTySleuSerIleuGluGlyLeuCyAsnLeuThrIleGluGluPheArgLeuThr 260
Qy 1130 TATATAATCATTTTTCAGATGATATTATTAATCTC---AATTGCTTGGCAATATTCTT 1186
Db 261 TyryLeuAspTyryTyryLeuAsnIleIleAspLeuPheAsnTySleuAlaAsnValSer 280
Qy 1187 GCATGCTCTTTCACAGGTGTACATATPAAACACATAGACATGTCTCTAGGCAATTTCAAA 1246
Db 281 SerPheSerIleuValSerValSerIleTySleuArgValGluAspPheSerTyraAsnPhArg 300
Qy 1247 TGGCAATCTTATCAATCATTTAGATGTCATCTTAAGCTTTTCAAGCTGAGTCACT 1306
Db 301 TrpGlnHisIleuGluLeuValAsnCyTySleuPheGluGlnPheProThrLeuGluLeuGlu 320
Qy 1307 TTTCTTAAAAGTTGAGCTTTTAATCTACCAACAGAGAGATTCAGCTTTGCTCAGTTGGCT 1366
Db 321 SerIeuTySleuArgLeuThrPheThrAlaAsnTySleuGlyTySleuAlaPheSerGluValAsp 340
Qy 1367 CTGCGAAGTCTCAGATATCTAGATCTTAGTGAAGAAATCCATGAGCTTTAGAGGTTGCTGT 1426
Db 341 LeuProSerLeuGluLeuLeuAspLeuSerTyraAsnGlyLeuSerPheTySleuGlyCyS 360
Qy 1427 TCTTATCTGATTTTGGACAAACCAACTGAACTTATGACTCAGCTTCAATGCTGTCT 1486

```

Db      361 SerGlnSerAspPheGlyThrThrSerLeuYsTYrLeuAspLeuSerPheAsnAspVal 380
Qy      1487 ATCTGATGAGTGGCAACTTCATGGGTCTAGAGAGCTGGAATATACCTGCACTTTCAGCAGC 1546
Db      381 IleThrMetSerSerAsnPheLeuGlyLeuGlnYsLeuGlnHisLeuAspPheGlnHis 400
Qy      1547 TCCACTTTAAAAAGTCAGAGAAATTCAGTGTCTTATCTCTTGAAGAACTTCTTATAC 1606
Db      401 SerAsnLeuYsGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleYr 420
Qy      1607 CTGACATCTCTTACATTAATCCAAATATGACTTGTGATGCAATTTCTTGAGCTTGTATC 1666
Db      421 LeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAspIleLeuLeu 440
Qy      1667 AGTCTCAACACTTTAAAAATGCGTGGCAATTTCTTCAAGAACACACCCTTCAATGTC 1726
Db      441 SerLeuYsValLeuYsMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIle 460
Qy      1727 TTTACAAACACAAACAACTTAACTTCTGATCTTCTTAAATGCCAACTGGACAGATA 1786
Db      461 PheThrAspLeuYsAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnLeu 480
Qy      1787 TCTAGGGGGGATTTTGACACACTCTACAGACTCCGCTTATTAATGATGACACAAAC 1846
Db      481 SerProThrAlaPheAspThrLeuAsnYsLeuGlnValLeuAsnMetSerHisAsnAsn 500
Qy      1847 CTACTGTTCTGGATCCATCCCATATTAACAGCTGTACTCCCTCAGAGACTCTTATGTC 1906
Db      501 PhePheSerLeuAspThrPheProTYrYsCysLeuProSerLeuGlnValLeuAspYr 520
Qy      1907 AGTTCAATGCCATAGACATCCAAAGAA--ATACTGCAACATTTTCCAAAGATCTA 1963
Db      521 SerLeuAsnHisIleMetThrSerAsnAsnGlnGlnIleGlnHisPheProSerLeu 540
Qy      1964 GCCGCTTCATCTGACTTAATTAATCTGCTGTATATATGTAATACAAATTTCTTG 2023
Db      541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeu 560
Qy      2024 CAGTGGGTCAAGSACCAAGAAATGTTCTTGGAATGTTGAACAAATGAAATGTCATCA 2083
Db      561 GlnTrpIleYsAspGlnArgGlnLeuLeuValGlnAlaGlnArgMetGlnCysAlaThr 580
Qy      2084 CCTATAGACATGAAGGCTCCCTGTGTGTGAATTTTACGAATTCACCTGTTATATAC 2143
Db      581 ProSerAspYsGlnGlnYMetProValLeuSerLeu--AsnIleThrCysGlnMetAsn 599
Qy      2144 AAGACTATCATCAGTGTATCGGTGCTCAGTGTCTTGTTGTTGACCATGATTTCTG 2203
Db      600 LysThrIleIleGlyValSerValPheSerValLeuValIleSerValAlaValLeu 619
Qy      2204 ATATACCACTTCTATTTTACCTGATCTTATTTGCTGCTGCTGAATAAATACAGCAGAGA 2263
Db      620 ValTYrYsPheTYrPheHisLeuMetLeuValAspGlyCysIle**TYrGlyArgGly 639
Qy      2264 GAAAGCATCTATGATGATTTGTGTATCTTACTCGAGCCAGAAATGAGACTGGGTGAAGC 2323
Db      640 GlnAsnIleTYrAspAlaPheValIleTYrSerSerGlnAsnAspTrpValArgAsn 659
Qy      2324 GAGCTGGTAAAGATTTGAAGAGAGAGTCCCGCTTACGCTTTCAGCTTTCATTAACG 2383
Db      660 GluLeuValYsAsnLeuGlnGlnGlyValProPheGlnLeuCYLeuHisIleTYrArg 679
Qy      2384 GACTTATTCCTGGTGTAGCATTTGCTGCCAATCATCCAGAGAGAGCTTCCAGAGAGC 2443
Db      680 AspPheIleProGlyValAlaIleAlaAsnIleIleHisGlnGlyPheHisIleYsSer 699
Qy      2444 CGAAAGTATTTGGTGTGTCTAGACATTTATCCAGACCGTGTGTATCTTTGAA 2503
Db      700 ArgYsValIleValIleValSerGlnHisPheIleGlnSerArgTrpCysIlePheLeu 719
Qy      2504 TATGAGATTGCTCAGACATGGCAGTTTCTGAGTACCGCTTCGACATATCTTCAATGTC 2563
Db      720 TYrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 739

```

```

Qy      2564 CTGAGAAAGTGAAGATCCTTGTGAGCAGAGTCAATTTGATCGCTTCTTAC 2623
Db      740 LeuGlnYsValGlnYsThrLeuLeuArgGlnGlnValGlnLeuTYrArgLeuSer 759
Qy      2624 AGAAACACTTACTCTGAGTGGAGACAAATCTGTGGAGACACATCTTGTGAGAGA 2683
Db      760 ArgAsnThrTYrLeuGlnTrpGlnAspSerValLeuGlnGlnHisIlePheTrpArgArg 779
Qy      2684 CTCAAAAAGCCCTTGTGATGAGAAAGCCCTTGAATCCAGATGAA 2728
Db      780 LeuArgYsAlaLeuLeuAspGlyArgSerTrpAsnProGlnGln 794

RESULT 12
ID      AD057800
XX      AD057800 standard; protein. 795 AA.
AC      AD057800;
DT      12-AUG-2004 (first entry)
DE      Hamadryas baboon toll-like receptor 4 SEQ ID NO:21.
XX      toll-like receptor 4; TLR4; old world monkey; antibacterial;
KW      immunosuppressive; antiasthmatic; Gram-negative bacterial infection;
KW      sepsis; severe sepsis; septic shock; asthma; hamadryas baboon.
XX      Papio hamadryas.
XX      WO2004042365-A2.
XX      21-MAY-2004.
XX      03-NOV-2003; 2003WO-US036247.
XX      01-NOV-2002; 2002US-0423113P.
XX      (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX      Messier W;
XX      WPI; 2004-400726/37.
XX      DR      N-PSDB; AD057798, AD057799.
XX      PT      Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX      in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX      PT      sequence of the Old World monkey with that of a human.
XX      PS      Disclosure; SEQ ID NO 21; 111pp; English.
XX      CC      The invention relates to a novel method for identifying a nucleotide
XX      change in a TLR4 polynucleotide sequence of an old world monkey
XX      comprising comparing the TLR4 polynucleotide sequence of the Old World
XX      CC      monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX      CC      method of the invention has antibacterial, immunosuppressive, and
XX      CC      antiasthmatic activity. The method is useful in identifying a nucleotide
XX      change in a TLR4 polynucleotide sequence of an Old World monkey where the
XX      CC      change may be associated with reduced sensitivity to Gram-negative
XX      CC      bacterial infection. The methods, agents and composition are useful in
XX      CC      treating sepsis, severe sepsis or septic shock and asthma. The present
XX      CC      sequence represents hamadryas baboon TLR4.
XX      SQ      Sequence 795 AA;

Alignment Scores:
Pred. No.:      2,71e-272
Score:          2781.50
Percent Similarity: 81.01%
Best Local Similarity: 67.67%
Query Match:    46.80%
DB:             8
Gaps:           3
Length:         795
Matches:        538
Conservative:   106
Mismatch:       148
Indels:         3

```

US-09-396-985B-5 (1-3395) x AD057800 (1-795)

QY	350	GTACTTCTTAATATTATTAACCTACCAATGCATGCATGCAGATCTCAGCAAAATCCCTCATGCAC	403
Db	1	ValValAlProbaenIlleThrTyrGlnCysMetGluLeuAsnPhenTyrIleProaspaa	20
QY	410	ATCCCTTAATTCACCAAGAACTTAAGTCTGACCTTCAACCCCTCGAAGATCTTAAAGAAC	469
Db	21	IleProPheSerThrIleAsnLeuAspLeuSerPheAsnProLeuArgIleuGlySer	40
QY	470	TATAGCTTACCAATTCTCACAACCTTCAGTGGCTGGATTATTCACAGGTGTGAATGTAG	529
Db	41	TyrSerPheLeuArgPheProGluLeuGlnValIleAspLeuSerArgCysGluIleGln	60
QY	530	ACAAATGGAAGACAGGCGATGGCATGGAACCGAGCTCTCAACCTTGATGTCAGCAGA	589
Db	61	ThrIleGluAspGlyAlaIaryGlnSerIleuSerHisIleSerThrIleuIleuThrGly	80
QY	590	AACCTTATCAGAGTATTTTCCCGAGGAAGTATTTTCTGACATACAAATTTAGAGATCTG	649
Db	81	AsnProIleGlnSerIleuLeuIleuGlnAlaIlePheSerGlyLeuSerSerIleuGlnIleu	100
QY	650	GTGGCTGTGGACCAAAAATGACCTCTCTAGAGGGTTTCCATATTTGGACAGCTTATATCC	709
Db	101	ValAlaValAlaGluThrAsnLeuAlaSerIleuGluAsnPheProIleGlyHisIleuYsrThr	120
QY	710	TTAAAGAAATCTAAATGTGGCTCATATCTTATACATCTCTTAAAGTGTGGCTGAATATTTT	769
Db	121	LeuYsrGluLeuAsnValAlaHisAsnLeuIleGlnSerPheIleuYsrProGluTyrPhe	140
QY	770	TCTAATCTGACAAACCTAGAACATGTGGATCTTTCTTATTAACATAATTCAACTATTCT	829
Db	141	SerAsnLeuThrAsnLeuGlnIleHisLeuAspLeuSerSerAsnIleGlnIleuThr	160
QY	830	GTCAAGAAGATTACAGTTTCTAGTGAAGAAATCCCGAGTCATATCTCTTAAAGCTGTCT	889
Db	161	CysIleYsrAspLeuGlnValIleuHisGlnMetProLeuProAsnLeuSerLeuAspLeuSer	180
QY	890	TTAAACCCCAATTGACTCCATTCAGAGCCCAAGCCCTTTCAGGAGATTAGGCTCCAGATTG	949
Db	181	LeuAsnProIleAsnPhenIleGlnProGlyAlaPheIleGlyValIleArgIleuHisIleu	200
QY	950	ACTCTTAAGAAAGTAAATTTTAAATAGCTCAATGTACTGAATAATGTGCTTCAAAACATGACT	100
Db	201	ThrLeuArgSerAsnPhenAspLeuAsnValMetIleYsrCysIleGlnGlyLeuAla	220
QY	1010	GGTTTACATGCTCCATGGTGTGATCTCTGGAGAAATTAAATAAGAAAGCATCTGCAAGGT	106
Db	221	GlyLeuGlnValHisArgIleuValIleuGlyGlnPheArgAsnGluArgAsnLeuGlnIleu	240
QY	1070	TTTGACCGTTCTGTGATGGAAGGACTATGCAATGTGACGATTCATGATGATTCAGGTTAAC	112
Db	241	PheAspYsrSerAlaLeuGlnIleuGlyLeuCysAsnLeuThrIleGluIleuPheArgLeuThr	260
QY	1130	TATATATAATCATTTTTCAGATGATATTTTAAATCTC---AATAGCTTGGCAATATTTCT	118
Db	261	TyrLeuAspTyrTyrIleuAspAsnIleIleAspLeuPheAsnCysLeuAlaAsnAlaSer	280
QY	1187	GCAATGTCTTTCACAGGTGTACATATATAAACACATGACAGATGTTCTTAGCATTTCAA	124
Db	281	SerPheSerLeuValSerValAsnIleIleYsrArgValGluAsnPhenSerTyrIleAsnPhenArg	300
QY	1247	TGGCAATCTCTTATCAATCATATAGATGTCACTCTTAAGCCTTTTCCAAAGCTGAAGCTTAACT	130
Db	301	TTPGlnHisIleuGlnIleuValAsnCysIleYsrPheGluGlnPheProThrIleuGlnIleuGln	320
QY	1307	TTTCTTAAAGTTGGACCTTAACTTACCAACAGAGAGGATATCAGCTTTGGTCAAGTGGCT	136
Db	321	SerLeuIleYsrArgLeuThrPheThrAlaAsnIleYsrGlyIleAsnAlaPheSerGluValAsp	340
QY	1367	CTGCCAAGTCTCAGATATCTAGATCTTAAAGTAAATGCCATGACGCTTAAAGGTTGCTGT	142
Db	341	LeuProSerIleuGlnIleuLeuAspLeuSerArgIleAsnGlyLeuSerPheIleuYsrGlyCysCys	360

QY	1427	TCGTAATTCGATTTTGGACAACAACAACTGAAAGTACTTAAGCTCACTCACTCAATGAGTGC	1486
		
Db	361	SerGlnSerIlePheGlyThrIleThrSerLeuIleGlyThrLeuAspLeuSerPheAsnAspVal	380
QY	1487	ATCCGATGAGTGGCACTTCATAGGGCTGTAAGAAGCTGGAAATGACCTGGACCTTTCACAC	1546
		
Db	381	IleThrMetGlySerAsnPheLeuGlyLeuGlnIleMetGlnIleValAspPheGlnHis	400
QY	1547	TCCACTTAAAAAGGCTCAGAAATTCCTAGTGTCTTATCTCTTGGAAAACTTCTTAC	1606
		
Db	401	SerAsnLeuIleGlyMetSerGlnPheSerValPheLeuSerLeuValGlnMetIleLeu	420
QY	1607	CTTGACATCTTTACACTAATATCAAAATGACTTTGATGGCATTTCTTGGCTTGATC	1666
		
Db	421	LeuAspIleSerIleIsthrIleIsthrThrValAlaPheAsnGlyIlePheAspGlyLeuLeu	440
QY	1667	AGTCCAAACACTTTAAAAATGGCTGGGCAATCTTTCAAAGAGCAACCCCTTTCAAAATGTC	1726
		
Db	441	SerLeuIleValLeuIleGlyMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIle	460
QY	1727	TTTACAAACAACAACAACTTAAACAATTCCTGGATCTTTCTTAATGCTCACTGGAAACAGATA	1786
		
Db	461	PheThrAspLeuIleValAsnLeuThrPheLeuAspLeuSerGlnIleGlnGlnLeu	480
QY	1787	TCTAAGGGGGATATTGGACACCTGTACAGCTCCAGTTATTAAAACTAGTCCACAAAC	1846
		
Db	481	SerProThrAlaPheAspThrLeuAsnIleGlnValLeuAsnMetSerHisValAsn	500
QY	1847	CTACTGTTCTGGATCCATCCCATTAATTAACAGTGTAACTCCSCCAGAGCTCTTGATTC	1906
		
Db	501	PhePheSerLeuAspValPheProTyrIleGlySerLeuProSerLeuGlnValLeuAspTyr	520
QY	1907	AGTTTCAATCCGATAGAGACACTCAAAAGCA--ATACGCAACAATTTTCCAAAGACTTA	1963
		
Db	521	SerLeuAsnHisIleMetThrSerIleAsnGlnIleIleProGlnIlePheProSerSerLeu	540
QY	1964	GCCGCTTTCATCTGCATATATATATCTGTGGCTGTATATGTGAATATCAGAAATTTCTTG	2023
		
Db	541	AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnIleGlnSerPheLeu	560
QY	2024	CAGTGGGTGACAGAACCAAGAAATGTTCTGTGTAATGTGAACAATAAGTAATGTGCA	2083
		
Db	561	GlnTrrIleIleValAspGlnIleArgGlnLeuLeuValGlnAlaGlnMetGlnCysValThr	580
QY	2084	CCTATGACATGACAAAGGCTCCCTGGATGTGGATTTTACAAATCACTCCGTTATATATC	2143
		
Db	581	ProSerAspIleGlnIleMetProValLeuSer---ValAsnIleThrCysGlnMetAsn	599
QY	2144	AAGACTATCATCAGTGTATCGGTGAGTCAAGTGTGCTGTGTAGACCACTGATGCAATTTCTG	2203
		
Db	601	LysThrIleIleGlyValIleSerValPheSerValLeuValIleSerValIleAlaValLeu	619
QY	2204	ATATTCGCACTGTATTTTCACTGTGATCTATATGTGTGGCTGTAAAAAGTACAGACAGCA	2263
		
Db	620	ValTyrIlePheTyrPheIleValMetSerLeuLeuAlaCysValLeuTyrGlyValArgGly	639
QY	2264	GAAACACATCTGATGATCTGTATGTATCTATCCAGACCAAGATGAGCACTGGGTGACAAAC	2323
		
Db	640	GlnAsnIleTyrAspAlaPheValIleTyrIleSerIleGlnAspGlnIleAspTrrValAlaGln	659
QY	2324	GAGCTGTGAAGAAATTTGAAGAAGAGATGCCSCGCTTTCAGCTTTGGCTTCAATTAACAG	2383
		
Db	660	GlnLeuValIleValAsnLeuGlnGlnGlyValAlaProIlePheGlnIleIleCysValMetIleTyrArg	679
QY	2384	GACTTATATCTCGGTGTAGCCATGTGTGCTGCCAATCATCCAGAAAGCTTTCACAAAGC	2443
		
Db	680	AspPheIleIleProGlyValAlaIleAlaAlaAsnIleIleIleGlnIleGlyIlePheIleIleSer	699
QY	2444	CGGAAGATTAATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	2503
		
Db	700	ArgIleValIleIleValIleValIleSerGlnHisPheIleGlnIleSerAlaGlyTrrCysIlePheIle	719
QY	2504	TATGAGATTTGTCAGACATGTCAGATTTCTGAGTACGCGCTGTGGCATCATCTTCAATTTGTC	2563


```

Db      341 LeuProSerLeuGluPheLeuAspLeuSerArgSangIyluSerPheIySglYcysCys 360
Qy      1427 TCCTATTCGTGATTTTGGAAACAACCTGAGACTTATAGACCTCAGCTTCAATGGTGC 1486
Db      361 SerInSerAerPheGlyThrThrSerIeuSerIyLeuAerPheLeuSerPheAangIylVal 380
Qy      1487 ATCCGTGAGTGCACATTCATGGGCTTGAGNAGAGCTGAAATCTGCACTTTCACAC 1546
Db      381 IleThrSerSerAerAenPheLeuGlyLeuGluGluLeuGluIuhIleAerPheGluIuhIs 400
Qy      1547 TCACCTTAAAAAGTCAAGAAATTCAGTGTCTTATCTCTTGA AAAAATTCTTAC 1606
Db      401 SerAenIeuIySglImeSerGluPheSerValPheLeuSerIeuAurGAsnIleIyX 420
Qy      1607 CTGACATCTCTGATCACTAATACCAAAATGACCTTGAATGCAATTTCTTGGCTTATC 1666
Db      421 LeuAspIleSerHsIsthHsIsthArgValAlaPheAangIylIlePheAangIylLeuSer 440
Qy      1667 AGTCTCAACACTTTAAAAATGGCTGGCAATCTTTCAAGACAACACCCTTTCAAATGTC 1726
Db      441 SerIeuGluValIleuIySgMeAlaGlyAasSerPheGluGluAenPheLeuProAspIle 460
Qy      1727 TTTCAAAACACACAACAACTTAACATTCCTGATCTTTTAAATGCCAATGGAACAGATA 1786
Db      461 PheThrGluLeuAurGAsnIleuThrPheLeuAerPheLeuSerGIncySglIleuGluIleu 480
Qy      1787 TCTAGGGGGGATTTTGGACACACTCTACAGACTCCAGTATTAACATGAGTCAACAAC 1846
Db      481 SerProThrAlaPheAenSerIeuSerSerIeuGluValIeuAenMeSerHsIsthAsn 500
Qy      1847 CTACTGTTTCTGATTCACATCCATTAATTAACAGCTGTATCTCCACAGACTCTTGATTC 1906
Db      501 PhePheSerIeuAerPheThrPheProTylIySyluAenSerIeuGluValIeuAerPheYx 520
Qy      1907 AGTTTCAATGCCATAGACATCC--AAAGAAATCTGCAACTTTTCCAAAGAGCTA 1963
Db      521 SerIeuAenHsIsthIleMetThrSerIySglIleuGluGluIuhIsPheProSerIeu 540
Qy      1964 GCGGCTTCATCTGACTAATTAATTCGTGCTGTATGATGTAATACAGAAATTTCTG 2023
Db      541 AlaPheLeuAenIleuThrGluAasPheAlaCysThrCysGluHsIsthSerPheLeu 560
Qy      2024 CAGTGGGTCAAGACACAGAAATGTTTGGTGAATGTTGAACAATGAATGTCATCA 2083
Db      561 GluIthrIleIySgAerGluAerGluIleuLeuValGluValGluAerMeGluCylAlaThr 580
Qy      2084 CTTATAGACATGAAGGCTCCCTGGTGTGAATTTTACGAATTCACCTGTATATATAC 2143
Db      581 ProSerAerIySglImeSerProAlaIleuSerIeu--AenIleThrCysGluIleMetAen 599
Qy      2144 AAGACTATCATCAGTGTATGGTGTGAGTGTGCTGTGATGAGCACTGTAGCAATTTCTG 2203
Db      600 LysThrIleIleGlyValSerValIeuSerValIeuValIeuValIeuValAlaValIeu 619
Qy      2204 ATATACACTTCTATTTTCACTGATACTTATGCTGCTGTAAATAAGTACAGACAGAGA 2263
Db      620 ValTylIySgPheTylRphHsIleuMetIeuIleuAlaGlyGlyIleTylGlyAlaGly 639
Qy      2264 GAAAGCATGTATGATGCAATTTGTGATCTATCTGAGCCGAATGAGAACTGGGTGAAGAAC 2323
Db      640 GluAenIleTylAspAlaPheValAlaIleTylSerSerGluAerGluAerTylValAlaArgAsn 659
Qy      2324 GAGCGGTGAAGAAATTTGAAGAAGAGAGTGCCTTCAGCTTGGCTTCAATTAACAG 2383
Db      660 GluIeuValIySgAenIleuGluGluIylValProProPheGluIleuCysLeuHsIsthYx 679
Qy      2384 GACTTATTCCTGTGTAGCACTTGTCTGCAACATCATCTCAGAGGCTTCCACAAGAC 2443
Db      680 AspPheIleProGlyValAlaIleAlaIleAasIleIleHsIsthIleGluIyPheHsIsthSer 699
Qy      2444 CGAAAAGTATTTGTGTGTGTGTGTAGACATTTATCCAGACCGTGTGTATCTTTGAA 2503
Db      700 ArgIySgValIleValIleValIleValIleSerGluIsthPheIleGluIsthArgTylPheGlu 719

```

```

Qy      2504 TATGAGATTGCTCAGACATGGCAGTTTCTGAGTAGCCGCTCTGACATCATCTTCAATGTC 2563
Db      720 TyrGluIleAlaGluIthrTrpGluIlePheLeuSerSerArgAlaIleIleIlePheIleVal 739
Qy      2564 CTGAGAAAGTGAAGAAGTCTTGTGAGGACAGAGTGAATGTATGTATGCGCTTCTTAC 2623
Db      740 LeuGluIySgValGluIySgThrLeuAerArgGluValGluIleuTylRArgLeuLeuSer 759
Qy      2624 AGAAACCTTACCTCGAGTGGGAGAGCAATGCTCTGAGGAGAGCAATCTTCTGAGAGA 2683
Db      760 ArgAsthTrpIyLeuGluIyTrpGluAerSerValIleuGlyAArgHsIsthPheThrArgX 779
Qy      2684 CTCAAAAAGCCCTGTGATGAGAAAAAGCTTGAATCCAGAT-----GAAACATCA 2734
Db      780 LeuArgIySgAlaIleuLeuAerGluIySgThrPAsnProGluIleuThrValGluIyThrGly 799
Qy      2735 GAGGAAGACACAAGACCAACTTGTG 2761
Db      800 CysAsthTrpGluIleuAlaThrSerIle 808

RESULT 14
AD057782 standard; protein; 808 AA.
ID AD057782
AC AD057782;
XX 12-AUG-2004 (first entry)
DT 12-AUG-2004
DE Chimpanzee toll-1-like receptor 4 SEQ ID NO:3.
XX toll-1-like receptor 4; TLR4; old world monkey; antibacterial;
XX immunosuppressive; antiaesthetic; Gram-negative bacterial infection;
XX sepsis; severe sepsis; septic shock; asthma; chimpanzee.
XX Pan troglodytes.
XX WO2004042365-A2.
XX 21-MAY-2004.
XX 03-NOV-2003; 2003WO-US036247.
XX 01-NOV-2002; 2002US-0423113P.
XX (EVOL-) EVOLUTIONARY GENOMICS LLC.
XX Meslier W;
XX WPI; 2004-400726/37.
XX N-PSDB; AD057780, AD057781.
XX Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful
XX in treating sepsis and asthma, by comparing the TLR4 polynucleotide
XX sequence of the Old world monkey with that of a human.
XX Example 1; SEQ ID NO 3; 11pp; English.
XX The invention relates to a novel method for identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey
XX comprising comparing the TLR4 polynucleotide sequence of the Old world
XX monkey with corresponding TLR4 polynucleotide sequence of a human. The
XX method of the invention has antibacterial, immunosuppressive, and
XX antiaesthetic activity. The method is useful in identifying a nucleotide
XX change in a TLR4 polynucleotide sequence of an old world monkey where the
XX change may be associated with reduced sensitivity to Gram-negative
XX bacterial infection. The methods, agents and composition are useful in
XX treating sepsis, severe sepsis or septic shock and asthma. The present
XX sequence represents chimpanzee TLR4.
XX Sequence 808 AA;
XX Alignment Scores:

```

Pred. No.: 1.99e-271 Length: 808
 Score: 2773.00 Matches: 540
 Percent Similarity: 80.59% Conservative: 112
 Best Local Similarity: 66.75% Mismatches: 151
 Query Match: 46.66% Indels: 6
 DB: 8 Gaps: 4
 US-09-396-985b-5 (1-3395) x AD057782 (1-808)

350 GACTCTCTAATATATACCAATGCAATGCATGCAATCTGAGCAAAATCCCTGATGAC 409
 1 ValValProbenH1ethrTygIncyswecGluLeuAsnPhetYrLysIleProAspAsn 20
 410 ATCCCTTATTCACCAAGACCTAGATCTGAGCTTCAACCCCTGAAGATTGTAAGAAG 469
 21 LeupProPheSerThrlYsAsnLeuAspLeuSerPheAsnProLeuAArgH1sLeuAlySer 40
 470 TATAGCTTCACCAATTTCTCACAACTTCAGTGGCTGAGATTATTCAGAGGTGAAATTGAG 529
 41 TyrSerPhePheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIleGln 60
 530 ACAATTGAAGACAGACATGAGCATGAGCTTAAACAGCTCTCAACCTTGCTGACAGAGA 589
 61 ThrIleGluAspGlyAlaTygIleSerLeuSerH1sLeuSerThrlLeuH1leuThrGly 80
 590 AACCTATCAAGAGTTTCCCGCAAGATTCTTCGAGCTTCAACAAATTGAGAAATCTG 649
 81 AsnProIleGlnSerLeuH1sLeuGlnAlaPheSerGlyLeuSerSerLeuGlnLysLeu 100
 650 GTGGCTGTGAGACAAAAATGACCTCTGAGAGGCTTTCATATTTGACAGCTTATATCC 709
 101 ValAlaValAlaGluThrAsnLeuAlaSerLeuGlnAsnPheProIleGlyH1sLeuLysThr 120
 710 TTAAGAAACCTAATGTGGCTCATATCTTATATCTCTTAACTGCTGAATATTTT 769
 121 LeuLysGluLeuAsnValAlaH1sAsnLeuIleGlnSerPheLysLeuProGluLysPhe 140
 770 TCTAATCTGACAAACCTGAGAACATGTGATCTTCTTAACTAATTCATATTCATTTCT 829
 141 SerAsnLeuThrlAsnLeuGlnH1sLeuAspLeuSerSerAsnLysIleGlnSerIleTy 160
 830 GTCAAAAGACTTACAGCTTCTAGCTGAAAAATCCCAAGCTCAATCTCTTATAGACCTGTCT 889
 161 CysThrAspLeuArgValLeuH1sGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 180
 890 TTTAAACCAATGATCTCATTCACGCCAAGCTTTCAGGGAATTAGGCTCCATGAATTG 949
 181 LeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuH1sLysLeu 200
 950 ACTCTAAGACGTAATTTATATGATCTCAATATGCAATGCAAAATGTGCTCAAAACATGACT 1009
 201 ThrLeuAlaGlnAsnAsnPheSerSerLeuAsnValMetLysThrCysIleGlnGlyLeuAla 220
 1010 GATTATCATGTCCATCGGTGATCTTGGAGAAATTTAAATGAAGAATCTGGAAAGT 1069
 221 GlyLeuGlnValH1sArgLeuValLeuGlnGlnPheArgAsnGlnGlyAsnLeuGlnLys 240
 1070 TTTGACCGTTCTGTCATGGAAGACTATGCAATGTGAGCATGATGAGTTCAGGTTAAACA 1129
 241 PheAspLysSerAlaLeuGlnGlnLysCysAsnLeuThrlIleGlnGlnPheArgLeuAla 260
 1130 TATATTAATCATTTTTCAGATGATATTTATATATCTC--AATGTGTCGCAAAATTTCT 1186
 261 TyrLeuAspTyTyTyLeuAsnAspIleIleLeuAsnLeuPheAsnCysLeuThrlAsnValSer 280
 1187 GCATGTCTTTCACAGGTGTACATATAAACAACATAGACAGATGTTCTTAGGACATTTCAAA 1246
 281 SerPheSerLeuValSerValThrIleLysSerValLysAspPheSerTyAsnPheGly 300
 1247 TGGCATCTTATCATCATTTAGATGTCAATTTAAGCTTTTCCAAAGCTGAGTTCATCT 1306
 301 TrpGlnH1sLeuGlnLeuValAsnCysLysPheGlnGlnPheProThrlLeuLysLeuLys 320

1307 TTTCTTAAAGCTGGACCTTTTACTACCAAGAGAGATATCAAGCTTGTGTCAGTTGGCT 1366
 321 SerLeuLysArgLeuThrlPheThrlSerAsnLysGlnGlyAsnAlaPheSerGlnValAsp 340
 1367 CTGCCAAGCTTCAGATATCTTGATCTTATGTAAGAAATGCCATGAGCTTTAGAGCTTGCT 1426
 341 LeuProSerLeuGlnPheLeuAspLeuSerArgAsnGlnLysLeuSerPheLysGlyCysCys 360
 1427 TCTTATTCGATTTTGGAAACAACAACCTGAAGAACTTAGACCTCAGCTTCATAGTGTGC 1486
 361 SerGlnSerAspPheGlyThrlThrlSerLeuLysTyLeuAspLeuSerPheAsnIlyVal 380
 1487 ATCCGATGAGTGCACATTCATGAGGTCTTAGAAGAGCTGGAATACCTGAGCTTTCAGCAC 1546
 381 IleThrlMetSerSerAsnPheLeuGlnLysLeuGlnGlnLeuGlnH1sLeuAspPheGlnH1s 400
 1547 TCCACTTTAAAAAGTCCACAGAAATTCAGTGTCTTATCTCTTGAATAAACTTCTTTAC 1606
 401 SerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuArgAsnLeuIleTy 420
 1607 CTGACATCTCTTACATTAATACCAAAATTCATTCATGAGCATATTTCTTGCTGATC 1666
 421 LeuAspIleSerH1sThrlH1sThrArgValAlaPheAsnGlnLysIlePheAsnGlyLeuSer 440
 1667 AGTCTCAACACTTTAAAAATGCTGCGCAATCTTTTCAAGAACACACCCCTTCAATATGC 1726
 441 SerLeuGlnValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIle 460
 1727 TTTACAAACACACAAACCTTAACATTCCTGAGATCTTTCTAATGCCAACCTGAACAGATA 1786
 461 PheThrGluLeuArgAsnLeuThrlPheLeuAspLeuSerGlnGlnLeuGlnLeu 480
 1787 TCTAGGGGGATTTGACACACTTACAGACTCCAGTTATTAACATGACATGACAAACAC 1846
 481 SerProThrlAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerH1sAsnAsn 500
 1847 CTACGTGTTCTGATTCATCCATTAATTAACAGCTGATCTCCCTCAGAGACTCTGATTCG 1906
 501 PhePheSerLeuAspThrlPheProTyTyLeuGlySerLeuAsnSerLeuGlnValLeuAspTy 520
 1907 AGTTCAATGCGATAGACATCC--AAAGAAATCTGCAACATTTTCCAAAGAGCTTA 1963
 521 SerLeuAsnH1sIleMetThrlSerLysGlnGlnLysGlnH1sPheProSerSerLeu 540
 1964 GCCGCTTCAATCTGACTAATAATTTCTGCTGTAATGTGAATACAGAAATTTCTTG 2023
 541 AlaPheLeuAsnLeuThrlGlnAsnAspPheAlaCysThrCysGlnH1sGlnSerPheLeu 560
 2024 CAGTGGGTCAAGACACAGAAATGTTCTTGGTGAATGTTGAACAAATGAATGTGCATCA 2083
 561 GlnTrpIleLysAspGlnArgGlnLeuLeuValGluValGlnArgMetGlnCysAlaThr 580
 2084 CCTATAGACATGAAGGCTCCCTGCTGTGATTTTGAATTCACACCTGTTATATATAC 2143
 581 ProSerAspLysGlnGlyMetProValLeuSerLeu--AsnIleThrCysGlnMetAsn 599
 2144 AAGACTATCATCAAGTATGCTGTGCTCAGTGTCTTGTGAGGCACGTATGACATTTCTG 2203
 600 LysThrIleIleGlyValSerValLeuSerValLeuValAlaSerValAlaValLeu 619
 2204 ATATACCACTCTATTTTTCACCTGATCTTATCTGCTGCTTAAAGTAACAGACAGAGA 2263
 620 ValTyTyLysPheTyTyPheH1sLeuMetLeuLeuAlaGlyCysIleTyTyGlyArgGly 639
 2264 GAAAGACTATATGATGATTTGTATCTACGACCAAGATGAAGAATCTGGGTGAGAAAC 2323
 640 GluLeuIleTyArgAlaPheValIleTySerSerGlnAspGlnAspTyValArgAsn 659
 2324 GAGCTGTAAGAAATTTTGAAGAAAGAGTGGCCGCTTTCAGCTTGGCTTTCATTAACAG 2383
 660 GluLeuValLysAsnLeuGlnGlnGlyValProProPheGlnLeuCysLeuH1sTyArg 679
 2384 GACTTATTCCTGTGTAGCATTTGCTGCCAAATCATTCAGAGAAAGCTTCCAAAGAGC 2443

Dd		680	AapPhelleProGlyValAlaIleLeaIlaaenilleHnIsGlugLyPheHslySer	699
Oy		2444	CGGAAGTATATTGTGGTGTCCTACACACTTTATCCAGAGCCGTGGTATCTTTGA	2503
Dd		700	ArglysvAllileValValserGlnhsphellegInserArGrTriPcyalIephedu	719
Oy		2504	TATGAGATTGCTCAGACATGCAGTTTCTGAGTAGCCGCTCGGCATCATCTTCATTGTC	2563
Dd		720	TyrGiullileaglInthrTriplInpheusSerSeraGrAlaglylIellelleleVal	739
Oy		2564	CTTGAGAAGTGGAGAAGGCCCTTGGTGAGGCAGCGATCGAATTGTAACGCTTCTTGCC	2622
Dd		740	LeuGlnlysvAlaGlnlyshThrleuLeuArGrAlnValGlnleuTyrtgrleuLeuSer	759
Oy		2624	AGAAACACCTACCTCGAGTGGAGAGACAATGCTCTGGGAGGACACATCTTGGAGAAGA	2683
Dd		760	ArganInThryleGluIntripGlnspeserValleGlyArghIlellehetrparGrAg	779
Oy		2684	CTCAAAAAAGCCCCCTGTGGATGGAAAAGCCCTTGAAATCCAGAT-----GMAACATCA	2733
Dd		780	LeuArGlysvAlaleuLeuhspsGilysserTrpanProGluGlyThrValGlyThrgly	799
Oy		2735	GAGGAAGAACAGAACCAACACTTGG 2761	
Dd		800	CysaentrpGlngluAlathresterile 808	
RESULT 15				
ID	ADOS7785		standard, protein; 808 AA.	
XX	ADOS7785;			
XX	AC			
XX	DT	12-AUG-2004	(first entry)	
DE			Gorilla toll-like receptor 4 SEQ ID NO:6.	
KW			toll-like receptor 4; TLR4; old world monkey; antibacterial;	
KM			immunosuppressive; antiasthmatic; Gram-negative bacterial infection;	
KX			sepsis; severe sepsis; septic shock; asthma; gorilla.	
OS			Gorilla gorilla.	
PN		WO2004042365-A2.		
PD		21-MAY-2004.		
XX				
XX		03-NOV-2003;	2003MO-US036247.	
XX				
PR		01-NOV-2002;	2002US-0423113P.	
PA			(EVOL-) EVOLUTIONARY GENOMICS LLC.	
Pt	Messier W;			
DR	WPI; 2004-400726/37.			
DR	N-PsDB; ADOS7783, ADOS7784.			
PT			Identifying a nucleotide change in a TLR4 polynucleotide sequence, useful	
PT			in treating sepsis and asthma, by comparing the TLR4 polynucleotide	
PS			sequence of the Old World monkey with that of a human.	
Example 1;	SEQ ID NO 6; 111bp; English.			
The invention relates to a novel method for identifying a nucleotide				
change in a TLR4 polynucleotide sequence of an old world monkey				
comprising comparing the TLR4 polynucleotide sequence of the Old World				
monkey with corresponding TLR4 polynucleotide sequence of a human. The				
method of the invention has antibacterial, immunosuppressive, and				
antiasthmatic activity. The method is useful in identifying a nucleotide				
change in a TLR4 polynucleotide sequence of an Old World monkey where the				
change may be associated with reduced sensitivity to Gram-negative				
bacterial infection. The methods, agents and composition are useful in				

CC	treating sepsis, severe sepsis or septic shock and asthma. The present		
CC	sequence represents gorilla TLR4.		
XX			
SQ	Sequence 808 AA;		
Alignment Scores:			
Pred. No.:	3.29e-270	Length:	808
Score:	2761.00	Matches:	538
Percent Similarity:	80.35%	Conservative:	112
Best Local Similarity:	66.50%	Mismatches:	153
Query Match:	46.46%	Indels:	6
DB:	8	Gaps:	4
US-09-396-985B-5 (1-3395) x ADO57785 (1-808)			
QY	350 GTACTCTCAATATTTACCTACCAATGCAGATGAGATCTCAGCAAAATCCCTCATGAC	409	
DB	1 ValValProbanilethrrYrYgIncysMeGcluleuasnhetYrlyslleProbaasn	20	
QY	410 ATCCCTTAATTCACCAAGAAACCTAGATCTGAGCTTCACCCCTGAAGATCTTAAGAAC	469	
DB	21 LeupProbeserThrrYsaenleuaspLeuserPheasnProleuAargHleuGlySer	40	
QY	470 TATAGCTTCACCAATTTCTCACAACCTCAGTGGCTGGATTTATTCAGGTGTGAATGAG	529	
DB	41 TyserPhePheSerPheProGlnleuGlnValleuaspLeuserAryGylGln	60	
QY	530 ACAATTCGACGAAGATGGCATGGCTGTAAACAGCTTCACACCTTGATGATGACAGAGA	589	
DB	61 ThrilleGlnabpGylalYrGlnSerleuSerHlsleuserThrrleuileleuthrGly	80	
QY	590 AACCTTACAGAGATTTTTCCCGACGAAGATTTTTCTGAGATTAACAAATTTAGAAATCTG	649	
DB	81 AsnProileGlnSerleuAlaLeuGlnYalApheserGlyleuSerSerleuGlnlyLeu	100	
QY	650 GTGGCTGTGGAGACAAAAATGACCTCTCTAGAGGGTTCCATATTCAGACGCTTATATCC	709	
DB	101 ValAlaValGlnThrAnleuAlaSerleuGlnabpPheProileGlyHlsleuYsThr	120	
QY	710 TTTAAAGAAACCAAAATGGGCTCATATCTTAATCATCTTAAAGTGGCTGAATATTTT	769	
DB	121 LeuYsgilleuasnValAlaHlsasnleuileGlnSerPheYsleuProGlnlyrPhe	140	
QY	770 TCTATCTGACAAACCTAGAACATGATGGATCTTCTTATACATATATTCAAACTATTTCT	829	
DB	141 SerasnleuthrAnleuGlnlyrYleuaspLeuserSerasnYslleGlnSerIleYr	160	
QY	830 GTCAAAGACTTACAGTTTCTACGTGAATAATCCCAAGTCAATCTCTTTAGACCTGTCT	889	
DB	161 CysThrPheleuAargValleuHlsGlnMerProleuLeuAnleuSerleuAspLeuser	180	
QY	890 TTTAAACCAATTCAGCTCCATTCAGCCCAAGCCCTTCAGAGAAATTTAGGCTCCAGTAATG	949	
DB	181 LeuasnProMetCThrPheileGlnProGylAlaPheYsgilleaYrGlnHlsYsleu	200	
QY	950 ACTCTAAGAAATTAATTTATAGCTCAAAATCTAGTGAATAATGTGCTTCAAAACATACT	1009	
DB	201 ThrleuAargasnAnPheaspSerleuasnValMetYsThrYsilleGlnlyleuAla	220	
QY	1010 GGTTCATCTTCATCGGTGATCTGTGGAGAAATTTAAATGAAAGAAATCTGGAAGT	1069	
DB	221 GlyleuGlnValAargYsgleuValleuGlnYglnPheAryasnGlnlyYsaenleuGlnly	240	
QY	1070 TTTGACCGCTTGTGCATGAGGAAGACTATGCAAATGTGACATGATGATGATTCAGTTTACA	1129	
DB	241 PheaspYsSerAlaaleuGlnlyYleuYsasnleuThrrilleGlnlyleuPheAryleuAla	260	
QY	1130 TATATAAATCATTTTTCGATGATGATTTATTAATCTC--AATGCTGGCAAAATATTTCT	1186	
DB	261 TyrleuasnAryrYrYleuaspAspilleleaspnePheasnYsleuthrAnValSer	280	
QY	1187 GCAATGCTTTCACAGGTGATCATATAAACATCATACAGATGTTCTTAGGCAATTTCAAA	1246	

Db 281 SerPheSerLeuValSerValThrIleGluIArgValIysAspPheSerIyrAsnPhgGly 300
 Qy 1247 TGGCAATCCTTATCATAGATAGATGATCATCTTAAGCCTTTTCCAAAGCTGAGTCTACCT 1306
 Db 301 TrpGlnHisLeuGluLeuValAsnCySlysPheGlyGlnPheProThrLeuLysLeuLys 320
 Qy 1307 TTTCTTAAAGTTGGACCTTTTAACCAACAGAGAGATATCAGCTTTTGTCAGTTGGCT 1366
 Db 321 SerLeuLysArgLeuThrPheThrSerLeuLysGlyGlyAsnAlaPheSerGluValAsp 340
 Qy 1367 CTGCCAAGCTTCAGATATCTAGATCTTAGTGAATGCCATGAGCTTTAGAGTTGCTGT 1426
 Db 341 LeuProSerLeuGluPheLeuAspLeuSerIyrGanGlyLeuSerPheLysGlyCySlys 360
 Qy 1427 TCTTATTCGTATTTGGAAACAACACCTGAAGTCTTAGACCTTCAGCTTGAATGAGTGC 1486
 Db 361 SerGlnSerAspPheGlyThrThrSerLeuLysIyrLeuAspLeuSerPheAsnIylVal 380
 Qy 1487 ATCCGTAGAGTGCACATCTGATGGGCTTAGAGAGCTGAAATACCTGACCTTCAGAC 1546
 Db 381 IleThrMetSerSerAsnPheLeuGlyLeuGluGlnLeuGlnHisLeuAspPheGlnHis 400
 Qy 1547 TCCACTTTAAAGAGTCAACAGATTCAGAGTGTCTTATCTCTTGAATAAATTCTTAC 1606
 Db 401 SerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuAspIyr 420
 Qy 1607 CTGACATCTCTTACATTAATACCAAAATGACCTTGAATGATTTCTTGGAATTCCTGATC 1666
 Db 421 LeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 440
 Qy 1667 AGTCTCAACACTTTTAAAGTGGCTGGCAATCTTTCAAGACACACCCCTTCAAAATGTC 1726
 Db 441 SerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIle 460
 Qy 1727 TTTACAAACACAACTTAACATTCCTGATCTTTTAAATGCGCAATGCGAACAGATA 1786
 Db 461 PheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCyGlnLeuGlnLeu 480
 Qy 1787 TCTAGGGGGTATTGACACACTCTACAGACTCCAGTATTAAACATGAGTCACACAC 1846
 Db 481 SerProThrAlaPheAsnSerLeuSerLeuGlnValLeuAsnMetSerHisAsnAsn 500
 Qy 1847 CTACTGTTCTGATCCATCCATTAATAACAGCTGTACTCCCTCAGAGCTCTGATTGC 1906
 Db 501 PhePheSerLeuAspThrPheProIyrIysCySlysLeuAsnSerLeuAspIyrValLeuAspIyr 520
 Qy 1907 AGTTTCAATCCCATAGACATCC---AAAGCAATAGTCACATTTTCCAAAGAGTCA 1963
 Db 521 SerLeuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPheProSerSerLeu 540
 Qy 1964 GCCGCTTCATCTGACTTAATTAATCTGTGCTGTATATGTGAATATCAGAAATTTCTTG 2023
 Db 541 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCyThrCySglnHisGlnSerPheLeu 560
 Qy 2024 CAGTGGCTCAAGAGACCAAGAAATGTTCTTGGGAATGTTGAACAAATGAATAGTGCATCA 2083
 Db 561 GlnTrpIleLysAspGlnArgGlnLeuLeuValGluValGluArgMetGlnCyAlaAlaThr 580
 Qy 2084 CCTATAGACATGAAAGCCTCCCTGGTGTGTGAATTTTACAAATCCACCTGTATATATAC 2143
 Db 581 ProSerAspLysGlnGlyMetProValLeuSerLeu---AsnIleThrCyGlnMetAsn 599
 Qy 2144 AAGACTATCATCAGTGTATCGGTGCTCAGTGTGCTTGTGGTACGCCATGTAGCATTTCTG 2203
 Db 600 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValValAlaValLeu 619
 Qy 2204 ATATACCACTTCTATTTTCACTGATCTTATGCTGCTGTAATAAGTATACAGCAGAGA 2263
 Db 620 ValIyrLysPheIyrPheHisIleuMetLeuLeuAlaGlyCySleIleIyrGlyIyrGly 639
 Qy 2264 GAAAGCATCTATGATGATCTTGTGTATCTAGACCCAGAAATGAGAGCTGGGTGAGAAAC 2323
 Db 640 GluAsnValIyrAspAlaPheValIleIyrSerSerGlnAspGluAspTrpValArgAsn 659

Qy 2324 GAGCTGTAAAGATTTTGAAGAGAGAGTGGCCGCTTTCAGCTTTCCTTCAATTAACAG 2383
 Db 660 GluLeuValLysAsnLeuGlnGlnGlyValProThrPheGlnLeuCySleuHisIleIyrArg 679
 Qy 2384 GACTTATTCCTGTGTAGCCATTCGTGCCAACATCATCCAGAAAGCTTCCACAAAGAC 2443
 Db 680 AspPheIleProGlyValAlaIleAlaIleAlaAsnIleIleHisGlnGlyPheHisLysSer 699
 Qy 2444 CGGAAATTAATGCGTGGTGTGTAGACACTTATCCAGAGCCGTTGTGTATCTTGA 2503
 Db 700 ArgIysValIleValValSerGlnHisPheIleGlnSerArgIyrCySlePheGln 719
 Qy 2504 TATGAGATTCCTCAGACATGCGACATTTCTGAGTACCGCTTCGACATCTTCATTTGTC 2563
 Db 720 TyrGlnIleAlaGlnThrTrpGlnPheLeuSerSerArgAlaGlyIleIlePheIleVal 739
 Qy 2564 CTGAGAAAGTGAAGAAAGCTCTGTAGAGCAGAGTGCATTTGTATCGCTTCTTAC 2623
 Db 740 LeuGlnLysValGlnLysThrLeuLeuArgGlnGlnValGluLeuIyrArgLeuLeuSer 759
 Qy 2624 AGAAACACCTTACCTCGAGTGGAGAGACAAATGCTTGGGAGGCACTTCTGAGAGA 2683
 Db 760 ArgAsnThrIyrLeuGlnTrpGluAspSerValLeuGlyArgHisIlePheTrpArgArg 779
 Qy 2684 CTCAAAAAAGCCCTGTGATGAGAAAGCCTTGAATCCAGAT-----GAAACATCA 2734
 Db 780 LeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnGlyThrValGlyThrGly 799
 Qy 2735 GAGGAGAGACAGAGACAACTTGTG 2761
 Db 800 CysAsnTrpGlnGlnAlaThrSerIle 808

Search completed: March 29, 2005, 17:02:25
 Job time : 215.403 secs

This Page Blank (uspto)

Db	19	ProPheThrPro-IleProLeuLeuValAlaLysCysArgPheIleThrGluVala	38
Qy	355	TCCTATATATACCTCAACATGCAATGATCAGAAATCTCAGAAAAATCCCTCAATCAATCCC	414
Db	38	1ProAsnIleThrTyrgInCysMetGluLeuAsnPheTyrlsIleProAspAsnLeuPr	58
Qy	415	TTATTCACCAAGAACTAGATCTTAGCTTCAACCCCTGGAAGATCTTAAAGACTATAG	474
Db	58	oPheSerThrIysAsnLeuAspLeuSerPheAsnProLeuArgHisLeuGlySerTyrSe	78
Qy	475	CTTCACCAATTTCTCAACATTTCACTGAGCTGATTTATCCAGGTGTGAAATTGAGACAT	534
Db	78	rPhePheSerPheProGluLeuGlnValIleAspLeuSerArgCysGluIleGlnThrI	98
Qy	535	TGAACACAAAGGATGCGATGGCTTAAACAGCTCCCAACCTTGGATGACAGGAAACC	594
Db	98	eGluAspGlyAlaTyrgInSerIleSerHisIleuSerThrIleuIleuThrGlyAsnPr	118
Qy	595	TATCAAGAGTTTTTCCCGAGGAAGTTTTTCTGACATAACAATTTAGAAATCGTGTGC	654
Db	118	oIleGlnSerIleuAlaLeuGlyAlaPheSerGlyLeuSerSerIleuGlnIlysLeuAla	138
Qy	655	TGTGAGACCAAAAATGACCTCTTAGAGGGTTCCATATTTGACAGCTTATATCTTAA	714
Db	138	aValGluThrAsnLeuAlaSerIleuGlnAsnPheProIleGlyHisLeuIyStrIleuLy	158
Qy	715	GAAACATAATGTGGCTCAATATCTTATACATTCCTTTAAGTTGGCTGAATATTTTTCTAA	774
Db	158	sGluLeuAsnValAlaHisAsnLeuIleGlnSerThelysLeuProGluTyrlPheSerHis	178
Qy	775	TCTGCACAAACCTGAACATGTGGATCTTTCTTATACATATTCACATATTTCTGTCAA	834
Db	178	nLeuThrAsnLeuGlnIHisIleAspLeuSerSerAsnIyIleGlnSerIleTyrcysTh	198
Qy	835	AGACTTACAGTTCTTACGTGAAAAATCCCAAGTCAATCTCTTTAAGACCTGTCTTAAA	894
Db	198	rAspLeuArgValIleuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAs	218
Qy	895	CCCAATTTGCTCCTTCAAGCCCAAGCCCTTCAAGGAATTTTGGCTCCATTAATTTGACCT	954
Db	218	nProMetAsnPheIleGlnIProGlyAlaPheLeuGluIleArgLeuHisIlyIleuThrIle	238
Qy	955	AAGAAGTATTTTAAATAGCTCAAAATGTAAGTGAATAATGTGCTTCAAAACATGACTGTTT	1014
Db	238	uArgAsnAsnPheAspSerIleuAsnValMetCysThrCysIleGlnGlyLeuAlaGlyLe	258
Qy	1015	ACATGTCCATCGGTGATCTTGGGAAATTTAAAATGAAAGAACTGGAAGTTTGA	1074
Db	258	uGluValHisArgLeuValIleuGlyIlePheArgAsnGluIysLeuAsnLeuGluTyrsPheAs	278
Qy	1075	CCGTTCTGTCAATGGAAGGACTATGAAATGTGACATATAGTTACAGTTAACTAATAT	1134
Db	278	lPysSerIleAlaLeuGlnGlyLeuCysAsnLeuThrIleGluGluPheArgLeuAlaTyrlle	298
Qy	1135	AAATCATTTTTCAGATGATATTTATTAATCTC--AATGTCTGCAAAATATTTCTGCAT	1191
Db	298	uAspTyrlTyrlleuAspAspIleIleIleAspLeuPheAsnTyrlsLeuThrAsnValSerSerHis	318
Qy	1192	GTCCTTTCACAGGTGATCATATTAACATACATAGACATGTTCTTCAGGCAATTTCAATGGCA	1251
Db	318	eSerIleuValSerValThrIleGluArgValIysAspPheSerTyrlAsnPheGlyTyrlpG	338
Qy	1252	ATCCTTATCAATCATTAAGTGCATCTTAAAGCTTTCCAAAGCTGAATCACTTTTCT	1311
Db	338	nHisLeuGluLeuValAsnCysLysPheGlyGlnIlePheProThrIleuTyrlsLeuTyrsSerIle	358
Qy	1312	TAAAAGTTGGAATTTAACTACCAACAGAGAGATATCAAGCTTTGGTCAAGTGGCTGTGCC	1371
Db	358	uLysArgLeuThrIlePheThrSerAsnIyIleGlyIysAsnIlePheSerGluValAspLeuPr	378
Qy	1372	AAGTCTCAGATATCTTAGATCTTATGAGAAATGCCATGAGCTTTAGAGGTGCTGTTCTTA	1431

D	378	OSerLeuGIuPheLeuAspLeuSerAArgaGnGlyLeuSerPheIysGlyCyScySerGI	398
Q	1432	TTTCGATTTTGGAAACAAACACCTGAAGTACTTAGACCTCAGCTTCATGGGTGCATCCT	1491
D	398	nSerAspPheGlyThrThrSerLeuIyryrLeuAspLeuSerPheAsnGlyValIleTh	418
Q	1492	GATAGAGTCCAACTTCATGGGTCTAGAAGAGCTGGAAATACCTGACCTTTCAAGCACTCCAC	1551
D	418	ImetSerSerAsnPheLeuGlyLeuGIuGlnIleLeuAspPheGlnIHisSerAs	438
Q	1552	TTTAAAAAGGTGCAGAAATTCAGAGTTCCTTATCTTGAAAAAACTTCCTTTACCTTGA	1611
D	438	nLeuIySerImetSerGIuPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAs	458
Q	1612	CATCTCTTACCTATATCCAAAATTTGACTTGATGAGCATATTTCTTGCTTGATCAGCTCT	1671
D	458	pIleSerIleThrIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSerSerIle	478
Q	1672	CAACACTTTAAAAATGGCTGGCAATTCCTTTCCAAAGACAACACCCTTCCAAATGCTTTAC	1731
D	478	uGIuValLeuIyMetIaGIyAsnSerPheGlnGlnIAsnPheLeuProAspIlePheTh	498
Q	1732	AAACACAAACAACCTTAATCATTCCTCGATCTTTCTTAAATGGCAATGGAAACAGATATAG	1791
D	498	rGIuLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGIuGlnIleuSerPr	518
Q	1792	GGGGGTAATTTGACACACTCTACACACTCCAGCTTATTTAAACATGAGTACAAACACTACT	1851
D	518	oThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerIleAsnAsnPheP	538
Q	1852	GTTTCTGATCCATCCCATTTATTAACAGCTGACTCCCTCAGACCTTGATTTGACAGTTT	1911
D	538	eSerLeuAspThrPheProTyrlYrsCySLeuAsnSerLeuGlnValLeuAspTyrlSerIe	558
Q	1912	CAATCCGATTAAGACATCC--AAAGAAATCTGCACATTTTCCAAAGTCAAGCGCT	1968
D	558	uAsnIleIleThrSerIySylsGlnGluLeuGlnIlePheProSerSerLeuAlaPhe	578
Q	1969	CTTCATCTGACTATATATCTGTGGCTGTGATATGTGAATATACAGAAATTTCTTGACAGTG	2028
D	578	eLeuAsnLeuThrGlnPheAsnPheAlaCyPThrCyGlnIleGlnSerPheLeuGlnTr	598
Q	2029	GGTCAAGACACGAAAAATGTTCTTGCGAATGTTGAACAAAATGAATGTGCATCCTAT	2088
D	598	pIleYAspGlnArgGlnLeuLeuValGluValGluArgMetGlnCysAlaThrProSe	618
Q	2089	AGACATGAAGCCCTCCCTGGGTGGTGAATTTTACGAATTCACACCTGTATATATACAAGAC	2148
D	618	rAspIySerGlnIyMetProValIleuSerLeu--AsnIleThrCySglnMetAsnIySth	637
Q	2149	TATCATCGTATACGGGTGCAGTGTGCTGTGGTGAAGCACTGTACATTTCTGATATATA	2208
D	637	rIleIleGlyAlaSerValIleuSerValIleValIleSerValValAlaValIleuValIy	657
Q	2209	CCACTTCTATTTTCACTGATACTTATTTGCTGAGCTGTAAAAAGTACAGACAGAGAGAAAG	2268
D	657	rIySerPheTyrlrPheIHisLeuMetLeuLeuAlaGlyCyAlleTyrlGlyArgGlyIuAs	677
Q	2269	CATCTATATATGCATTTTGATCTACTGTAGGCACAAATGAAGACCTGGGTGAGAAACAGCT	2328
D	677	nIleTyrlAspAlaPheValIleTyrlSerSerGlnAspIuAspTrpValAlaArgAsnGlyIe	697
Q	2329	GGTAAAGAAATTTAGAAAGAGAGGCCCGCTTCAGTTTGACCTTCATACAGAGCACTT	2388
D	697	uValIyAsnLeuGIuGlnGlyAlaProProPheGlnIleuCySLeuIHisTyrlArgPhePhe	717
Q	2389	TATTCCTGTGTAGCCATTTGCTGCACAATCATCATCAGAAAGCTTCCACAAGACCGGAA	2448
D	717	eIleProGlyAlaIleAlaIleAlaAsnIleIleHisGIuGlyPheHisIySerArgIy	737
Q	2449	AGTTATTTGTGGTGTCTAGACACTTTATCAAGACCGGTGGTGTATCTTTGAATATGA	2508
D	737	eValIleValAlaIleSerGlnIHisPheIleGlnIleSerArgTrpCySIIlePheGlnTyrlG	757

Qy 2509 GATTGCTCAGACATGAGCAGTTTCTGAGAGCCGCTGGCATTCATTGTCCTTGA 2568
 |||||
 Db 757 uilealaglnhrtrpqlnphleuseSerxhAladlyllelleheillevalleuGl 777
 |||||
 Qy 2569 GAAAGTGAAGATGCTTGTCTGAGGACAGCAGCTGAATTGATGCTTCTTACAGAAA 2628
 :|||
 Db 777 nlyValglulrlyThrleuLeuArgglnGlnValgluldeuLyraThrgleuLeuSerArgAs 797
 |||||
 Qy 2629 CACCTACCTGAGTGGGAGGACAAATGCTCTGGAGAGGACATCTTCTGAGAAAGCTCAA 2688
 |||||
 Db 797 nhrThyrluenglulrTgluAspSerValleuGlyArghisillepethrPArGyluar 817
 |||||
 Qy 2689 AAAAGCCTGTGATGAGAAAAGCCTTGATCCAGAT-----GAAACATCAGAGA 2739
 :|||
 Db 817 glyhAlaileuLeuaspGlylySerTrpAsnProGlnGlyThrValglThrglyCyAs 837
 |||||
 Qy 2740 AGAACAGAGACCAACACTTGTG 2761
 |||||
 Db 837 ntrpGlnGlnAlaThrSerile 844
 |||||

RESULT 2

US-08-514-014-4
 ; Sequence 4, Application US/08514014
 ; Patent No. 5707829
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John
 ; APPLICANT: Kelleher, Kerry
 ; APPLICANT: Carlin, McKenough
 ; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
 ; STREET: 87 Cambridgepark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/514,014
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; REFERENCE/DOCKET NUMBER: G16000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 661 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-514-014-4

Alignment Scores:

Pred. No.: 1,4e-53 Length: 661
 Score: 609.00 Matches: 194
 Percent Similarity: 46.51% Conservative: 133
 Best Local Similarity: 27.60% Mismatches: 303
 Query Match: 10.25% Indels: 73
 Db: 1 Gaps: 21

US-09-396-985B-5 (1-3395) x US-08-514-014-4 (1-661)

Qy 208 TACAGTTGTCATGCTTT-----CTCAGCGGCTCCGCTGGTCAGAAAAATGCGAG 258
 :|||
 Db 3 PheaspValSerCysPhepethrPValValleuPheSerhlaGlyCylys----- 19
 |||||
 Qy 259 GATGATGCTCTCTTGATCATGCTGGGACTGTGATCATGGCATGTGCTTCTGCTGCT 318
 :|||
 Db 20 -----ValleuThrSerTrpAspGln-Met----- 27
 |||||
 Qy 319 GAGACAGAAAGCTTGAATCCCTGCAATAGAGTACTTCTTAATATTAACCTTCAATGAT 378
 |||||
 Db 28 -----CyslleGlyLysglnAlaAsnLythrYraenCyse 40
 |||||
 Qy 379 GGATCAGATCTCAGCAAAATCCCTCATGACATCCCTTATTCAGCAAGAACTAGATCT 438
 :|||
 Db 40 uAsnleuGlyleuSerGlnleuProAspThrleuProAsnThrThrgluPheleuGluPh 60
 |||||
 Qy 439 GAGCTTCAACCCCTGGAAGATCTTAAGACCTATAGCTTCAACAAATTTCTCAACACTTCA 498
 :|||
 Db 60 eSerPheAsnPhleuProthrIleHisAsnArgThrPheSerArGlyleuMetAsnleuth 80
 |||||
 Qy 499 GTGGCTGATTTATCCAGGTGTGAATTTGAGACATTTGAACAGACAGGATGGCTT 558
 :|||
 Db 80 rPheleuAspLeuThrArGcysGlnIleAsnTrpIleHisgluAspThrPheGlnSerh 100
 |||||
 Qy 559 AAACAGCTCTCAACCTTGGTGAAGTGAAGAAACCTATCAAGAGTTTTCAGGAGAG 618
 :|||
 Db 100 hIleGlnleuSerThrleuValleuThrGlyAsnProleuIlePheleuAlaGluThrSe 120
 |||||
 Qy 619 TTTTCTGACCTAACAAATTTAGAAATGTGGTGTGGAGACAAAAATGACCTCTCT 678
 :|||
 Db 120 rleuAsnGlyProlyserleuLyshIleuPheleuIleGlnThrGlyIleSerAsnle 140
 |||||
 Qy 679 AGAGGTTTCATTTGAGACGCTTATATCTTAAAGAACTAATGTGGCTCAATCT 738
 :|||
 Db 140 uGluPheIleProValHisAsnleuGluAsnleuGlySerleuLyserAsnhi 160
 |||||
 Qy 739 TATACATCTCTTGAAGTGGCTGAATTTTCTTAATCTGACAAACCTTGAACATGTGCA 798
 :|||
 Db 160 eIleSerSerIlelysheProlyAspPhePro--AlaArgAsnleuLysValleuAs 179
 |||||
 Qy 799 TCTTCTTAATACTAATATTCAAATATTTCTGTCAAGACTTACAGTTTCTACGTGAAA 858
 :|||
 Db 179 pPheGlnAsnAsnAlaIleHisTrylleSerArGlnAspMetArGserleuGluGln-- 198
 |||||
 Qy 859 TCCCAAGTCAATCTCTTGTAGACCTGTCTTAAACCAATTAAGTCTCAAGGCCA 918
 :|||
 Db 199 ----AlaIleAsnleuSerleuAsnPhleuAsnGlyAsnAsnValylsglylleGluLeuG 217
 |||||
 Qy 919 AGCCTTCAGGAATTAGGCTCCATGAAATTGACCTTAAGAGTAATTTAATACCTAAA 978
 :|||
 Db 217 yAlaPheAspSerThrValPheGlnSerLeu-----AsnPheGlyGlyThrPr 233
 |||||
 Qy 979 TGTACTGAATAATGCTTCAAAAATGATGCTGTTTACATGCTCAGTCGATCTTGGG 1038
 :|||
 Db 233 oAsnleuSerValIlePheAsnGlyleuGlnAsnSerThrThrglnSerleuTrpleuG 253
 |||||
 Qy 1039 AGAATTTAAATGAAGAATCTGGAAGATTGACCGTTCTGTCAAGAGACATGAT 1098
 :|||
 Db 253 yThrPheGluAspIleAspAsp--GluAspIleSerSerAlaMetleuLysGlyLeuCy 272
 |||||
 Qy 1099 CAATGTGAGCATGATGATGCTTACGATCAATATTAATTAATTTTCAATGAT 1155
 :|||
 Db 272 eGluMetSerValGluSerleuAsnleuGlnGlu--HisArgPheSerAspIleSerSe 291
 |||||
 Qy 1156 TTATATCTCAATGCTTGTGCAATATTTCTGCAATGCTTCTTCAAGAGTGTACATATAA 1215
 :|||
 Db 291 rThrThrPheGlnCysPheThrGlnleuGlnGluLeuAspLeuThrAlaThrIleleuLy 311
 |||||
 Qy 1216 ACACATAGCAGATGCTTCTGAGCATTTCAAAATGCAATCTTATCAATCATTAAC 1270
 :|||
 Db 311 s-----GlyleuProSerGlyMetLys-----GlyleuAsnleuLeuLySlySle 326
 |||||

```

Qy 1271 -----TTCATCTTAAAGCCT-----TTCCAAA 1293
Db 326 uValleuSerValaAsnHisPheargInLeuCyGlnHiseralAlaAsnProse 346
Qy 1294 GCTGAGCTCTACCTTTTCTTAAAGTTGACCTTAACTACCAAGAGATACAGCTT 1353
Db 346 rLeuThrHisLeuYrHisLeuArgLy-----AsnVallybVleuHisLeuGlyVa 363
Qy 1354 TGGTCAGCTG--GCTGCGCAAGCTCAGATATCTGATCTGATGGTGAAGATGCCAG 1410
Db 363 lGlyCysleuGlnuLyseuGlnLeuGlnThrLeuAsnLeuSerHisAsnArgIleG 383
Qy 1411 CTTTAGAGCTGCTCTTCTTATCTGATTTTGAACAACAACAGCTGAAGTACTTGA 1470
Db 383 uAlaSerAspCysCysSerleuGlnLeuLyAsnLeuSerHisLeuGlnThrLeuAnle 403
Qy 1471 CAGCTTCAATGGTCTCATC--CTGATGAGTGCACAACTTCAAGGCTGAGAGCTGGA 1527
Db 403 uSerHisAsnGlnuProleuGlnLeuGlnSerGlnAlaPheLyGlnuCybProGlnLeuG 423
Qy 1528 ATACCTGGACTTTGAGCAGCTCAGCTTAAAGAGTCAAGAAATTCAGTCTTATC 1587
Db 423 uLeuLeuAsnProleuAlaPheThrArgLeuHisIleAsnAlaProGlnSerProPheGln 443
Qy 1588 TCTTGAAGAACTCTTCTTACCTTGAATCTTGAATCTTGAATCTTGAATCTTGA 1647
Db 443 nLeuHisPheleuGlnValleuAnleuThrTyCybPheleuAsnThrSerArgGlnHis 463
Qy 1648 CATATTTCTGGCTTGATCAGCTGCAACATTTAAAGAGCTGGCAATTTCTTCAAGA 1707
Db 463 sLeuLeuAlaGlyLeuProValleuArgHisLeuAnleuLyseGlyAsnHisPheGln 483
Qy 1708 CAACAGCCTT-----TCAATGCTTTTACAACAACAACAACAATTCATCTCCGATCT 1761
Db 483 rGlyThrIleThrHisThrAsnLeuLeuGlnThrValGlySerleuGlnValleuIlele 503
Qy 1762 TTCTAAATGCCAGCTGGAACAGATATCTAGGGGGGTATTGACACAGCTTACAGCTCA 1821
Db 503 uSerSerCysGlyLeuLeuSerIleArgGlnAlaPheHisSerleuGlnuLybMetse 523
Qy 1822 GTTATTAACATGAGTCAACAACACTTACTG-----TTTGTGATCA--TCCCATTA 1872
Db 523 rHisValaAsnLeuSerHisAsnSerLeuThrCysAspSerIleAspSerLeuSerHisle 543
Qy 1873 TAAACAGCTGATCCCTCAGAGCTCTTGAATGAGCTTCAATGAGATGAGATCCAA 1932
Db 543 uLybGlyIleTy-----LeuAnleuAlaAlaAsnSerIleAsnIleIleSe 559
Qy 1933 AGGAATCTGCAACATTTTCCAAAGAGCTAGCCGCTTCAATCTGATTAATCTGT 1992
Db 559 rProArgLeuLeuProIleLeuSerGlnGlnSerThrIleAnleuSerHisAsnProle 579
Qy 1993 TGCCTTGATATGGAATATCAGAATTTCTTGCAGTGGTCAAGACCAAGAAATGTTCT 2052
Db 579 uAspCysThrCysSerAsnIleHisPheLeuThrTyArgIlybAsnLeuHisLybSe 599
Qy 2053 GGTGAATGTTGAACAATGAATGATGATGATGATGATGATGATGATGATGATGAT 2112
Db 599 uGlnGlySerGlnuGlnuThrCysAlaAsnProSerLeuArgIlyVallybSe 619
Qy 2113 GGATTTTACGAATTC-----ACCTGTATATATATACAAAGTATCATCAGTGT 2160
Db 619 rAspVallybLeuSerCysGlyIleThrAlaIleGlyIlePhePheleuIleValPhele 639
Qy 2161 ATCCAGTGTCACTGCTTGTGTGTAGCCATGATGATGATGATGATGATGATGAT 2220
Db 639 uLeuLeuLeuAlaIleLeuLeuPhePheAlaVallybTybLeuLeuArgTlybTyG 659
Qy 2221 TCACCTG 2227
Db 659 nHisIle 661

```

RESULT 3

```

US-08-833-823-4
; Sequence 4, Application US/08833823
; Patent No. 5969093
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Keilher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,823
; FILING DATE: 10-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/514,014
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI6000
; TELEPHONE: (617) 876-5851
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 661 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-833-823-4

Alignment Scores:
Pred. No.: 1,4e-53 Length: 661
Score: 609.00 Matches: 194
Percent Similarity: 46.51% Conservative: 133
Best Local Similarity: 27.60% Mismatches: 303
Query Match: 10.25% Indels: 73
DB: 2 Gaps: 21

US-09-396-985b-5 (1-3395) x US-08-833-823-4 (1-661)
Qy 208 TACAGTTCATGATGCTT-----CTCAGCGCCTCCGCTGTTGACAGAAATGCCAG 258
Db 3 PheAspValSerCysPhePheThrValValleuPheSerHisGlyCysLyS----- 19
Qy 259 GATGATGCTCTTGTGATGCTGGCTGGAGCTGTGATCAGATGATGCTTCTTCCGCT 318
Db 20 -----ValIleThrSerTyrAspGln-Met----- 27
Qy 319 GAGACGAGAGCTGGAATCCCTGATGAGAGTACTTCTTAATTTACTTACCAATGCAT 378
Db 28 -----CysIleGlnuLybGlnuAlaAsnLybThrTybAsnCybG 40
Qy 379 GGATCAGATCTGACAAATCCCTCATGATCAGATCCCTTATTTACCAAGAACTGATCT 438
Db 40 uAsnLeuGlybLeuSerGlnuIleProAspThrLeuProAsnThrThrGlnuPheLeuGlnu 60
Qy 439 GAGCTTCAACCCCTGAAAGATCTTAAGAACTTAAGTTCACCAATTTCTCACAACTTCA 498

```



```
; PRIOR FILING DATE: 1996-07-12
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-982-308B-23

Alignment Scores:
Pred. No.: 1.72e-42 Length: 784
Score: 502.00 Matches: 210
Percent Similarity: 41.09% Conservative: 136
Best Local Similarity: 24.94% Mismatches: 324
Query Match: 8.45% Indels: 172
DB: 4 Gaps: 32

US-09-396-985B-5 (1-3395) x US-09-982-308B-23 (1-784)
QY 386 AATCTGAGCAAAATCCCTCATGATCCCTATTCAACCAAGACCTAGATCTGAGCTTC 445
DB 42 SerLeuAsnSerIleProSerGlyLeuThrGluAlaValIysSerLeuAspLeuSerAsn 61
QY 446 AACCCCTGAGATCTTTAAGAGGCTTAGCTTCAACCAATTTCTCAACATTCAGTGGCTG 505
DB 62 AsnArgIleThrTyrIleSerAsn-----Ser 70
QY 506 GATTATTCACAGGTGTGAATTTAGACAACTTGACAAAGCAGCATGGCTTAAACAG 565
DB 71 AspLeuGlnArgCysVal-----Asn 77
QY 566 CTCCTCAACCTTGCTGACTGACAGAAACCCATCAAGAGTTTTCCTCCAGAAAGTTTCT 625
DB 78 LeuGlnAlaLeuValIleThrSerAsnGlyIleAsnThrIleGluGluAspSerPheSer 97
QY 626 GGACTTAACAATTTAGAGAACTGTGGCTGTGAGACAAAAATGACCTCTTAGAGAGT 685
DB 98 SerLeuGlySerLeuGluIleLeuAspLeuSerTyrAsnTyrLeuSerAsnLeuSerSer 117
QY 686 TTCATATTGGACAGCTTATATCTTAAAGAACTAAATGTGGCTCAATATTATACAT 745
DB 118 SerTyrPheIysProLeuSerSerIleThrPheLeuAsnLeuGluIysAsnProTyrIys 137
QY 746 TCCTTTAAGTTGGCTGATATATTTCTATCTGAACAACCTAGAACATGTGATCTT--- 802
DB 138 ThrLeuGlyGluThrSerLeuPheSerHisIleuThrIysLeuGlnIleLeuArgValGly 157
QY 803 -----TCCTTAACCTATATTCAAACTATTTCTGTCAAGAAGCTTACAGTTTCTAGT 853
DB 158 AsnMetAspThrPheThrIysIleGlnArgIysAspPheAlaGlyLeuThrPheLeuGlu 177
QY 854 GAAATATCCCAAGTCATCTCTTTAGACCTGTCTTAAACCAATGACTCCATTCAA 913
DB 178 Glu-----LeuGlnIleAspAlaSerAspLeuGlnSerTyrGlu 190
QY 914 GCCCAAGCTTTGAGGAATTAGG-----CTCCAT-----GAA 946
DB 191 ProIysSerLeuIysSerIleGlnAsnValSerHisIleuIleuHisMetIysGlnHis 210
QY 947 TTGACTCTAAGAACTAATTTAATAGCTCAAAATGTACTGAAATGTGCTTCAA----- 1000
DB 211 IleLeuLeuLeuGluIlePheValAspValThrSerSerValGluCysLeuGluLeuArg 230
QY 1001 -----AATGACTGGTTTCAATGCTCATGCTGGTTGATCTTGGAGAAATTTAAAT--- 1051
DB 231 AspThrAspLeuAspThrPheHisPheSerGluLeuSerThrArgIysGluThrAsnSerLeu 250
QY 1052 -----GAAAGAACTGGAAGATTGTAAGCTTGTGACGTTGTCATGAGAA----- 1090
DB 251 IleIysIysPheThrPheArgAsnValIysIleThrAspGluSerLeuPheGlnValMet 270
QY 1091 -----GACTATGCAATGTGAGCATTTGATGAGTTTCAGGTTTACA 1129
```

```
DB 271 LysLeuLeuAsnGlnIleSerGlyLeuLeuGluIlePheAspAspCysThrLeuAsn 290
QY 1130 TATATAATCATTTT---TCAGATGATATTATTAATCTCAATGCTTGGCAAAATATTCT 1186
DB 291 GlyValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyIysValGlu 310
QY 1187 GCATGCTCTTCAACAGGTGTACATATATAACATAGCAGATGTCTTACGCAATTTCCAA 1246
DB 311 ThrLeuThrIleArgArgIleHisIle-----ProArgPheTyrLeu 324
QY 1247 TGGCAATCTTATCAATCATTAGATGTCATCTTAAGCCTTTCCAAAGCTGATCTTACT 1306
DB 325 PheTyrAspLeuSerThrLeuTyrSerLeuThrGluArgValIysArgIleThrValGlu 344
QY 1307 -----TTCTTAAAGTTGAGCTTTACTTACTTACCAACAGAGAGATATCAGCTTT 1354
DB 345 AsnSerIysValIleLeuValProCysLeuLeuSerGlnHis----- 358
QY 1355 GGTCAATGGCTCTGCCAAGTCTCAGATATCTAGATCTTAGTGAATGCCATGAGCTTT 1414
DB 359 -----LeuIysSerLeuGluTyrLeuAspLeuSerGluAsnLeuMetVal--- 373
QY 1415 AGAGTTGCTGTTCTTATTCGATTTTGAACAAACCTGAGTACTTAGACCTTCAGC 1474
DB 374 -----GluGluTyrLeuIysAsnSer 380
QY 1475 TTCAATGCTGTCATCCGATGAGTGCACACTTCATGGCTTAGAAGCTGGAATACCTG 1534
DB 381 -----AlaCysGluAspAlaTyrProSerLeuGlnThrLeuAlaValArg 395
QY 1535 GACTTTCAGACATCCACTTTTAAAAAAGTCCACAAATTCACAGTGTCTTATCTTGA 1594
DB 396 GlnAsnHisIleuAsnIleSerLeuGluIysThrGlyGlu-----ThrLeuLeuThrLeuIys 413
QY 1595 AATCTTCTTACCTTGACATCTCTTACACTTAATACAAATTTGACTTGAATGCAATATT 1654
DB 414 AsnLeuThrAsnIleAspIleSer----- 421
QY 1655 CTGGCTGATCAGTGTCAACACTTTAAATGCTGGCAATCTTTCAAAAGCAACACC 1714
DB 422 -----LysAsnSerPhe-----HisSer 427
QY 1715 CTTTCAAAATGCTTTTCAAAACACAACTTAACATCTCTGATCTTTTAAATGCCAA 1774
DB 428 MetProGluThrCysGlnTyrProGluIysMetIysTyrLeuAsnLeuSerSerThrArg 447
QY 1775 CTGAAACAGATATCTAGGGGGGTATTGACACACTTACAGACTCCAGTTATTAACATG 1834
DB 448 IleHisSerValThrGlyCysIleProIysThr-----LeuGluIleLeuAspVal 464
QY 1835 AGTCACACAAACCTA---CTGTTT---CTGATCCATCCCATTAATAACAGCTGTAC--- 1885
DB 465 SerAsnAsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuIysGluLeuTyrIle 484
QY 1886 -----TCCTTCAGGACTCTT 1900
DB 485 SerArgAsnIysIleuMetThrLeuProAspAlaSerIleuLeuProMetLeuValLeu 504
QY 1901 GATTGCACTTCAATGCAATAGACACA---TCCAAAGAAATACTGCAACATTTTCCAAAG 1957
DB 505 LysIleSerArgAsnAlaIleThrThrPheSerIysGluIleuAspSerPhe---His 523
QY 1958 AGTCTAGCCGCTTTCATCTGACATAATTAATTCGTGCTTGTATATGTAATATCAGAT 2017
DB 524 ThrLeuIysThrLeuGluAlaGlyGlyAsnAsnPheIleCysSerCysGluPheLeuSer 543
QY 2018 TTCTTGACGGGTGTCAGACAGCAAGAAATGTTCTTGATGATGTTGAA-----CAA 2068
DB 544 PheThrGln-----GluGlnGlnAlaLeuAlaIysValLeuIleAspTyrProAlaAsn 561
QY 2069 ATGAATGTGCATGACCTTATGACATGAAAGCCTCCTGCTGTGGAT-----TTTACG 2122
DB 562 TyrLeuCysAspSerProSerHisValArgGlyGlnGlnIleValIleAspValArgLeuSer 581
```



```

Qy 385 GAATCTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGAACTAGATTCAGCT 444
Db 63 gashleuthrargleuproabpelyleprogllythrinalaleutrpheuaspe 83
Qy 445 CAACCCCTGAGAGATCTTAAGAGCTATAGCTTCACCAATTTCTGCAACTTCAGTGCT 504
Db 83 rashnleuSerSerIleProProAlaIaPhearghbnleuSerSerIleAlaPhele 103
Qy 505 GGATTTATCCAGCTGTGAAATTTGAGACAAATGGAACAAGCATGGCATGGCTTAAACA 564
Db 103 uashnleuIngllyglInleuGlySerleuGlnProGlnAlaleuLeuGlyLeuGluAs 123
Qy 565 GCTCTCAACCTTGGATGAGACAGAAACCTATCAAGATTTTTCAGGAAAGTTTTC 624
Db 123 nleuCyehisleuhsleuGlnuarghbnleuargSerleuAlaValIgllythrPheAl 143
Qy 625 TGACACTAACAAATTTAGAAATCTGGTGGCTGTGAGACAAAAATGACCTCTTAGAGGG 684
Db 143 atyThrProAlaleuAlaleuLeuGlyLeuSerashnarghbnleuSerArgLeuGluAs 163
Qy 685 TTTCATATTTGAGACGCTTATATCTTAAAGAACTAATAGGCTCATATCTTATACA 744
Db 163 pglyleuPheglIngllyleuGlyashnleuTrpAspleuashnleuGlyTrpashnSerleu-- 182
Qy 745 TTCTTTAAGTTGGCTGAA---TATTTTCTAATCTGCAAAACCTAGAAACATGGAGATCT 801
Db 183 ----AlaValaleuProabpAlaIaPhearglyleuGlyglyleuArgIleuValle 201
Qy 802 TTCTTATTAAC-----TATATTCAAACTATTTCTGCAAGACTTACAGTTTCTACG 852
Db 201 ualIgllyashnargleuAlaIaIytrleuGlnProAlaleuPheSerGlyleuAlaIglInleuAr 221
Qy 853 TGAATAATCCCAAGTCATCTCTCTTTGACCTGTCTTAAACCAATGATGCTCATTC 912
Db 221 gglu-----LeuashpleuSerArgashnAlaleuArgAlaIlely 234
Qy 913 AGCCCAAGCTTTGAGGGAAT---AGGCTCATGATTTGACTGTCAAGAAATTTTAA 969
Db 234 balashnValPhealagInleuProargleuGlnlyshleuTryleu----- 249
Qy 970 TAGCTCAAAATGACTGAATAATGTGCTTCAAAACATGACTGTTACATGTCATCGGTT 1029
Db 249 ----- 249
Qy 1030 GATCTTGGAGAAATTTAAAAATGAAAGAAATCTGAAAAGTTTACCGTCTGTCATGGA 1089
Db 250 -----AspArgashnleu----- 253
Qy 1090 AGGACTATGCAATGATGACATTTGATGAGTTACAGTTAACATATATATATTTTTCAGA 1149
Db 253 ----- 253
Qy 1150 TGATATTTATATCTCAATCTGCTGGCAAAATTTCTGCAATGCTTTCACAGGTGTACA 1209
Db 254 -----lealalavalalaleuProgllyalPheleuGlyleu-- 265
Qy 1210 TATATAAACATAGACAGATGTTCTTAGGCAATTTCAATGSCAATCTTATATATCATTTAG 1269
Db 266 -----LysAlaleuArgTrpleuashpleuSer----- 274
Qy 1270 ATGTCATCTTAAGCTTTTCCAAAGCTGATCTACCTTTTCTTAAAGTTGACCTTTTAA 1329
Db 274 ----- 274
Qy 1330 TACCAACAGA-----GAGATATACAGCTTTGGTCACTGGCTGCGCCAAAG 1374
Db 275 -HisashnArgValalaglyleuLeuGlnuarghbnPheProgllyleuLeu-----Gl 291
Qy 1375 TCTCATATCTTATAGATCTTATAGAAATGCGATGAGCTTTAGAGGTTGCTGTTTATTC 1434
Db 291 yLeuArgValleuArgleuSerHisashnAlaIlealaserleuArgProArgTrpPheGl 311

```

```

Qy 1435 TGATTTTGGACAAACAACTGAGACTTATGACCTGACCTTCAATGCTGTC---ATCCT 1491
Db 311 uashpleu-----HisPheleuGlnuGlnleuGlnleuGlyHisashnArgIleArgGlnle 329
Qy 1492 GATAGTGCCAACTTCATGGCTCTTGAAGAGCTGGAATATCTGGACTTTACAGACTCCAC 1551
Db 329 ualIgllyuargSerPheglIngllyleuGlnleuGlnvalleuThrleuashPheHisashnGl 349
Qy 1552 TTTAAAAAGCTCAACGAATTTCTGAGTGTCTTATCTTGAATAAACTTTTACCTTGA 1611
Db 349 nleuGlnleuVal--LysValIglYalalPheleuGlyleuThrashnValalalalMetas 368
Qy 1612 CATCTCTTACACTAATACCAAAATTTGACTTGTATGAGCATATTTCTTGGCTTATGATCCT 1671
Db 368 nleuSerGlyashnCyshleuArgashnleuProglInvalPheArgGlyleuGlyLysle 388
Qy 1672 CAACACTTTAAAAATGGCTGGCAATTC----- 1699
Db 388 uHiserleuHisleuGlnuGlySerCyshleuGlyArgIleArgProHisThrPheAlaGl 408
Qy 1700 -----TTCAAGAGACAAACCTTCAAAATGTC----- 1726
Db 408 yLeuSerGlyleuArgTrpleuPheleuLysAspashnGlyleuValIglYIleGlnuGln 428
Qy 1727 -----TTTAAACAACAACTTAACATTCCTGATCTTCTTAATGSCAACTGGAACA 1782
Db 428 nSerleuTrpGlyleuAlaglnleuLeuGlnleuashpleuThrSerashnleuThrHis 448
Qy 1783 GATATCTAGGGGGTATTTTGAACACTCTTACAGACTGCACTGATTTTAAACAGTACAGAA 1842
Db 448 shleuProHisleuPheglInleuPheglIngllyleuGlnuGlyTryleuLeuLeuSerHisAs 468
Qy 1843 CAACCTACTGTTTGTGATTCATCCCATTTATTAACAGCTGATCTCCCTCAGAGACTTTGA 1902
Db 468 nArgleuAlaglnleuProAlaaspAlaleuGlyProleuGlnArgalalPheTrpleuAs 488
Qy 1903 TTGCAATTCATGCAATGAGACATCCAAAGAAATCTGCAACATTTTCCAAAGAGTCT 1962
Db 488 pValSerHisashnargleuGlnuAlaleuProgllySerleuLeuAlaserleuGlyArgle 508
Qy 1963 AGCCGTCTTCAATCTGACTAATAATCTGTGCTTGTATATGTGAATATCAGAAATTTCTT 2022
Db 508 uArgTryleuashnleuArgashnSerleuArgTrPheThrProGlnProProgllyLe 528
Qy 2023 GCAG-----TGCGTCAAGACACGAAAAATGTTCTTGCTGAATGTGAACAAATGAATG 2076
Db 528 uGlnArgleuTrpleuGlnly-----AsnProTrpAspCy 540
Qy 2077 TGATCACTATATAGAC-----ATGAAGGCTTCCTGCTGTTTGA 2115
Db 540 sSerCyProleuLysalaleuArgashPhealaleuGlnashnProSerAlaValalProAr 560
Qy 2116 TTTTACGAATTCACCTGT-----TATATATACAAAGAC 2148
Db 560 gPheValIglalalaleuCyglIngllyAspArgCyglInProProValTrpThrTrpYashnAs 580
Qy 2149 TATCATCAGGTATCG 2164
Db 580 nIleThrCysAlaser 585

```

RESULT 7
 US-09-353-585-2
 Sequence 2, Application US/09353585
 Patent No. 6287865
 GENERAL INFORMATION:
 APPLICANT: Dixon, Mark S
 Jones, David A
 Jones, Jonathan DG
 TITLE OF INVENTION: Plant pathogen resistance genes and uses
 thereof
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon & Vanderhye PC

[illegible]

```

Db          1104 entYrArgArgAen 1109

RESULT 8
US-09-353-585-3
; Sequence 3, Application US/09353585
; Patent No. 6287865
GENERAL INFORMATION:
APPLICANT: Dixon, Mark S
            Jones, David A
            Jones, Jonathan DG
TITLE OF INVENTION: Plant pathogen resistance genes and uses
                    thereof
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 6287865th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: United States of America
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EBO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/353,585
FILING DATE: 15-JUL-1999
CLASSIFICATION: C12N 15/29, 15/82, A01H 5/00, A01N 65/00, C12Q
                    1/68
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/930,277
FILING DATE: 27-OCT-1997
APPLICATION NUMBER: PCT/GB96/00785
FILING DATE: 01-APR-1996
APPLICATION NUMBER: GB 9506658.5
FILING DATE: 31-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ms Mary J Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 62-69
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1112 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Tomato
STRAIN: Cf2
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-353-585-3

Alignment Scores:
Pred. No.:          6,226-21          Length:          1112
Score:              294.00            Matches:          185
Percent Similarity: 35.43%            Conservative:     108
Best Local Similarity: 22.37%         Mismatches:       270
Query Match:        4.95%             Indels:           264
DB:                  3                 Gaps:             32

US-09-356-985B-5 (1-3395) x US-09-353-585-3 (1-1112)
Qy          326 GGAAGCTGAATCCCTGCATAGAGGTACTTCTTAATTATACC-----TACCAATGCATG 379
Db          397 GlySerIleProAlaSerLeuGlyAsnIleuAanAanLeuSerArgIleuYrIleuYrAen 416
Qy          380 GATCGAATTCGACGAATAATCCCTCATGATGATCATCCCTTAT-----TCAACCAAGAACTTA 433

```

```

Db      417 AsnGlnLeuSerGlySerIleProGluGlnIleGlyTyrLeuSerSerIleThrTyrLeu 436
      434 GATGTGAGCTTCAACCCCTGAGAGATCTTAAAGACTATGCTTACCAATTTCTCAAA 493
      437 AspLeuSerAsnAsnSerIleAsnGlyPheIleProIleSerPheGlyAsnMetSerAsn 456
      494 CTTGAGGGCTGATTTATCCAGGTGGAATGGAATGGAACAAATGGAACAGGCGAT 553
      457 LeuAlaPheLeuPheLeuTyrGluAsnGlnLeuAlaSerSerValProGluGlnIleGly 476
      554 GCGTTAAACAGCTCTCAACCTTGATCTGACAGAAAACCTCAAGAGTTTCCCA 613
      477 TyrLeuArgSerLeuAsnValLeuAspLeuSerGluAsnAlaLeuAsnGlySerIlePro 496
      614 GGAAGTTTTCGTGACCTAACAAATTTAGAGATCTGGTGGCTGGAGACAAATGACC 673
      497 AlaSerPheGlyAsnLeuAsnAsnLeuSerArgLeuAsnLeuValAsnAsnGlnLeuSer 516
      674 TCTCTAGAGGTTCCATATTGACAGCTTATCCTTAAAGAACTAAATGCGTCAT 733
      517 GlySerIleProGluGlnIleGlyTyrLeuArgSerLeuAsnValLeuAspLeuSerGlu 536
      734 AATCTTATACATTCCTTAAAGTGCCTGAATATTTTCTAATCTGACAAACCTGAACAT 793
      537 AsnAlaLeuAsnGly----SerIleProIleSerPheGlyAsnLeuAsnAsnLeuSerArg 555
      794 GTGATCTTTCTTAACTAATATTCAACTATTTCTGTCAAAGACTTACAGTTCTACGT 853
      556 LeuAsnLeuValAsnAsnGlnLeuSerGlySerIleProGluGlnIleGlyTyrLeuArg 575
      854 GAAATCCCAAGTCAATCTCTCT----- 877
      576 SerLeuAsnAspLeuGlyLeuSerGluAsnAlaLeuAsnGlySerIleProIleSerLeu 595
      877 ----- 877
      596 GlyAsnLeuAsnAsnLeuSerMetLeuTyrLeuTyrAsnAsnGlnLeuSerGlySerIle 615
      878 -----TTAGACTGTCTTTAAACCAATT 901
      616 ProGluGlnIleGlyTyrLeuSerSerIleThrTyrLeuSerLeuGlyAsnAsnSerLeu 635
      902 GACTCATTCAGGCCCAAGCCTTCAGGAGATAGG---CTCCAGTAATGACTCTTAGA 958
      636 AsnGlyLeuIleProIleSerPheGlyAsnMetArgAsnLeuGlnAlaLeuIleLeuAsn 655
      959 AGT-----AATTTTAATAGCTCAATGTA 982
      656 AspAsnAsnLeuIleGlyGlnIleProSerSerValCysAsnLeuThrSerLeuGlnVal 675
      983 CTGAAATG-----TGCCTTCAAAACATGACT 1009
      676 LeuTyrMetProArgAsnAsnLeuGlyGlyValProGlnCysLeuGlyAsnIleSer 695
      1010 GGTTTACATGTCATCGGTGATCTTGGGAGATTTAATAATGAA----- 1054
      696 AsnLeuGlnValLeuSerMetSerSerAsnSerPheSerGlyGlnLeuProSerSerIle 715
      1055 AGCAATCTGAAAGT-----TTTGACGCTTGTCAATGGAAGACTA--- 1096
      716 SerAsnLeuThrSerLeuGlnIleLeuAspPheGlyArgAsnAsnLeuGlnGlyAlaIle 735
      1097 ----TGC-----AATGTAGCATGTAGATTGAGTTAACAATATATATCATTTT 1144
      736 ProGlnCysPheGlyAsnIleSerSerLeuGlnValPheAspMetGlnAsnAsnGlyLeu 755
      1145 TCAGATGATATT-----TATAATCTCAATGCTTGGCAAAATATTTCGATATGCT 1195
      756 SerGlyThrLeuProThrAsnPheSerIleGlyCys-----SerLeuIleSerLeuAsn 773
      1196 TTCACAGGTGATATATAAACACATATGACATGTTCTCAGGCATTTG----- 1243

```

```

Db      774 LeuIleGlyAsnGlnLeuGlnIleAsp-----GlnIleProArgSerLeuAspAsnCysGly 791
      1244 AAATGGCAATCCATTATCAATCATTAATGATGCATTTAG---CCTTTTCCAAAGCTG--- 1297
      792 LysLeuGlnValLeuAspLeuGlyAspAsnGlnLeuAsnAspThrPheProMetTyrLeu 811
      1298 ---AGTTCACCTTTTCTTAAAGTTGGACTTTAACTACCAACAGAGAGAT----- 1345
      812 GlyThrLeuProGluLeuArgValLeuArgLeuThrSerAsnLysIleGlyProIle 831
      1346 ---ATCAGCTTGGTCAAGTTGGCTGCTGCCAAGCTCAGATATCTAATCTTATGAAAT 1402
      832 ArgSerSerArgAlaGluIleMetPheProAspLeuArgIleIleAspLeuSerArgAsn 851
      1403 GCCATGAGCTTTAGAGGTTGCTGTATTGATTTTGAACAAACACTGAATAC 1462
      852 AlaPheSer-----GlnAspLeuProThrSerLeuPheGlnHis 864
      1463 TTAGACCTCAGCTTCAATGCTGCATCTGTAGTAGAGCCAACTTCATGGGCTTGAAGAG 1522
      865 Leu-----LysGlyMetArgThrValAspLysThr-----MetGluGln 877
      1523 CTGGAATACCTGACCTTTCAGCACTCCACTTTAAAGAGTCAACAGATTTCTAGTGTTC 1582
      878 ProSerTyrGluSerTyrTyrAspAspSerValValValThrLys----- 893
      1583 TTATCTTGTAAGAAACTTCTTACCTTGACATCTCTTACATAACCAAAATGACTTT 1642
      893 ----- 893
      1643 GATGGCATATTTCTTGCGTTGATCAGTCACTCAACCTTTAAATGCGTGGCAATTCCTTC 1702
      894 ---GlyLeuGlnLeuGlnIleValArgIleLeuSerLeu----- 905
      1703 AAAGACAACACCTTTCAAATGCTTTTCAAAACAAACAAACTTAATTCCTGATCTT 1762
      906 -----TyrThrValIleAspLeu 911
      1763 TCTTAATGCCAATCGAAGACAGATATCTAAGGGGGTATTGACACACTCTACAGCTCAG 1822
      912 SerSerAsnLysPheGluGlnHisIleProSerValLeuGlyAspLeuIleAlaIleArg 931
      1823 TTATTTAAACATGAGTTCACCAACACTTACTGTTCGTGATCCATCCATTTAAACAGCT 1882
      932 IleLeuAsnValSerHisAsnAlaLeuGlnGlyTyrIleProSerSerLeuGlySerLeu 951
      1883 TACTCCTCAGAGACTCTTGAATGCACTTTCATTCGCTACAGACATCCAAAGAAATCTG 1942
      952 SerIleLeuGlnSerLeuAspLeuSerPheAsnGlnLeuSer----- 965
      1943 CAACATTTTCCAAAGACTCAGCC-----GTCCTCAATTCGACTAAT 1984
      966 GlyGlnIleProGlnGlnLeuAlaSerLeuThrPheLeuGlnPheLeuAsnLeuSerHis 985
      1985 AATTCGTGCTGTATATATGATATCAGAAATTTCTGAGTGCGTCAAGAACAGAA 2044
      986 Asn-----TyrLeuGln-GlyCys-IleProGlnGlyProGlnP 998
      2045 ATGTTCTTGGAATGTTGAACAAATGATGCATCACCCTATAGACATGAAAGGCTCC 2104
      998 heatGThrPheGlu-----SerAsnSerTyrGlnIlyAsnA 1010
      2105 CTGGTGTGATTTTAC----- 2121
      1010 spGlyLeuArgGlyTyrProValSerLysGlyLysAspProValSerGlyLysA 1030
      2122 -----GAATTCACCTGTTATATATCAAGACTATC 2152
      1030 snTyrThrValSerAlaLeuGlnAspGlnGlnSerAsnSerGlnPhePheAsnAspPheT 1050
      2153 ATCAG-----TGTATCGGTGTCAGTGTCTGTG 2182
      1050 rpyAlaAlaLeuMetGlyTyrGlySerGlyLeuCysIleGly----- 1064

```

QY 2183 GTAGCAGCTGAGATTCTGATATACACTTCTATTTTCACTGATCTATTTGCTGGC 2242
 Db 1065 -----IleSerIleIleTyrlleuIleSerThcIlyAsnleuArgTrpL 1080
 QY 2243 TGTAAAA-----GTACAGCAGAGGAGAAAGCATCTAT 2275
 Db 1080 euAlaArgIleIleGluGluIleuGluHisIleIleMetGlnArgTrpLys----- 1097
 QY 2276 GATCATTTTGATGATCTACTGAGCCAGATAGAGAGCTGGTGAAGAGAGCTGTAAAG 2335
 Db 1098 -----LysGlnArgIleGlnArgA 1104
 QY 2336 AATTGAGAGAGAGAGT 2352
 Db 1104 snTyArgArgArgArgsn 1109
 RESULT 9
 US-08-190-802A-50
 ; Sequence 50, Application US/08190802A
 ; Patent No. 5519003
 ; GENERAL INFORMATION:
 ; APPLICANT: Mochly-Rosen, Daria
 ; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
 ; NUMBER OF INVENTIONS: Thereof
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: P.O. Box 60850
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306-0850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/190, 802A
 ; FILING DATE: 01-FEB-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fabian, Gary R.
 ; REGISTRATION NUMBER: 33,875
 ; REFERENCE/DOCKET NUMBER: 8600-0139
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 324-0880
 ; TELEFAX: (415) 324-0960
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 603 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
 ; INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
 ; US-08-190-802A-50
 Alignment Scores:
 Pred. No.: 1.02e-20 Length: 603
 Score: 290.50 Matches: 156
 Percent Similarity: 37.85% Conservative: 87
 Best Local Similarity: 24.30% Mismatches: 244
 Query Match: 4.89% Indels: 155
 Db: 1 Gaps: 24
 US-09-396-985B-5 (1-3395) x US-08-190-802A-50 (1-603)

QY 374 TGCATGATCAGATCTCAGCAAAATCCCTGATGACATCCCTTATTTCAACCAAGACCTTA 433
 Db 60 CysSerSerIyAsnleuThrHisIleuProAspAspIleProValSerThrArgAlaIeu 79
 QY 434 GATCTGAGCTTCAACCCCTGAGAGCTTAAAGATCTTAAAGATCTTACCAATTTCTACAA 493
 Db 80 TrpLeuAspGlyAsnAsnleuSerSerIleProSerAlaIlePheGlnAsnleuSerSer 99
 QY 494 CTTCAGTGGCTGAGATTTATTCAGGTGGAATTTAGACAAATTTGAACAAATTTGAGCAT 553
 Db 100 LeuAspPheLeuAsnleuGlnGlySerTrpLeuArgSerleuGlnProGlnAlaIeu 119
 QY 554 GAGCTTAAACAGCTCTGACACCTTGATCTGACAGAAACCTTAAAGAGATTCTTCCCA 613
 Db 120 GlyLeuGlnAsnleuTyTyTyLeuHisIleuGlnArgAsnArgAlaIleVal 139
 QY 614 GGAAGTTTCTGAGATACAAATTTAGAGATTTGTGGTGGTGGAGACAAATGACC 673
 Db 140 GlyLeuPheThrHisThrProSerleuAlaSerleuSerleuSerAsnleuGly 159
 QY 674 TCTCTAGAGGTTTCCATTTGACAGCTTATATCTTAAAGAACTTAAAGTGGTCAT 733
 Db 160 ArgLeuGlnGluGlyLeuPheGlnGlyLeuSerHisIleuTrpAspLeuAsnleuGlyTrp 179
 QY 734 AATCTTATACATCTCTTAAAGTTGCTGAA---TATTTTCTAATCTGACAAACCTGAA 790
 Db 180 AsnSerleu-----ValIleuProAspThrValPheGlnGlyLeuGlyAsnleuHis 197
 QY 791 CATGTGATCTTCTTAAAC-----TATATTCAAATATTTCTGCAAGACTTA 841
 Db 198 GlnleuValleuAlaGlyAsnIyAsnIyLeuThrTyIleuGlnProAlaIeuPheGlyIeu 217
 QY 842 CAGTTTCTAGTGAAATCCCAAGTCAATCTCTTAAACCTGTCTTAAACCAAT 901
 Db 218 GlyIleuArgIleu-----LeuAspLeuSerAspAsnAlaIeu 230
 QY 902 GATCCATTCAGAGCCCAAGCTTTCAGGAAAT---AGCTCCATGATGACTTAAGA 958
 Db 231 ArgSerValIyAsnAlaAsnValPheValHisIleuProArgleuGlnIyIleuAsp 250
 QY 959 AGTAATTTTAAATAGCTCAAAATGTAAGTGAATGCTTCAAAACATGATGTTTACAT 1018
 Db 251 ArgAsnleu----- 253
 QY 1019 GTCCATGCGTTGATCTTGGAGAAATTTAAAAATGAAAGATCTGAAAGTTTGAACCGT 1078
 Db 254 IleThrAlaValAlaProGlyAlaPheIleuGlyMetIyAsnAlaIeuArgTrpLeuAsp--- 272
 QY 1079 TCTGTCAVGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1138
 Db 273 -----LeuSer 274
 QY 1139 CATTTTCAAGATATTTTAAATCTCAATGCTTGGCAATATTTCTGCAATGCTTTTC 1198
 Db 275 His-----AsnArgAlaIleGlyLeuMetGlnAspThrPhe 286
 QY 1199 -----ACAGGTACATATTAACACATAGCAAT-----GTT 1231
 Db 287 ProGlyLeuIleuGlnIleuHisValIleuArgIleuAlaHisAsnAlaIleAsnSerleuArg 306
 QY 1232 CCTAGGATTTCAAAATGAGCAATCTTATCAATATTTAGATGATCTTAAAGCTTTTCCA 1291
 Db 307 ProArgThrPheIyAsn----- 311
 QY 1292 AAGCTGAGTCACTTTCTTAAAGTTGAGCTTAACTTAACTTAACTTAACTTAACTTAACT 1351
 Db 312 -----AspLeuHisPheIleuGlnIleuGlnIleuGlnIyAsnArg----- 325
 QY 1352 TTGGTCAATG-----GCTTGGCAAGCTTCAATATCTGATGATTT 1393
 Db 326 IleArgGlnIleuGlnIyArgTrpPheGlnGlyIleuGlnIleuGlnIleuValleuThrIeu 345
 QY 1394 AGTAGAATGCAATGAGCTTATAGAGTGTGCTTATCTGATTTTGGAAACAAACAC 1453

Db 346 AsnAspSerGlnIleThrGlnValArgValGlyAlaPheSer-----GlyLeuPheAsn 363
Qy 1454 CTGAAGTACTTGAACCTCAGCTTCAATGGTGTCT--ATCCTGATGAGTGCACATTATG 1510
Db 364 ValAlaValMetAsnLeuSerGlyAsnCySLeuArgSerLeuProGlnArgValPheGln 383
Qy 1511 GGCTAGAAAGAGCGGAATACCTGAGCTTTCAGACCTCCACTTTAAAAAAGGTACAGAA 1570
Db 384 GilyeuAspIySLeuHISerLeuHISerLeuHISerCySLeuGlyHISValArgLeu 403
Qy 1571 TTCTCAGTGTCTTATCTCTTGA AAAAATTCTTACCTTGAACATCTCTTACATATATACC 1630
Db 404 HisThr----- 405
Qy 1631 AAAATTGACTTATGATGGCATTTCTTGGCTTGAATCAGTCTCAACACTTTAAAAATGGCT 1690
Db 406 -----PheAlaGlyLeuSerGlyLeuArgArgLeuPheLeu--- 417
Qy 1691 GGCAATTTCTTCAAGACAAACCCCTTCAAAATGTC-----TTTACAAACACA 1738
Db 418 -----ArgAspAsnSerIleSerSerIleGlyGlnSerLeuAlaGlyLeu 433
Qy 1739 ACAAACTTAACATTCCTGATCTTTCTAATGCCAACTGGAACAGATATCTAGGAGGATA 1798
Db 434 SerGlyLeuLeuGlyLeuAspLeuThrThrAsnArgLeuThrHISLeuProArgGlnLeu 453
Qy 1799 TTTTACACACTCTACAGACTCCATATTAACATGAGTCAACAAACCTACTCTTCTG 1858
Db 454 PheGlnGlyLeuGlyHISLeuGlyIyIyLeuLeuLeuSerIyAsnGlnLeuThrLeu 473
Qy 1859 GATCCATCCCATTAATAACAGCTGTAATCCTCTCAGACTCTTGATGAGATTGCAATGCG 1918
Db 474 SerIleGlyValLeuGlyIyProLeuGlnArgAlaPheThrLeuAspIleSerHISAsnHIS 493
Qy 1919 ATAGAGACA--TCCAAAGAAATCTGCACAACTTTCCAAAGACTAGCCGCTTTCAT 1975
Db 494 LeuGlnThrIleuAlaGlyGlyLeuPheSerSerLeuGlyArg--ValArgIyLeuSer 512
Qy 1976 CTGACTAATATTTCTGTTGCTTGATATGTAATATCAAGATTTCTTGACAGTGGGTCAAG 2035
Db 513 LeuArgAsnAsnSerLeu-----GlnThrPheSerProGlnProGly 526
Qy 2036 GACCAGAAATGTTCTTGATGATGTTGCAAAATGAAATGAAATGCACTCATGAGCATG 2095
Db 527 LeuGlnArgLeuThrLeu--AspAlaAsnProThrAspCySerCySProLeuIyAla 545
Qy 2096 AAGGCTCCCTGCTGTTGGAT-----TTTACGAATTCACCTGT 2134
Db 546 LeuArgAspPheAlaLeuGlnAsnProGlyValIyAlaProArgPheValGlnThrValCyS 565
Qy 2135 -----TATATATACAAGACTATCATCAGTGTATCGGTGTC 2170
Db 566 GilyeuAspAspCySglnProValIyThrIyAsnAsnIleThrCySAlaGlyProAla 585
Qy 2171 AGTGTG 2176
Db 586 AsnVal 587

RESULT 10
US-08-477-346-50
Sequence 50, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Theoreof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSES: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington

STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 603 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
US-08-477-346-50

Alignment Scores:
Pred. No.: 1,02e-20 Length: 603
Score: 290.50 Matches: 156
Percent Similarity: 37.85% Conservative: 87
Best Local Similarity: 24.30% Mismatches: 244
Query Match: 4.89% Indels: 155
DB: 3 Gaps: 24

US-09-396-985b-5 (1-3395) x US-08-477-346-50 (1-603)

Qy 374 TGCATGATCAGATCTCAGCAAAATCCCTCAAGCATCCCTTATTCACCAAGAACTTA 433
Db 60 CysSerSerIyAsnLeuThrHISLeuProAspAspIleProValSerThrArgAlaLeu 79
Qy 434 GATCTGAGCTTCAACCCCTGAAGATCTTAAGAAGCTATAGCTTCAACCAATTTCTCAAA 493
Db 80 ThrLeuAspIyAsnAsnLeuSerSerIleProSerAlaIaPheGlnAsnLeuSerSer 99
Qy 494 CTTCAGTGTGCTGATTTATCCAGGTGTGAATGACAATGACAATGACAAGCATGGCAT 553
Db 100 LeuAspPheLeuAsnLeuGlnGlySerTrpLeuArgSerLeuGlnProGlnAlaLeuLeu 119
Qy 554 GGCTTAACCAAGCTCTCAACCTTGCTGACAGAAACCCCTATCAAGAGTTTCCCA 613
Db 120 GilyeuGlnAsnLeuIyIyLeuHISLeuGlyIyAsnArgLeuValAsnLeuAlaVal 139
Qy 614 GAAAGTTTCTGAGCAATTAATTTAGAAATCTGCTGCTGAGAGCAAAAATGACC 673
Db 140 GilyeuPheThrHISThrProSerLeuAlaISerLeuSerLeuSerSerAsnLeuLeuGly 159
Qy 674 TTCTAGAGGGTTTCCATATTTGACAGACTTATATCTTAAAGAACTAAATGGGCTCAT 733
Db 160 ArgLeuGlyGlyLeuPheGlnGlyLeuSerHISLeuThrAspLeuAsnLeuGlyTrp 179
Qy 734 AATCTTATACATTCCTTAAGTGGCTGAA--TATTTTCTAATCTGACAAACCTTGA 790
Db 180 AsnSerLeu-----ValIyAlaLeuProAspThrValPheGlnGlyLeuGlyAsnLeuHIS 197


```

RESULT 12
US-08-487-072A-50
: Sequence 50, Application US/08487072A
: Patent No. 6423684
: GENERAL INFORMATION:
: APPLICANT: Mochly-Rosen, Daria
: APPLICANT: Ron, Dorit
: TITLE OF INVENTION: MD-40 - Derived Peptides and Uses
: TITLE OF INVENTION: Theeot
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morison & Foerster
: STREET: 2000 Pennsylvania Avenue, NW
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1812
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/487,072A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 2550-0025.20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 887-0763
: INFORMATION FOR SEQ ID NO: 50:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 603 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: INDIVIDUAL ISOLATE: Insulin-like growth factor bind.
: INDIVIDUAL ISOLATE: pro. complex-rat, Fig. 33
US-08-487-072A-50
:
: Alignment Scores:
: Pred. No.: 1,02e-20 Length: 603
: Score: 290.50 Matches: 156
: Percent Similarity: 37.85% Conservative: 87
: Best Local Similarity: 24.30% Mismatches: 244
: Query Match: 4.89% Indels: 155
: DB: Gaps: 24
US-09-396-985B-5 (1-3395) x US-08-487-072A-50 (1-603)
QY 374 TGCATGATCAGATCTCAGCAAAATCCCTCAGCATCCCTTATTCAACCAAGACTTA 433
||| ::|||::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 CysSerSerIysAsnIeuThrHisIeuProAspApIleProValSerThrArgAlaIeu 79
QY 434 GATCTGAGCTTCAACCCCTCGAAGATCTTAAAGAGCTTATAGCTTCACCAATTTCTCAAA 493
||| ||| ||| ||| ||| ||| ::| | | | | | | | | | | | | | | | | | | | | |
Db 80 TrpIeuAspIyAsnAsnIeuSerSerIleProSerAlaAlaPheGlnAsnIeuSer 99
QY 494 CTCACAGGCGTGGATTTATTCACAGGTGTGAATTTGAGACAATTGAAGACAAGCATGGCAT 553
||| ||| ::|||::| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 100 LeuAspPheIeuAsnIeuGlnGlySerTrpIeuArgSerIeuGlnProGlnAlaIeuIeu 119
QY 554 GGCCTTAAACCAAGCTTCAACCTTGGTACTGACAGAGAAACCTTATCAAGAGTTTCCCA 613
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 GlyIeuGlnAsnIeuTyTrpIeuHisIeuGlnIuArgAsnArgIeuArgAsnIeuAlaVal 139
614 GGAAGTTTTCGAGCTAACAAATTTAGAGAACTGGTGGCTGTGGAGACAAAATGACC 673

```

[illegible]

Db 406 -----PheAlaGlyLeuSerGlyLeuArgArgLeuPheLeu--- 417
Qy 1691 GGCAATCTTTCAAGACACACCTTTCAAAATGTC-----TTTACAAACACA 1738
Db 418 -----ArgAspAsnSerIleSerSerIleGluGlnSerLeuAlaGlyLeu 433
Qy 1739 ACAAACTTAACATCTTCGATCTTTCTTAATGCAACGATGCAATATCTAGGGGGGTA 1798
Db 434 SerGlnLeuLeuGlnLeuAspLeuThrThrAsnArgLeuThrIleLeuProGlnLeu 453
Qy 1799 TTGACACACTCTACAGACTTCGACTTAAACATGATGACCAACCACTTCTGTTCTG 1858
Db 454 PheGlnIleGlyLeuGlyIleGlnIleGlyLeuLeuSerIleGlnIleThrLeu 473
Qy 1859 GATCCATCCCATTTAATTAACAGCTGCTACTCCCTGACAGCTCTGATGCAATTCATTCGC 1918
Db 474 SerAlaGluValLeuGlyProLeuGlnArgAlaPheThrLeuAspIleSerHisAsnHis 493
Qy 1919 ATAGAGACA---TCCAAAGGATATCTGCAACATTTTCCAAAGAGTCCGCTTCAAT 1975
Db 494 LeuGlnThrLeuAlaGluGlyLeuPheSerSerLeuGlyArg---ValArgIleLeuSer 512
Qy 1976 CTGACTAATATCTGTGCTGTGATATGATATGATATGCAATTTCTTGACGTGGGTCAAG 2035
Db 513 LeuArgAsnAsnSerLeu-----GlnThrPheSerProGlnProGly 526
Qy 2036 GACCAAGAAATGTTCTTGCTGTAATGTTGAACAAATGAAATGTCATCCTATAGACATG 2095
Db 527 LeuGlnArgLeuThrLeu---AspAlaAsnProThrAspCysSerCysProLeuIleAla 545
Qy 2096 AAGGCTCCCTGGTGGTGGAT-----TTTGAATTCACCTGT 2134
Db 546 LeuArgAspPheAlaLeuGlnAsnProGlyValValProArgPheValGlnThrValCys 565
Qy 2135 -----TATATATACAAAGCTATCATCATGATGATCGGTGTC 2170
Db 566 GluGlyAspAspCysGlnProValIleThrIleAsnAsnIleThrCysAlaGlyProAla 585
Qy 2171 AGGTG 2176
Db 586 AsnVal 587

RESULT 13
US-09-949-016-10995
; Sequence 10995, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10995
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10995

Alignment Scores:
Pred. No.: 4.87e-20 Length: 623
Score: 284.00 Matches: 169
Percent Similarity: 35.55% Conservative: 88
Best Local Similarity: 23.37% Mismatches: 265
Query Match: 4.78% Indels: 201

DB: 4 Gaps: 24
US-09-396-985b-5 (1-3395) x US-09-949-016-10995 (1-623)
Qy 238 GGTGGTTGCAAAAATGCCAGATGATGCTCTTGGCATCTGGCTGGGACTGTGATCAT 297
Db 12 AlaAlaCysProAlaCys-ArgMet-----AlaLeuArgIleGlyCylLeuAlaLeuAl 29
Qy 298 GGCAATGTTCTTCC-----TGCCTGAGACCAAGAAAGTTGAAT----- 337
Db 29 AlaLeuLeuLeuSerIleProValAlaLeuGlyProArgSerLeuGlnIleValAlaAspProG 49
Qy 338 -----CCCTGACATA-----GA 348
Db 49 YThrProGlyGluAlaGluGlyProAlaCysProAlaAlaCysValCysSerIleArgAsp 69
Qy 349 GGTACTTCTTAATATTAATCTTACCAATGATGATCAGATCTCAAGATCTCAAGAAAATCCCTCATGA 408
Db 69 AspAlaAspGluLeuSerValPheCysSerSerArgAsnLeuThrArgLeuProAspG 89
Qy 409 CATCCCTTATTCACCAAGAACCTAGATCTGACCTTCAACCCCTGAAGATCTTAAGAG 468
Db 89 ValProGlyGlyThrGlnAlaLeuThrLeuAspGlyAsnAsnLeuSerValProPr 109
Qy 469 CTATAGCTTCACCAATTTCTCACAACTTCAGTGGCTGATTTATCCAGTGTGAATGA 528
Db 109 AlaAlaPheGlnAsnLeuSerSerLeuGlyPheLeuAsnLeuGlnIleGlyGlnLeuG 129
Qy 529 GACAATTGAAGACAGGATGCGATGCTTAAACAGCTCTCAACCTTGATCTGACAG 588
Db 129 YSerLeuGlnProGlnAlaLeuLeuGlnIleGlnIleAsnLeuCysHisIleuHisLeuGlnI 149
Qy 589 AAACCCATGAAGATTTTCCCGCAGAGATTTTTCGACSTAAACAATTAAGAAATC 648
Db 149 GlnGlnIleuArgSerLeuAlaLeuGlnIlePheAlaHisThrProAlaLeuAlaSerLe 169
Qy 649 GGTGGCTGTGGAACAAAATGAACCTCTAGAGGGTGTTCATATTTGACAGCTTATATC 708
Db 169 UGlyLeuSerAsnAsnArgLeuSerArgLeuGlnIleAspGlyLeuPheGlnIleGlySe 189
Qy 709 CTTAAAGAACTTAATGTGGCTCATTAATCTTATATCATCTTTAAGTGGCTGA---TA 765
Db 189 IleuThrAspLeuAsnLeuGlyIleThrAsnSerLeu-----AlaValLeuProAspAla 207
Qy 766 TTTTTCATATCTGACAAACCTAGAACATGAGATCTTCTTATAC-----TATAT 816
Db 207 AsnArgGlyLeuGlySerLeuArgIleValIleuAlaGlyAsnArgLeuAlaIle 227
Qy 817 TCAAACTATTTCTGTCAAAAGACTTACAGTTTCTACGTGAAGAAATCCCAAGTCAATCTCTC 876
Db 227 UGlnProAlaLeuPheSerGlyLeuAlaGluLeuArgGlu----- 240
Qy 877 TTTAGACTGTCTTTAAACCAATTTGACTCCATTTCAAGCCCAAGCTTT---CAGGGAAT 933
Db 241 -LeuAspLeuSerArgAsnAlaLeuArgAlaIleIleValAsnValPheValGlnLeuPr 260
Qy 934 TAGCTTCATGAATGTGCTTAAAGATTAATTTTAATAGTCAAAATGTG 993
Db 260 ArgLeuGlnIleLeuIleu----- 267
Qy 994 CTTTCAAAACATGACTGTGTTTACATGTCATCGGTGATCTTGGAGAAATTTAAATGA 1053
Db 268 -----As 268
Qy 1054 AAGGAATCTGAAAAGTTTGAACGTTCTGTGCATGAGAGACTATGCAATGTAGCATTTGA 1113
Db 268 PArgAsnLeu----- 271
Qy 1114 TGAAGTTAGGTTAAACATATTAATATCATTTTTCAGATGATATTTAATGTCATTTGCTT 1173
Db 272 ----- 1172
Qy 1174 GGCAAAATATTTCTGCAATGTCTTTCAAGGTGTATATTAACACATAGACAGATGTTCC 1233

```

Db      272  ealalavalaprogilapheleuglyleu-----283
Qy      1234  TAGGATTTCAAATGGCAATCCTTATCATGATTAGATGTCATTAGCCTTTCCAA 1293
Db      284  -Lysalaleuarglyrleuaspleuser-----292
Qy      1294  GCTGAGTCTACCTTTCTTAAAGTTGGACTTAACTACCAACAGA-----1339
Db      293  -----Hisbshargvalalaglyleu 300
Qy      1340  -GAGGATATCAGCTTTGGTCAGTTGGCTCGCCAAAGTCAGATATCTTAGATCTTAGTAG 1398
Db      300  ugliasprhrpherpoglyleu-----glyleuargvalleuargleuserhi 317
Qy      1399  AAATGCCATGAGCTTTAGAGGTGCTGTTCTTATCTCATTTTGGAAACAAACCTGAA 1458
Db      317  sashalallealeseleuargproarghrphelayspleu-----HisphleuGI 335
Qy      1459  GTACTTAGACCTCAGCTTCAATGGTGC---ATCCTGATGAGTGCACATTCATGGCTCT 1515
Db      335  ugliuleuglnleuglyhisbshargillearglnleualaglyuargserpherglyle 355
Qy      1516  AGAAGAGCTGGAATACCTGGAACCTTCAGCACTCCACTTAAAAAAGTCACAGAAATCTC 1575
Db      355  ugliuleuglnleuvalleuthrleuasprhisbshnleuglnleuval---LysalagI 374
Qy      1576  AGTGTCTTATCTCTGAAAAACTTCTTACCTTCAGATCTTACCTAATACCAAAAT 1635
Db      374  yalaphleuuglyleuthrshasnvalalavalmetshleuserglyaencybleuargas 394
Qy      1636  TGACTTATGAGCAATTTCTTGGCTGATGATGATGATGATGATGATGATGATGATGATG 1695
Db      394  nleuprogiluglnvalpheargglyleuglyleuhsisereuhsisereuhsisereu 414
Qy      1696  TTCT-----1699
Db      414  rCyleuuglyargileargprohisrhrphethrCyleuserglyleuargargleuPh 434
Qy      1700  -TTCAAGACCAACCCCTTCAATGTC-----TTTACAAACACACAAACTT 1746
Db      434  eleuhsbshasnleyleuvalaglyleuglnleuhsisereuhsisereuhsisereu 454
Qy      1747  AACATTCCTGATCTTTTAATGACCACTGGAACAGATATCAGGGGATTTTGAACAC 1806
Db      454  uleuglnleuaspleuhsisereuhsisereuhsisereuhsisereuhsisereuhsis 474
Qy      1807  ACTCTACAGACTCCAGTTATTAACATGATGATGATGATGATGATGATGATGATGATG 1866
Db      474  yleuglyyleuuglyuylrleuhsisereuhsisereuhsisereuhsisereuhsisere 494
Qy      1867  CCATTTAACAAGCTGTAATCCCTCAGACTCTTGATGATGATGATGATGATGATGATGAT 1926
Db      494  palaleuuglyproleuglnargalaphetrleuasprhisbshasnleuglnuI 514
Qy      1927  ATCCAAAGGATATCGCAACATTTTCCAAAGAGTACCGCTTCATCTGACATAATA 1986
Db      514  aleuhsisereuhsisereuhsisereuhsisereuhsisereuhsisereuhsisere 534
Qy      1987  TTCTGTTGCTGTATGATGATATCAGAAATTTCTTGACG-----TGGTCAAGACCA 2040
Db      534  nserleuarghrphethrproglinproglinleuhsisereuhsisereuhsisereu 553
Qy      2041  GAAATGTTCTTGGAATGTTGAACAAATGATGATGATGATGATGATGATGATGATGAT 2092
Db      554  -----AsnprotrpaspysglyCysproleuhsisereuhsisereuhsisereu 566
Qy      2093  -----ATGAAGGCTCCCTGCTGTGATTTTGAATTTGCAATTCACCTGT----- 2144
Db      566  gAspPhealeuuglnleuhsisereuhsisereuhsisereuhsisereuhsisereu 586
Qy      2135  -----TATATATACAGACTATCATGATGATGATGATGATGATGATGATGATGAT 2172

```

```

Db      586  yAspAspCysglinProalaTyThrTyAsnAsnIleThrCysAlaSerProProGI 606
Qy      2173  TGTGCTT 2179
Db      606  uValVal 608

RESULT 14
US-09-191-647-7
; Sequence 7, Application US/09191647
; Patent No. 6046015
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey
; APPLICANT: Kld, Thomas
; APPLICANT: Brose, Katja
; APPLICANT: Tesier-Lavigne, Marc
; TITLE OF INVENTION: Modulating Robo: Ligand Interactions
; FILE REFERENCE: B98-031-3
; CURRENT APPLICATION NUMBER: US/09/191,647
; EARLIER FILING DATE: 1998-11-13
; EARLIER APPLICATION NUMBER: 60/065,544
; EARLIER FILING DATE: 1997-11-14
; EARLIER APPLICATION NUMBER: 60/081,057
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1480
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-191-647-7

Alignment Scores:
Pred. No.: 1,12e-19 Length: 1480
Score: 282.50 Matches: 161
Percent Similarity: 33.29% Conservative: 88
Best Local Similarity: 21.52% Mismatches: 246
Query Match: 4.75% Indels: 254
DB: Gaps: 25

US-09-396-985B-5 (1-3395) x US-09-191-647-7 (1-1480)
Qy      374  TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 433
Db      308  Cysargglyuhsisereuhsisereuhsisereuhsisereuhsisereuhsisereu 327
Qy      434  GATGTGAGCTTCAACCCCTGGAAGATCTTAAAGACTTATGCTTACCAATTTTCACAA 493
Db      328  Argleuuglnleuhsisereuhsisereuhsisereuhsisereuhsisereuhsisere 347
Qy      494  CTTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 553
Db      348  leuarglyleuaspleuhsisereuhsisereuhsisereuhsisereuhsisereuhsis 367
Qy      554  GGCTTAACCAAGCTCTCAACCTTGATGATGATGATGATGATGATGATGATGATGATG 613
Db      368  glyleuhsisereuhsisereuhsisereuhsisereuhsisereuhsisereuhsisere 387
Qy      614  GGAAGTTTCTTGGAATTAACAAATTTAGAGATCTGCTGCTGGAAGACAAATGAC 673
Db      388  glyalpheuglyleuglyserleuargleuhsisereuhsisereuhsisereuhsisere 407
Qy      674  TCTTAAGAGGTTCCATTTTGAACAGCTTATATCTTAAAGAACTTAATGATGATGAT 733
Db      408  CysellearglysbapalaphaargAspleuhsisereuhsisereuhsisereuhsisere 427
Qy      734  AATCTTATACATTCCTTAAAGTGCCTGAATATTTTCTAATCTGACAAACCTGAAACAT 793
Db      428  Asnasnleuglnleuhsisereuhsisereuhsisereuhsisereuhsisereuhsisere 446
Qy      794  GTGATCTTCTTATTAACCTATATTAACAACTATTTCTGCAAGCTTACAGTTTCTACGT 853
Db      447  Valhisleuhsisereuhsisereuhsisereuhsisereuhsisereuhsisereuhsisere 464

```

```

QY 854 GAAATCCCAAGCAATCTCTTTAGACCTGTCTTTAAACCCCAATTCATCCATTCAA 913
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 465 Aspyr-----LeuHisysAsnProIleGluThrSerGly 476
QY 914 GCCCAACCTTTACAGGAATTAGCTCCATGAATTCATGAAGT-----961
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 477 AlaArgCysGluSerProLysArgMetHisArgArgIleGluSerLysArgGlu 496
QY 962 AATTATATAGCTCAATATGTAAGAAATGCTTCATAAATCATGATCGTTTACATGTC 1021
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 497 LysPheLysCysSer-----501
QY 1022 CATCGTTGATCTTGGAATTTAAATGAAGAATCTGAAAGTTTTCAGCGTTCT 1081
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 502 -----TrpGlyGluLeu-----ArgMet 507
QY 1082 GTCATGGAAGCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1141
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 508 LysLeuSerGlyGluCysArgMetAspSerAsp-----518
QY 1142 TTTTCAGATGATATTTATTAATCTCAATTCCTGCAATATTTTCGCAATGCTTTTACA 1201
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 519 -----CysProAlaMetCysHisCysGluGlyThrThrValAspCysThr 533
QY 1202 GGTGTACATATTAACAACATAT---GCAGATGTTCTTACGCGATTTTCAATGCGCATCTTA 1258
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 534 GlyArgArgLeuLysGluIleProArgAspIleProLeuHis-----547
QY 1259 TCATATCATAGATCATCTTAAGCCTTTTCCAAAGCTGATCACTTTTCTTAAAGT 1318
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 548 -----Thr 548
QY 1319 TGACCTTAATCAACAAGAGATATTCAGC-----TTTGGT 1357
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 549 ThrGluLeuLeuLeuAsnAspAsnGluLeuGlyArgIleSerSerAspGlyLeuPheGly 568
QY 1358 CAGTTGGCTCTGCCAAGCTTCAGATATCTAGATCTTATGTAAGAAATGCGCATGACCTTTAGA 1417
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 569 Arg-----LeuProHisLeuValLysLeuGluLeuLysArgAsnGlnLeuThr-----584
QY 1418 GGTGTCTGTTCTTATTTCTGATTTTGGAAACAACCACTGAAGTCTTACAGCTTC 1477
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 584 -----584
QY 1478 AATGTGTCATCTGATGATGCGCAAC---TTGATGGGTCTAGAAGAGCTGAATACCTG 1534
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 585 ---GlyIle-----GluProAsnAlaPheGluGlyAlaSerHisIleGlnGluLeu 600
QY 1535 GACTTTCAGCACTCCACTTTAAAAAAGGTCAAGAAATTCAGTGTCTTATCTTTGAA 1594
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 601 GlnLeuGlyGluAsnLysIleLysGluIleSerAsn---LysMetPheLeuGlyLeuHis 619
QY 1595 AAATCTTCTTATCTTGCATCTTCTTACATTAATCCAAATATGCTTGTATGCGATATTT 1654
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 620 GlnLeuLysThrLeuAsnLeuLysArgAsnGlnIleSerCysValMetProGlySerPhe 639
QY 1655 CTTCGCTTCAGCTCACTCAACTTTAAAAAATGCTGCGCATCTTTCTTC-----1702
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 640 GlnHisLeuAsnSerLeuThrSerLeuAsnLeuAlaSerAsnProPheAsnCysAsnCys 659
QY 1702 -----1702
Db 660 HisLeuAlaTrpPheAlaGluCysValArgLysLysSerLeuAsnGlyAlaAlaArg 679
QY 1703 -----AAAGC-----1708
Db 680 CysGlyAlaProSerLysValArgAspValGlnIleLysAspLeuProHisSerGluPhe 699
QY 1708 -----1708
Db 700 LysCysSerSerGluAsnSerGlyLysLeuGlyAspGlyTyrCysProProSerCys 719
QY 1709 -----AACACCTTTTCAAAATGTC-----1726

```

```

Db 720 ThrCysThrGlyThrValValAlaCysSerArgAsnGlnLeuLysGluIleProArgGly 739
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 1726 -----1726
Db 740 IleProAlaGluThrSerGluLeuTyrLeuGluSerAsnGluIleGluGlnIleHisTyr 759
QY 1727 -----TTTCAAAACAACAACAACTTAACATTCCTGATCTTTCTTAAATGCCAATGGA 1780
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 760 GluArgIleArgHisLeuArgSerLeuThrArgLeuAspLeuSerAsnAsnGlnIleThr 779
QY 1781 CAGATATCTAGGGGGGATATTTGACACATCTACAGACTCCAGTTATTTAAACATGATCAC 1840
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 780 IleLeuSerAsnTyrThrPheAlaAsnLeuThrLysLeuSerThrLeuIleIleSerTyr 799
QY 1841 AACACCTCTGTTTTCGATTCATCCATTTAAACAGATGATCCCTCCAGACCTTT 1900
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 800 AsnLysLeuGlnCysLeuGlnArgHisAlaLeuSerGlyLeuAsnAsnLeuArgVal 819
QY 1901 GATTGCAGTTTCATGCAATGAG---ACATCCAAAGAAATACGCAATTTTCCAAAG 1957
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 820 SerLeuHisGlyAsnArgIleSerMetLeuProGluGlySerPheGluAspLeu---Lys 838
QY 1958 AGTTGACCGCTTTCATCTGACTAATATTTCTGTTGCTGTATGTATGTAATTCAGAT 2017
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 839 SerLeuThrHisIleAlaLeuGlySerAsnProLeuTyrCysAspCysGlyLeuTyr 858
QY 2018 TTCTTCGACAGTGGGTCAAGAACCAAGAAATGTTTGTGTGAATTTGAACAAATGAATGT 2077
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 859 PheSerAspTrpIle-----LysLeuAspTyrValGluProGlyIleAlaArgCys 875
QY 2078 GCATCACTTATGACATGAAGGCTCTGCTGTTGATTTTCAATTCACAC-----2131
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 876 AlaGluProGluGlnMetLysAspLysLeuIleLeuSerThrProSerSerPheVal 895
QY 2132 -----TGTATAT-----2139
Db 896 CysArgGlyArgValArgAsnAspIleLeuAlaLysCysAsnAlaCysPheGluGlnPro 915
QY 2140 ATCAAGACTATCATGATGATTCGGT-----GTCAGTGTGCTGT---2181
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 916 CysGlnAsnGlnAlaGlnCysValAlaLeuProGlnArgGlyTyrGlnCysLeuCysGln 935
QY 2182 -----GTTAGCCACTGT 2193
Db 936 ProGlyTyrHisGlyLysHisCys 943

```

```

RESULT 15
US-09-540-245A-7
Sequence 7, Application US/09540245A
Patent No. 6270984
GENERAL INFORMATION:
APPLICANT: Goodman, Corey
APPLICANT: Kid, Thomas
APPLICANT: Brose, Katja
APPLICANT: Tessier-Lavigne, Marc
TITLE OF INVENTION: Modulating Robo: Ligand Interactions
FILE REFERENCE: B98-031-3
CURRENT APPLICATION NUMBER: US/09/540,245A
CURRENT FILING DATE: 2000-03-31
PRIORITY FILING DATE: 1997-11-14
PRIORITY FILING DATE: 1998-04-07
PRIORITY FILING DATE: 1998-04-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 7
LENGTH: 1480
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-540-245A-7

```

Alignment Scores:

Pred. No.: 1,12e-19 Length: 1480
 Score: 282.50 Matches: 161
 Percent Similarity: 33.29% Conservative: 88
 Best Local Similarity: 21.52% Mismatches: 246
 Query Match: 4.75% Indels: 254
 DB: 3 Gaps: 25

US-09-396-985B-5 (1-3395) X US-09-540-245A-7 (1-1480)

```

QY 374 TGCATGATCGAATCTTCAGAAAATCCCTCATGACATCCCTTATTACCAAGAACCTTA 433
DB 308 CysArgGluysSerLeuThrSerValProValThrLeuProAspArgThrThAspVal 327
QY 434 GATCTGAGCTTCACCCCTGAAAGATCTTAAGAACTATAGCTATTCACCAATTTTCACA 493
DB 328 ArgLeuGluGlnAhnPheIleThrGluLeuProProlySerPheSerPheArgArg 347
QY 494 CTTCAGTGGCTGATTTATTCAGAGGTGAAATTTGAGCAATTTGAGCAAGCAAGCATGGCAT 553
DB 348 LeuArgArgIleAspLeuSerSerAsnAsnIleSerArgIleAlaIleAspAlaLeuSer 367
QY 554 GGCCTTAACCGCTCTCAACTTGGTACTGACAGAAACCTTATCAGAGTTTTCCTCCA 613
DB 368 GlyLeuysGlnLeuThrThrLeuValLeuTyrgIlyAsnIlyIleYAspLeuProSer 387
QY 614 GGAAGTTTCTCGACATACAAATTTAGAAATCTGGGTGGTGGAGACAAAATGACC 673
DB 388 GlyValPheYsgIlyLeuGlySerLeuArgLeuLeuLeuAlaAsnGluIleSer 407
QY 674 TCTCTAGAGGGTTTCATATTGACAGCTTATATCTTAAAGAACTAAATGGCTCAT 733
DB 408 CysIleArgIysAspAlaPheArgAspLeuIleSerLeuSerLeuLeuTyArg 427
QY 734 AATCTTATCACTTCTTAACTGCTGAGATATTTTCTAATCTGACAAACCTTAAGACAT 793
DB 428 AsnAsnIleGlnSerLeu--AlaAsnGlyThrPheAspAlaMetIlySerMetIlyThr 446
QY 794 GTGATCTTTCTTAACTATATTCATATTCAAACTATTTCTGCAAGCACTTAAGTTCTACGT 853
DB 447 ValIleuAlaIlyAsn--ProPheIleCysAspCysAsnLeuArgTyArgIleuAla 464
QY 854 GAAATCCCAAGTCAATCTCTTTAGACCTGTCTTAAACCAATTAAGTCTCATTCACA 913
DB 465 AspIyr-----LeuIleIlyAsnProIleGluThrSerGly 476
QY 914 GCCAAGCCTTTCAGGAATTAGCTCCATGAATTAAGCTTAAGAGAGT----- 961
DB 477 AlaArgCysGluSerProIlySerArgMetHisArgArgIleGluSerLeuArgGlu 496
QY 962 AATTTAATAGCTCAAAATGTACTGAATAATGTCCTTCAAAAACATGACTGTTTACATGTC 1021
DB 497 LysPheIysCysSer----- 501
QY 1022 CATCGTGTGATCTTGGAGAAATTTAAATGAAAGAAATCTGAAAGTTTGAACGTTCT 1081
DB 502 -----TrpGlyGluLeu-----ArgMet 507
QY 1082 GTATGGAAGACTATGCAATGTGAGCATTTGATGATGAGTTAACAATATAATCAT 1141
DB 508 LysLeuSerGlyGluCysArgMetCAspSerAsp----- 518
QY 1142 TTTTCAGATGATATTATTAATCTCAATTTGCTGGCAAAATATTTCGCAATGCTTTTACA 1201
DB 519 -----CysProAlaMetCysHisCysGluGluIlyThrValAspCysThr 533
QY 1202 GGTGTACATATAAACACATA--GCAGATGTTCTTAGGCACTTTCAATGGCAATCCTTA 1258
DB 534 GlyArgArgLeuYsgIlyIleProArgAspIleProLeuHis----- 547
QY 1259 TCATATCATTTAGATGATCTTAAGCCTTTTCAAAAGCTGAGTCACTTTTCTTAAAGT 1318
DB 548 -----Thr 548
  
```

```

QY 1319 TGCATTTAACTACCAACAGAGATATATCAGC-----TTTGGT 1357
DB 549 ThrIleuLeuLeuAhnAspAsnGluLeuGlyArgIleSerSerArgIlyLeuPheGly 568
QY 1358 CAGTTGCTCTGCGCAAGCTTCAGATATCTAGATATCTTGAATTTAGAAATGCCATGAGCTTTAGA 1417
DB 569 Arg-----LeuProHisLeuValIlyLeuGluIleuYsgArgAsnGlnLeuThr----- 584
QY 1418 GGTTCGTGTTCTTATTTCTGATTTTGGAAACAAACACTGAAGTACTTAAGACTTCAGCTTC 1477
DB 584 ----- 584
QY 1478 AATGGTCAATCTGATAGAGTCCAAC--TTCATGGGTCTAGAGAGCTGAATATCTTG 1534
DB 585 ---GlyIle-----GluProAsnAlaPheGluGlyAlaSerHisIleGlnGluLeu 600
QY 1535 GACTTCAGACATCCACTTTAAAAAGGTACAGAAATTCAGTGTCTTATCTTTGAA 1594
DB 601 GlnLeuGlyGluAhnIlyIleYsgIlyIleSerAsn--LysMetPheLeuGlyLeuHis 619
QY 1595 AAATCTTCTTACCTTGACATCTCTTACATTAATTAACAAATTTGACTTTGATGGCATATT 1654
DB 620 GlnLeuysThrLeuAhnLeuTyArgAspAsnGlnIleSerCysValMetProGlySerPhe 639
QY 1655 CTTCGCTTGAATCAGTCTCAACACACTTTAAATGGCTGGCAATTCCTTC----- 1702
DB 640 GlnIleuAhnSerLeuThrSerLeuAhnLeuAlaSerAsnProPheAsnCysAsnCys 659
QY 1702 ----- 1702
DB 660 HisLeuAlaTrpPheAlaGluCysValArgIlySerLeuAhnGlyAlaAlaArg 679
QY 1703 -----AAAGAC----- 1708
DB 680 CysGlyAlaProSerIlyValArgAspValGlnIleYsgAspLeuProHisSerGluPhe 699
QY 1708 ----- 1708
DB 700 LysCysSerSerGluAhnSerGluGlyCysLeuGlyAspGlyTyArgCysProProSerCys 719
QY 1709 -----AACACCTTTCAAAATGTC----- 1726
DB 720 ThrCysThrGlyThrValAlaIleCysSerArgAsnGlnLeuYsgIlyIleProArgGly 739
QY 1726 ----- 1726
DB 740 IleProAlaGluThrSerGluLeuTyLeuGluSerAhnGluIleGluGlnIleIleTyArg 759
QY 1727 -----TTTACAAACACAAACCTTAACATTCCTGATCTTTCTTAATGACCACTGGA 1780
DB 760 GluArgIleArgHisLeuArgSerLeuThrArgLeuAspLeuSerAsnAhnGlnIleThr 779
QY 1781 CAGATATCTAGGGGGGTATTGTGACACACTTACAGACTTCCAGTTATTTAAACATGAGTCA 1840
DB 780 IleLeuSerAhnTyThrPheAlaAhnLeuThrIlySerSerThrIleIleSerTyArg 799
QY 1841 AACACCTTACTGTTTCTGATCCATCCATTAATAACAGCTGATCTCCTCAGACTCTT 1900
DB 800 AsnIlySerGlnCysLeuGlnArgHisAlaIleuSerGlyLeuAhnAhnLeuArgVal 819
QY 1901 GATTGACGTTTCAATGCAATGAG--ACATCCAAAGAGATATGCAACATTTTCCAAAG 1957
DB 820 SerLeuHisGlyAhnArgIleSerMetLeuProGluIlySerPheGluAspLeu--Lys 838
QY 1958 AGTTCAGCCGCTTTCATCTGATTAATTAATTTGTTGCTGTATATGTGTAATTCAGAAAT 2017
DB 839 SerLeuThrHisIleAlaLeuGlySerAhnProLeuTyArgCysAspCysGlyLeuTyArg 858
QY 2018 TTCTTGCAAGTGGGTCAAGACCAAGAAATGTTCTTGATGATGTGGAACAAAGAAATGT 2077
DB 859 PheSerAspTrpIle-----LysIleuAspTyArgIleuProGlyIleAlaArgCys 875
QY 2078 GCATCACTTATAGACATGAAGGCTCCGTGTTGATTTTACGAATTCACAC----- 2131
  
```

```
Db      876 AlagluProgluInMetLysAspLysLeuIleuSerThrProSerSerPheVal 895
QY      2132 -----TGTATAT----- 2139
Db      896 CysArgGlyArgValArgAsnAspIleuAlaLysCysAsnAlaCysPheGluInPro 915
QY      2140 ATACAAGACTATCATCAGTGTATCGGT-----GGTCAGTGTGCTTGT--- 2181
Db      916 CysGlnAsnGlnAlaGlnCysValAlaLeuProGlnArgGluTyrGlnCysLeuCysGln 935
QY      2182 -----GGTAGCCACTGT 2193
Db      936 ProGlyTyrHisGlyLysHisCys 943
```

Search completed: March 29, 2005, 17:38:10
Job time : 83.8263 secs

Result No.	Score	Query Match	Length	DB	ID	Description
1	597.5	10.1	661	2	156258	RP105 - mouse
2	465.5	7.8	766	2	T08664	Toll protein-like
3	398.5	6.7	1097	2	A29943	Toll protein precursor
4	374.5	6.3	1389	2	T13562	gene wheeler prote
5	371.5	6.3	1385	2	T13867	tlr protein - frutl
6	333.5	5.6	1134	1	A29944	chaoptin precursor
7	303.5	5.1	1066	2	T15864	hypothetical prote
8	301.5	5.1	603	3	JC6128	insulin-like growt
9	301	5.1	605	2	UC5239	insulin-like growt
10	294	4.9	1112	2	T10504	disease resistance
11	290.5	4.9	603	3	JC1382	insulin-like growt
12	285.5	4.8	1051	2	T13174	sp10 protein - fr
13	282.5	4.8	1466	2	B3665	slit protein 2 pre
14	282.5	4.8	1480	2	A3665	slit protein 1 pre

15	282.5	4.8	1523	2	T13955	MEGFI1 protein - r
16	281.5	4.7	605	2	A41915	infin-like growth
17	274	4.6	1592	2	A33988	adenylate cyclase
18	270.5	4.6	1143	2	T10636	hypothetical prote
19	270	4.5	907	2	UG0193	G protein-coupled
20	267	4.5	1016	2	T30553	disease resistance
21	267	4.5	1531	2	T42218	slit-1 protein hom
22	264.5	4.5	1037	2	B85089	receptor protein k
23	261	4.4	1232	2	T05332	hypothetical prote
24	259	4.4	910	2	G84648	probable disease r
25	256	4.3	560	2	A60164	platelet membrane
26	254	4.3	907	2	J60176	Platlet G protein-c
27	252	4.2	1068	2	B96769	hypothetical prote
28	252	4.2	1120	2	B86479	hypothetical prote
29	249	4.2	662	2	S42799	garp precursor - h
30	249	4.2	855	2	T17460	disease resistance
31	247.5	4.2	910	2	B66770	hypothetical prote
32	247.5	4.2	1778	2	AF1116	internalin protein
33	247	4.2	890	2	T00800	disease resistance
34	246.5	4.1	853	2	T17461	disease resistance
35	245.5	4.1	951	2	A96770	hypothetical prote
36	245	4.1	800	2	H84740	hypothetical prote
37	244	4.1	1091	2	A58332	glial cell membran
38	243.5	4.1	738	2	T119938	hypothetical prote
39	243	4.1	1784	2	G36615	hypothetical prote
40	242.5	4.1	603	2	T24315	hypothetical prote
41	239	4.0	855	2	T07015	Cf-4a protein - to
42	237	4.0	994	2	H96510	probable disease r
43	236.5	4.0	622	2	GC7973	synleaurin - huma
44	236.5	4.0	983	2	G84524	probable disease r
45	235.5	4.0	2026	1	ORBY	adenylate cyclase

ALIGNMENTS

RESUL

I56258
 RP105 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I56258
 J:Miyaake, K.; Yamashita, Y.; Ogata, M.; Sudo, T.; Kimoto, M.
 J. Immunol. 154, 3333-3340, 1995
 A:Title: RP105, a novel B cell surface molecule implicated in B cell activation, is a member of the TNF receptor superfamily
 A:Reference number: I56258; NUID:95204928; PMID:7897216
 A:Accession: I56258
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-661 <RSS>
 A:Cross-references: UNIPROT:Q62192; GB:D37797; NID:g761711; PIDN:BAA07043.1; PID:g761712

Alignment Scores

Pred. No.:	5,35e-35	Length:	66
Score:	597.50	Matches:	18
Percent Similarity:	46.50%	Conservative:	12
Best Local Similarity:	27.87%	Mismatches:	35
Query Match:	10.05%	Indels:	41
DB:	2	Gaps:	15

US-09-396-985B-5 (1-3395) x 156258 (1-661

[illegible]

```

QY 467 AGCTAATGCTTCCACCAATTTCTCACAACCTTCAGTGGCTGATTTATTCAGGCTGATTAAT 526
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 70 AsnThrThrPheSerArgLeuIleAsnLeuThrPheLeuAspLeuThrArgCysGlnIle 89
QY 527 GAGCAATTAAGACAGCAAGCATGGCAGCTTTAAACAGCTCTCAGACCTTGATCTGACA 586
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 90 TyrTrpIleHisArgLeuThrPheGlnSerGlnHisArgLeuAspThrLeuValLeuThr 109
QY 587 GGAAACCCCTATCAGAGTTTTCGCCAGAGTTTTCCTGAGCAATCAAAATTTTGAGAT 646
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 110 AlaAsnProLeuIlePheMetArgIleThrAlaLeuSerGlyProValAlaLeuHis 129
QY 647 CTGGCTGCTGTGAGCAAAATGACCTCTGACAGGCTTTCATATGACAGCTTATA 706
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 130 LeuPhePheIleGlnThrCylIleSerSerIleAspPheIleProLeuHisAsnGlnHis 149
QY 707 TCTTTAAAGAACTAAATGAGCTCAATATCTTTATACATCTCTTAAGTCCCTGAATAT 766
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 150 ThrLeuGlnSerLeuTyrLeuGlySerAsnHisIleSerSerIleTyrLeuProIyGly 169
QY 767 TTTTCTATCTGACAAACCTAGAACATGTCATCTTTTATATATATCAAACTATT 826
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 170 PheProThr---GluValLeuValIleuAspPheGlnAsnAsnAlaIleHisTyrLeu 188
QY 827 TCTGTCAAGACTTACAGTTTCTACGTGAATATCCCAAGTCAATCTCTTTAGACCTG 886
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 189 SerIyGlnAspMetSerSerLeuGlnGln-----AlaThrAsnLeuSerLeuAsnLeu 206
QY 887 TCTTTAAACCAATGACTCCATTCAGCCCAAGCTTTCAGGGAATTAGGCTCCATGAA 946
   ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 207 AsnGlyAsnAspIleAlaGlyIleGluProGlyAlaPheAspSerAlaValPheGlnSer 226
QY 947 TTGACTTAAGAGTAATTTAATAGTCAATAGTACTGAATATGCTTCAAAACATG 1006
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 227 Leu-----AsnPheGlyGlyThrGlnAsnLeuLeuValIlePheIyGlyLeu 242
QY 1007 ACTGGTTACATGTCATCGGTTGATCTTGAGAGATTTAAATGAAGAGATCTGGAA 1066
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 243 LysAsnSerThrIleGlnSerLeuThrLeuGlyThrPheGln---AspMetAspAspIlu 261
QY 1067 AGTTTGAACGTTCTGTATGAGAGACTATGCAATGTGAGCATTTAGTACAGTTA 1126
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 262 AspIleSerProAlaValPheGlnGlyLeuCysGlnMetSerValGlnSerIleAsnLeu 281
QY 1127 ACATATATAAATCATTTTTCAGATGATATTAATATCATCATGCTTGGCAATATTTCT 1186
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 282 GlnIyHisTyrPhePheAsnIleSerSerAsnThrPheHisCysPheSerGlyLeuGln 301
QY 1187 GCAATGCTTTCACAGTGTATCATATTAACAACATAGACAGAT----- 1228
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 302 GluLeuAspLeuThrAlaThrHisIleuSerGluLeuProSerGlyLeuValGlyLeuSer 321
QY 1229 -----GTTCTTAGGCATTTCAATGGCAATCTTATTCATCATATAGATGT 1273
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 322 ThrLeuIySlyIleValIleuSerIleAsnIySspHeGlnAsnLeu-----Cys 337
QY 1274 CATCTTAAGCCCT-----TTTCCAAAGCTGAGTCACTTTTCTTAAAGTTGACCTTA 1327
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 338 GlnIleSerAlaSerAsnProSerLeuThrHisIleuSerIleTyrGly----- 354
QY 1388 ACTACCAACAGAGAGATATACGTTTGTCAGTTGGCT---CTGCCAAGTCTCAGATAT 1384
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 355 AsnThrIySargLeuGlnLeuGlyThrGlyCysIleuGlnAsnLeuGlnAsnLeuArgGln 374
QY 1385 CTAGATCTTAGTAAATGCCATGAGCTTTAGAGCTTGCTGTTCTTATTTGATTTTGA 1444
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 375 LeuAspLeuSerHisAspAspIleGluThrSerAspCysAsnLeuGlnLeuArgAsn 394
QY 1445 ACAAAACACCTGAAGTACTAGACTCAGTTTCAATGAGTGCATC---CTAGTGGAGCC 1501
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 395 LeuSerHisIleuGlnSerIleuAsnMetSerTyrAsnGluProLeuSerLeuIySThrGlu 414
QY 1502 AACTTCATGGGTCTAGAAAGAGCTGGAATACCTGACCTTTCAGCACTTCACTTAAAAAG 1561

```

```

Db 415 AlaPheIySglCysProGlnIleuGlnLeuLeuAspLeuAlaPheThrArgLeuVal 434
QY 1562 GTCAAGAAATTCACAGTTCTTATCTGTGAAAACCTTTTACCTTTCAGCATCTTAC 1621
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 435 LysAspAlaGlnSerProPheGlnIleuHisIleuLeuIyValIleuAsnLeuSerHis 454
QY 1622 ACTAATACCAAAATGACTTGTAGTGGCATATTTCTTGAGCTTGTAGTCAACATTTA 1681
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 455 SerLeuLeuAspIleSerSerGlnGlnLeuPheAspIlyLeuProAlaLeuGlnHisLeu 474
QY 1682 AAAATGGCTGGCAATTTCTTCAAAAGACACACCTT-----TCAATGTCTTTACAAAC 1735
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 475 AsnLeuGlnGlyAsnHisPheProIyGlyAsnIleGlnIySThrAsnSerLeuGlnThr 494
QY 1736 ACAACAAATTTACATTTCTGATCTTTCTTAAATGCCAACTGGCAACAGATATCAGGGG 1795
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 495 LeuGlyArgLeuGluIleLeuValIleuSerPheCysAspLeuSerSerIleAspGlnHis 514
QY 1796 GTATTTGACACACTGTACAGACTCCAGTTATTAACAGTACGATGACAACTACTGTTT 1855
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 515 AlaPheThrSerLeuIySmetMetAsnHisValAspLeuSerHisAsnArgLeuThrSer 534
QY 1856 CTGGAT-----CCATCCCATTTATTAACACCTGTACTCCCTCAGACCTTTGATGTC 1906
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 535 SerSerIleGlnAlaLeuSerHisIleuIyGlyIleTyr-----LeuAsnLeu 550
QY 1907 AGTTCAATGCGCATAGAGACATCCAAAGAAATCTGCAACATTTTCCAAAGAGCTAGCC 1966
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 551 AlaSerAsnHisIleSerIleIleLeuProSerLeuLeuProIleLeuSerGlnIArg 570
QY 1967 GTCTTCAATGCTAATATATCTGTGCTGTATGATGTAATGCAATTCGAATTTCTTGACG 2026
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 571 ThrIleAsnLeuArgGlnAsnProLeuAspCysThrCysSerAsnIleTyrPheLeuGln 590
QY 2027 TGGGTCAAGACCAAGAAATGTTCTTGATAGTTGCAACAAATGAAATGTGATCACT 2086
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 591 TrpTyrIySglAsnMetGlnIySLeuGlnAspPheArgIleAspThrLeuCysGlnAsnPro 610
QY 2087 ATGACATGAAAGGCTCCCGTGGTGGATTTTACGAATTCACACCTGTAT----- 2137
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 611 ProLeuIyArgIyAlaArgLeuSerAspValThrIleuSerCysSerMetAlaAlaVal 630
QY 2138 ---ATATACAAAGACTATCATCATGATCGTATCGGTGCTGATGCTGTGAGCACTGTA 2194
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 631 GlyIlePhePheLeuIleValIlePheLeuValPheAlaIleLeuLeuIlePheAlaVal 650
QY 2195 GCATTTCTGATATACCACTTCTATTTTACCTG 2227
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 651 LysTyrPheLeuArgTyrIySglnHisIle 661

RESULT 2
T08664
Toll protein-like receptor DKFZp54710610.1 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08664
R:Pousetka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16466
A:Accession: T08664
A:Molecule type: mRNA
A:Residues: 1-786 <POU>
A:Cross-references: UNIPROT:Q15399; EMBL:AL050262
A:Experimental source: fetal brain; clone DKFZp54710610
C:Genetics:
A>Note: DKFZp54710610.1

Alignment Scores:
Pred. No.: 1, 71e-25 Length: 786
Score: 465.50 Matches: 203
Percent Similarity: 40.83% Conservative: 131
Best Local Similarity: 24.82% Mismatches: 287

```


Db	663	GLYmet-----GlnIleCysLeuH1seGlnIArgAnPheValProGlyLysSerIle	679
Qy	2408	GCTCCCAACATCATCTCCAGGAAGCGCTTCCACAGAGCCGGAAGATTATGTGTCGTCT	2467
Db	680	ValGluSenIleIle---ThrCysIleGlnLysSerTrpLysSerIlePheValLeuSer	698
Qy	2468	AGACACTTATTCACAGAGCCGTTGGTGTATCTTTGATATATGAGANTGCTCAGACATGGCA	2527
Db	699	ProAsnPheValGlnSerGlnTrpCysH1sArgLysLeuTrpPheAlaH1sH1sAlaLeu	718
Qy	2528	TTTCTGAGTACCCGCTCGGCATCATCTTCATCTGTCCTTGAAGAGT---GAGAAAGTCC	2584
Db	719	PheH1sGlnLysSerAsnSerIleuIleLeuIleLeuGlnProIleProGlnTrpSer	738
Qy	2585	TTGCTGAGGACAGAGTGAATTGATCGCCTTTAGACAGAAACACCTACCTGAGTGG	2644
Db	739	IleProSerSerTrpH1sLysLeuLysSerLeuMetAlaIaGArgTrpTrpLysGlnTrp	758
Qy	2645	GAGACAAATGCTCTGGGGAGGCACATCTTTGAGAGAGATCCMAAAAAGCCCTG	2688
Db	759	ProLysGlnLysSerLysArgLysLeuPheTrpAlaAsnLeuGalaAlaIle	776

RESULT 3

Toll protein precursor - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C:Accession: A29943
C:Hashimoto, C.; Hudson, K.L.; Anderson, K.V.
Cell 52, 269-279, 1988
A:Title: The Toll gene of *Drosophila*, required for dorsal-ventral embryonic polarity, and
A:Reference number: A29943; MUID:88135760; PMID:2449285
A:Accession: A29943
A:Molecule type: DNA
A:Residues: 1-1097 >HAS>
A:Cross-references: UNIPROT:P08953; GB:M19699; GB:J02682; NID:g158640; PTDN:AAA28941.1,
C:Genetics:
A:Gene: FlyBase:T1
A:Cross-references: FlyBase:FBgn0003717
C:Keywords: transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-1097/Product: Toll protein #status predicted <NAT>

Alignment Scores:

Pred. No.:	1,19e+20	Length:	1097
Score:	398.50	Matches:	120
Percent Similarity:	38.37%	Conservative:	125
Best Local Similarity:	24.05%	Mismatches:	317
Query Match:	6.71%	Indels:	221
DB:	2	Gaps:	34

US-09-396-985B-5 (1-3395) X A29943 (1-1097)

QY	212	GTCTTCGATGCTTTTCACAGGCGTCGGCTGGTGGAGAAAATGCGAGGATG-----	262
		:	
Db	258	VALAAGLeuMeCAsmnaArgValProLeuAlaThrLeuProSerLeuPheAlaAsn	317
		:	
QY	263	ATGCGCTCTTTCGATCTGGCTGGAGCTCGATCATGAGCATTTGCTTCCTGCGCTGAGA	322
		:	
Db	318	GLNProGluLeuGlnLe-----LeuArgLeuArgAlaGluLeuGlnInsertLeu---	333
		:	
QY	323	CCAGGAGAGCTTGAATCCCTGCATAGAGGATCTCTTAATATTTCCTACCAATGATGAGAT	382
Db	334	PROGlyAspLeu-----PheGlnHisSerThrGlnLeuThrLeuHisSerLeuGly	350
QY	383	CAGAAATCTAGAGAAA-----ATCCCTAGACATCCCTTATTGAACC	424
Db	351	AspAsnLeuLeuLysThrLeuProAlaThrLeuLeuGlnHisLeuVal-----AsnLeu	368
		:	
QY	425	AAGAACTTAGATCTGAGCTTCAACCCCTGAGAGATCTTAAAGAACTTAGAGCTTCAACCAAT	484
		:	
Db	369	LeuSerLeuAspLeuSerAsnAsnArgLeuThrHisLeuProAspSerLeuPheAlaHis	388
		:	

QY	485	TTCTCACAAGCTTCACTGCGCTGAGATTATTCAGAGGTGAAATTTAGACAATTTGAACAAGACAG	544
DB	389	ThrThrAsnLeuThrAspLeuArgLeuGluAspAsnLeuLeuThrGlyIleSerGlyAsp	408
QY	545	GCATGAGCATGGCTTTAAACACAGCTCTCAACCTTGATCTGACAGGAAACCCATACAGAGT	604
DB	409	IlePheSerAsnLeuGlnValAsnLeuValThrLeuValIleSerArgAsnArgLeuArgThr	428
QY	605	TTTTCCCAAGAGTTTTCTTGACACTAACAAATTTAGAAATCTG	649
DB	429	IleAspSerArgAlaPheValSerThrAsnGlyLeuLeuArgIleValSerHisLeuAspHisAsn	448
QY	650	-----GTGCGCTGTGAGACAAATAAGACCTCTCTA	679
DB	449	AspIleAspLeuArgLeuGlnProLeuLeuAspIleLeuLeuGlnThrGlnIleAsnSerPro	468
QY	680	GAGGATTTCCATATTTGACACAGCTTATATCCTTAAAGAACTAAATGTGGCTCATATCTT	739
DB	469	PheGlyIyrMetHisGlyIle-----LeuLeuThrLeuAsnLeuAspAsnSer	484
QY	740	ATACATTCCTTTAGTGGTCCGATATTTTCTAAATCTGACAAACCTAGAAACATGTGAT	799
DB	485	Ile---IlePheValTyrAsnAspTrpLeuAspHisThrMetLeuGlnLeuAspArgGluLeuAsp	503
QY	800	CTTTCTTATACATATATATTTCAAACTATTTCTGTCAAAAGCTTACAGTTTCTACGTGAAT	859
DB	504	LeuSerTyrAsnAsnIleSerSerLeuGlyTyrGluAspLeuAlaPheLeuSerGlnAsn	523
QY	860	CCCCAAGTCATCTCTCTTTAGACCTGTCTTTAAACCCATATGACTCCATTCAAAGCCCA	919
DB	523	-----	523
QY	920	GCCTTTCAGGAATTAAGGCTCATGAATTTAGCTCTAAGATATTTTAATTAAGCTCAAT	979
DB	524	-----ArgLeuHis-----	526
QY	980	GTACTGAAATATGTGCTTCAAAACATGACTGTGTTACATGTCATCGGTGATCTTGGA	1039
DB	527	-----ValAsnMetThrHisAsnIlyHisAsnIlyIleAspArgIleAlaLeuPro	540
QY	1040	GAATTTAAATAATGAAGAAGATCTGAAAGTTTAAACGCTGTCTGTCAAGAAAGACTATGC	1099
DB	541	Glu-----AspValHisLeuGlyGluGlyTyrAsn	550
QY	1100	AATGTGACATGTATGAGTTCAGGTTAATCATATATTAATCATTTTTCAGATGATATTTAT	1159
DB	551	Asn-----AsnLeuValHisValAsp-----LeuAsnAspAsnProLeu	563
QY	1160	AATCGATCTGTTGGCAAAATATTTTCGCATATGCTTTCACAGAGTGACATATAAACAC	1219
DB	564	ValCysAspCysThrIleLeuTrpPheIleGlnLeuValArgGlyValHisLeuProGln	583
QY	1220	ATAGCAGATGTCTCAGGCACTTTAAATGCAATCTTATCAATCACTTAGATGTCATCTT	1279
DB	584	TyrSer-----ArgGlnPheIlyAsnArgHisAspArgLeuVal-----	596
QY	1280	AAGCTTTTCCAAAGCTGAGTCACTTTTCTTAAAGTTGCACTTTACTACTCAACAGAGA	1339
DB	597	-----CysSerGlnProAsnValLeuGlnGlyThrProValArgGlnIle	611
QY	1340	GAGATATACAGCTTTGTCAGTGTGGCTGTGCAAGTGCACAGATACAGATCTTAAGTGA	1399
DB	612	GluPro-----GlnThrIleuIleCysProLeuAspPheSerAspAspProArg	627
QY	1400	AATGCCATGAGCTTTAGAGTTCG---TGTCTTATTTCTGATTTTGGAAACAACACTG	1456
DB	628	GluArgIlyCysProArgGlyCysAsnIlyHisValArg-----	640
QY	1457	AAGTACTTAGACCTCAGCTTCAATAGTGTCATCTCGATGAGTGGCAACTTATGGGTCTA	1516
DB	641	-----ThrTyrAspIlyAlaLeuValIleAsnCysHisSerGlyAsnLeu	655

```

QY 1517 GAAGAGCTGAATACCTGAGACTTTCAGACTCCATTAAAGGTCAGAAATTCACA 1576
Db 656 ThrihisValProAlaGluProAsnLeuHisLysAsnMetGlnLeuMetGlu----- 672
QY 1577 GTGTTCTTATCTTGAAAACTTCTTTCATCTTGACATCTCTTACATAATCCAAAAATT 1636
Db 673 -----LeuHisLeuGluAsnAsnThrLeuLeuArgProSerAlaAsnThrPro--- 689
QY 1637 GACTTTGATGGCATATTTCTTGCTTGATCAGTCCAAACATTAAATAAAGCGGCAGAT 1696
Db 690 -----GlyTyrGluSerValThrSerLeuHisLeuValGlyAsn 702
QY 1697 TCTTTCAAGACACACCCCTTTCAAATGCTTTTCAACACAGAAAATTAACTTCCTG 1756
Db 703 AsnLeu-----ThrSerLeaAspValAspGlnLeuProThrAsnLeuThrHisLeu 719
QY 1757 GATCTTTCTAATGCCAATCGAAACAGATATCTAGGGGGTATTTGACACACTCAGACA 1816
Db 720 AspLeuSer-----TyrAsnHis 725
QY 1817 CTCGAGTTATTAACATGATGACACAAACCTACTGTTTCGATCCATCCCATTAATAA 1876
Db 726 LeuGlnMetLeuAsn----- 730
QY 1877 CAGCTGACTCCCTCAGACTCTTGATTCAGTTTCAATCGCATAGACATCCAAAGCA 1936
Db 731 -----AlaThrValLeuGly 735
QY 1937 ATACTGCACATTTTCCAAAGAGTCTAGCCGCTTTCATCTGACTAATTAATCTGTTGCT 1996
Db 736 PheLeuAsnArgThrMetLeuTyrPArgSerVal---LysLeuSerGlyAsnProTyrMet 754
QY 1997 TGTATATGTAATATCAGAAATTTCTGCAAGTGGGTCAGAGCCAGAAAATGTTCTTGCTG 2056
Db 755 CysAspCysThrAlaLysProLeuLeuLeuPheThrGlnAspAsnPheGluArgIleGly 774
QY 2057 AATGTTGAACAATGAATGATGCATCACTTATGACATGAAGGCTCCCTGCTGTGGAT 2116
Db 775 AspArgAsnGlnMetMetCysValAsn---AlaGluMetProThrArgMetValGluLeu 793
QY 2117 TTATGCAATTCACCTGTTATATATACAAAGCTATC--ATCAGTGTATCGGTGTC--- 2170
Db 794 SerThrAsnAspIleCysProAlaGluLysGlyValPheIleAlaLeuAlaValValIle 813
QY 2171 -----AGTGTCTTGTTGTTAGCCACTGATCTTCTGATATACCACTTC----- 2215
Db 814 AlaLeuThrGlyLeuLeuAlaGlyPheThrAlaAlaLeuTyrTyrLysPheGlnThrGlu 833
QY 2216 -----TATTTTCAC--CTGATCTTATTTGCTGCTGCTGTTAAAGATACAGC 2257
Db 834 IleLysIleTyrPheLysAlaHisAsnLeuLeuTyrPheValThrGluGluAspLeu 853
QY 2258 AGAGAGAACATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2317
Db 854 AspLysAspLysLysPheAspAlaPheIleSerTyrSerHisLysAspGlnSerPheIle 873
QY 2318 AGAACAACAGCTGTTAGAAATTTAGAAAGAGAGTCCCGCTTTCAGCTTTCCTTCAT 2377
Db 874 GluAspTyrLeuValProGlnLeuGlnHisGlyProGlnLysPheGlnLeuCysValHis 893
QY 2378 TACAGGAGCTTATCTCTGCTGAGCCATTCGTCGACATCATCCAGAGAGGCTTCAC 2437
Db 894 GluArgAspIrrPheValGlyGlyHisIleProGluMetHisLeuArg---SerValAla 912
QY 2438 AAGAGCCGAGAAATTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2497
Db 913 AsperArgArgTyrIleIleValLeuSerGlnAsnPheIleLysSerGluTyrAlaArg 932
QY 2498 TTTGAATATGAGATTGCTCAGACATGACAGTTTCTGAGTACCCGCTGCGATCATCTTC 2557
Db 933 LeuGluPheArgAlaAlaHisLysSerAlaLeuAsnGluGluArgSerArgIleIleVal 952
QY 2558 ATTGTC-----CTTGAGAAAGTGAAGAGTCTCTGTCGAGCAGAG 2599

```

```

Db 953 IleLysIleSerAspIleGlyAspValGluLysLeuAspGlu----- 966
QY 2600 GTGCAATTTGATGCTCTTCTTACAGAAACACTCACTCGAGTGGGAGACATGCTCTG 2659
Db 967 ---GluLeuLysAlaTyrIleuLysMetAsnThrTyrIleuLysTyr----- 980
QY 2660 GGGAGGACATCTTCTGAGAGACTCAAAAAGCCCTG 2698
Db 981 GlyAspProTyrPheThrAspLysLeuArgPheAlaLeu 993

RESULT 4
T13852
gene: wheeler protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T13852
R:Eldon, R.; Kooyer, S.; D'aveilyn, D.; Duman, M.; Lawinger, P.; Botes, J.; Bellem, H.
Development 120, 885-899, 1994
A:Title: The Drosophila 18 wheeler is required for morphogenesis and has striking simila
A:Reference number: Z17796; MUID:95324375; PMID:7600965
A:Accession: T13852
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1389 <EID>
A:Cross-references: UNIPROT:Q24591; EMBL:L23171; NID:G415682; PID:G1019104; PIDN:AAA7920
C:GeneticS:
A:Gene: wheeler
A:Cross-references: FlyBase:FBgn0004364

Alignment Scores:
Pred. No.: 6,56e-19 Length: 1389
Score: 374.50 Matches: 250
Percent Similarity: 35.40% Conservative: 172
Best Local Similarity: 20.97% Mismatches: 361
Query Match: 6.30% Indels: 410
DB: 2 Gaps: 54

US-09-396-985b-5 (1-3395) x T13852 (1-1389)
QY 380 GATCAGATCTCAGCAAAATCCCTCATGACATCCCTTATTCACAAAGAACTAGATCTG 439
Db 154 AspAsnAsnIleArgGlnLeuProGluGluValTyrCysSerMetProSerLeuGlnLeu 173
QY 440 AGCTTCAACCCCTGAAGATCTTAAGAAGCTATAGCTTACCAATTC----- 487
Db 174 LeuAsnLeuThrGlnAsnArgIleArgSerAlaGluPheLeuGlyPheSerGluLysLeu 193
QY 488 -----TCACAACTTCAG 499
Db 194 CysAlaGlySerAlaLeuSerAsnAlaAsnGlyAlaValSerGlyGlySerGluLeuGln 213
QY 500 TGGCTGATTTATTCAGGTGTAATTTAGACAAATTGAGACAAAGCATGGCATGCG--- 556
Db 214 ThrLeuAspValSerPheAsnGlnLeuArgSerLeuProAsp---AlaTyrGlyAlaSer 232
QY 557 ---TTAAACAGCTCTCAACCTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 613
Db 233 ArgLeuArgArgLeuGlnThrIleThrSerLeuGlnHisAsnAsnIleSerThrLeuAlaPro 252
QY 614 GGAAGTTTCTGAGCATCAACAAATTTAGAGATCTGCTGCTGCTGAGACAAAATGAGC 673
Db 253 AsnAlaLeuAlaGlyLeuSerSerLeuArgValLeuAsnIleSerTyrAsnHisLeuVal 272
QY 674 TCTCTAGAGGGTTCATATTGACAGACTTATATCTTAAAGAACTAAATGTGCTCAT 733
Db 273 SerLeuProSerGluAlaPheAlaGlyAsnLysGluLeuArgGluLeuHisIleLeuGlnGly 292
QY 734 AATCTTATACATTCCTTTAAGTCCCTGAA----- 763
Db 293 AsnAspLeu-----TyrGluLeuProLysGlyLeuLeuHisIleArgLeuGlnGlnLeuLeu 310
QY 764 -----TATTTTCT 772

```

```

Db      311 ValLeuAspLeuSerGlyAsnGlnLeuThrSerHisValAspAsnSerThrPheAla 330
Qy      773 AATGTGCAAACTAGAACATGTGGATCTTTCTTATATCAATATTCAAATATT----- 826
Db      331 GlyLeuLeuArgLeuValLeuAsnLeuSerAsnAlaLeuThrArgGlyLeuGlySer 350
Qy      827 ---TCGTCAAGCTTACAGTTTCTTAGGAAATCCCAAGTCATCTCTCTTAGAC 883
Db      351 LysThrPheLeuSerGluLeuTyrPheLeuGln-----LleLeuAsp 363
Qy      884 CTGTCTTTAAACCAATTTGATCTTCAGCCCAAGCTTTGACGGAAATT---AGGCTC 940
Db      364 MetArgAsnAsnSerIleGlyHisIleGlnGlnGlyAlaPheLeuProLeuTyrArgAsnLeu 383
Qy      941 CATGAATTGACTTACAGAGTAAT-----TTTATATAGC 973
Db      384 HisThrLeuAsnLeuAlaGluAsnArgLeuHisThrLeuAspAsnArgIlePheAsnGly 403
Qy      974 TCAAAATGTACTG---AAATGTGCTTCAAAACATGACTGTGTTATGACATGCGGTG 1030
Db      404 LeuTyrValLeuThrIleValLeuThrLeuAsnAsn-----AsnLeuValSerIle 419
Qy      1031 ATCTTGCGAGAA---TTTAAAAATGAAAGAAATCTGAAAAGTTTTCACCGTCTC----- 1081
Db      420 ValGlnSerGlnAlaPheArgAsnCySerAspLeuLeuSerGluLeuAspLeuSerSerAsn 439
Qy      1082 -----GTCATGAAAGACTATGCAATGTGAGC----- 1108
Db      440 GlnLeuThrGlnValProGlnAlaValGlnAspLeuSerMetLeuIleuThrLeuAspLeu 459
Qy      1109 -----ATTGATGAGTTCAGGTTTAAATATATTAATCATTTTTCAGATGATATTT 1156
Db      460 GlyGlnAsnGlnIleSerGluPheLeu-----AsnAsnThrPhe 472
Qy      1157 TATATCTCAATTCGTGGCAAAATATTTCTGCAATGCT-----TTCACAGGTGATCAT 1210
Db      473 ArgAsnLeuAsnGlnLeuThrGlyLeuArgLeuLeuAspAsnArgIleGlyAsnIleThr 492
Qy      1211 ATAAAAACATAGACATGTTCCTAGGCATTTCAAAATGGCAATCCCTTATCATCATTTAGA 1270
Db      493 ValGlyMetPheGlnAspLeuProArg-----LeuSerValLeuAsn 506
Qy      1271 TGTGATCTTAAGCTTTTCCAAAGCTGAGTCTA---CCTTTCTTAAAGTGGACCTTTA 1327
Db      507 LeuAlaIleAspAsnArgIleGlnSerIleGlnArgGlyAlaPheAspIleAsnThrGlnIle 526
Qy      1328 ACTACCAACAGAGAGATATCAAGCTTT-----GGTCAAGTTGGCT---CTG 1369
Db      527 GlnAlaIleArgLeuAspIleAsnPheLeuThrAspIleAsnGlyIlePheAlaThrLeu 546
Qy      1370 CCAAGTCTCAGATATCTTAGATCTTAGAGAAATGCCATGAGCTTTAAGAGTGTCTTCT 1429
Db      547 AlaSerLeuLeuThrPheLeuAsnLeuSerGlnAsnHisLeuValIlePhe-----PheAsp 563
Qy      1430 TATCTGATTTTGGAAACAAACACTGAAGTACTTAGACCTCAATGATGGTGCATC 1489
Db      564 TyrAla---PheIleProSerAsnLeuIleAsnIleAsnIleHisGlyAsnTyrIleGln 582
Qy      1490 CTGATGAGTGCCACTTCATGGGTCTAGAAAG-----CTGAAATACCTGAGCTTT 1540
Db      583 AlaLeu---GlyAsnTyrTyrLeuLeuGlnGlnGlnIleArgValIleThrLeuAspAla 601
Qy      1541 CAGACCTCCACTTTAAAAAGGTCAACAGATTCACAGTGTCTTATCTCTTGAAGAACTT 1600
Db      602 SerHisAsnArgIleThrGlnIleGlyAlaMetSerValProAsnSerIleGln---Leu 620
Qy      1601 CTTTACCTTGACATCTCT-----TACATAATAC----- 1630
Db      621 LeuPheIleAsnAsnAsnIleIleGlyGlnIleGlnAlaAsnThrPheValAspIleThr 640
Qy      1631 -----AAATTTGACTTTGATGCGATATTTCTTGCGCTTGATCAGTCCACACTTTA 1681

```

```

Db      641 ArgLeuAlaArgValAspLeuTyrAlaAsnValLeuSerIleLeuSerLeuAsnAlaLeu 660
Qy      1682 AAATGGCT-----GGCAATTCT 1699
Db      661 ArgValAlaProValSerAlaGluValProValProGlnPheTyrLeuGlyGlyAsnPro 680
Qy      1700 TTCAAACACACACACCTTTCAATGTCTTTACAAACACAACTTAACTA----- 1750
Db      681 PheGlnCyAspCySerMetGluThrLeuGlnArgIleAsnAsnLeuThrThrArgGln 700
Qy      1751 -----TTCCTGATCTTTCTAAA----- 1768
Db      701 HisProHisValValAspLeuGlyAsnIleGlnCyLeuMetProHisSerArgSerAla 720
Qy      1768 ----- 1768
Db      721 ProLeuArgProLeuAlaSerLeuSerAlaSerAspPheValCysIleTyrGlnSerHis 740
Qy      1769 -----TCCCAACTGGAACAG----- 1783
Db      741 CysProProThrCysHisCysCysGluTyrGlnGlnCysGlnCysGlnValIleCysPro 760
Qy      1783 ----- 1783
Db      761 GlyAsnCySerCysPheHisAspAlaThrTrpAlaThrAsnIleValAspCysGlyArg 780
Qy      1784 -----ATATCTAGGGGGGTATTTGACACACTCTAC--- 1813
Db      781 GlnAspLeuAlaAlaLeuProAsnArgIleProGlnAspValSerAsp---LeuTyrLeu 799
Qy      1814 -----AGCTCCAG 1822
Db      800 AspGlyAsnAsnMetProGlnLeuGlnValGlnHisLeuThrGlyArgArgAsnLeuArg 819
Qy      1823 TTATTTAACTAGTGCACAAACCTACTGTTTCTGATCCATCCATTTAAACAGCTG 1882
Db      820 AlaLeuTyrLeuAsnIleAspAsnLeuMetThrLeuGlnAsnGlySerLeuAlaGlnLeu 839
Qy      1883 TACTCCCTGAGACCTTGATTTGACATTTCAATGCGATGAGACATCCAAAGCA----- 1936
Db      840 ValAsnLeuArgValLeuHisLeuGlnAsnAsnLeuLeuThrAlaLeuGlnGlyThrGln 859
Qy      1937 -----ATACTGCAACATTTT 1951
Db      860 PheArgSerLeuGlyLeuLeuArgGlnLeuTyrLeuHisAsnAsnMetLeuThrHisIle 879
Qy      1952 CCAAG-----AGTTAGCCGCTTCAATGACTGAATAATTTCT 1990
Db      880 SerAsnAlaThrPheGlnProLeuValSerLeuGlnValLeuArgLeuAspAsnAsnArg 899
Qy      1991 GTT----- 1993
Db      900 LeuSerSerLeuProHisLeuGlnTyrArgHisSerLeuGlnGlyLeuThrLeuGlnArg 919
Qy      1994 -----GCTGTATATGT---GAATATCAGAAATTTCTTGACATGGCTCAAGACCAAG 2041
Db      920 AsnAlaTrpSerCysArgCysGlnGlnLeuArgGlnLeuAlaGlnPheValSerAspAsn 939
Qy      2042 AAAATGTTCTTGATGATGTTGACAAATGATGAATGAATGCA---TCACCTATAGACATGAG 2098
Db      940 AlaMetValValArgAspAlaHisAspIleTyrCysLeuAspAlaGlyIleValArgGln 959
Qy      2099 GCCTCCCTGGTGGTGGATTTTACGAATTCACAC----- 2131
Db      2132 -----TGTTATATATACAG 2146
Qy      980 AlaSerAsnIleSerSerSerGlnAspLeuAlaGlyAlaIleGlyCysProCysTrpPro 999
Db      2147 ACTATCATCAGTGTATCGGTGTCAGTGTGCTTGTGGTAGCCACTGTAGCAATTTTGATA 2206
Qy      1000 AlaValLeu-----ValLeuIlePheLeuValValValLeuIleIleValPheVal 1016

```

```

QY 2207 TACGACTTCTATTTTCACTGTAATCTTATGCTGCGC-----TGTAA----- 2248
Db 1017 PheArgGluSerValArgMetTrpLeuPheAlaHisIleValArgValCysGluPro 1036
QY 2249 AAGTACACAGACAGAGAAAGCATCTATGATGATTTGTGATCTACTGACCCAGAAATGAG 2308
Db 1037 ArgPheGluAspAlaGlyLeuLeuTyrrAspAlaIleIleLeuHisSerGluIleuAspTyr 1056
QY 2309 GACTGGGAGAGAAAGAGAGCTGTTAAAGATTTAGAGAGAGAGTCCCGCTTTAGCTT 2368
Db 1057 GluPheValCysArgAsnIleAlaIleGluLeuGluHisGlyArgProPheArgLeu 1076
QY 2369 TGCCTTCTTACAGAGACTTATTTCTGATGAGCCATTTGCTGCCACATGATCCAG--- 2425
Db 1077 CysIleGlnGlnArgAspLeuProPro-----GlnAlaSerHisLeuGlnLeu 1092
QY 2426 ---GAGGCTTCCACAGAGCCGAGAAAGTTATGTGTGTGTGTGTAGACATTTATCCAG 2482
Db 1093 ValGlnGlyAlaArgAlaSerArgIleIleLeuValIleuThrArgAsnLeuAla 1112
QY 2483 AGCCGTGTGTATCTTTGATATGATGATGCTGAGACATGAGCACTTTCTAGTACGCC 2542
Db 1113 ThrGluTrpAsnArgIleGluPheArgAsnAla-----PheHisGluSerLeu 1128
QY 2543 TCTGCGCATCATC-----TTCATTGCTCTTGAGANA----- 2572
Db 1129 ArgGlyLeuAlaGlnIleuLeuValIleIleGluGluThrSerValSerAlaGluAlaGlu 1148
QY 2573 -----GTGAGAAAGTCTTGTCTGAGAGAGAGTGTGATTTGATTCGCTTTTAGCAGA 2626
Db 1149 AspValAlaGluLeuSerProTyrLeuLeuSerValProSerAsnArgLeuLeuThrCys 1168
QY 2627 AACACCTACCTCCGATGGAGAGACATGCTCTGGGAGGACATCTTTTGAGAAAGATC 2686
Db 1169 AspArgTyr-----PheTrpGluLeu 1176
QY 2687 AAAAAGCCCTGTTGATGAAAAAGCTTGAATCCAGATGAACATCA----- 2724
Db 1177 ArgTyrAlaIle-----ProIleGluLeuSerProArgGlyAsn 1189
QY 2735 -----GAGAGAAACAGAGAGCAACAACTTGTGACCTGAGAGTA----- 2773
Db 1190 AsnTyrThrLeuAspHisIleGluArgPheGlnProValSerProGlyMetIlePhe 1209
QY 2774 ---GAAACCTGCGCCCTAAACCCATTTGTTTCAATTTCCGAATGCTACAGTTATC 2830
Db 1210 ArgGlnAlaProProProProAlaTyrTyr----- 1219
QY 2831 TGGGTTTCTGCTGTGACAGAGGAGCCAGAGACAGAGCTTGAACCT----- 2880
Db 1220 ---CysThrGluGluMetGluAlaAsnTyrSerSerAlaThrAlaThrProSer 1237
QY 2881 CAAGACCTTCACAGGAGCAAGAGTAGACATGTG-----ATG 2919
Db 1238 ProArgProThrArgProGlyAlaAlaArgIleValaAspSerMetProMetProMet 1257
QY 2920 AAACCCCACTTTCATGTGTATCAGGTGTATGA 2955
Db 1258 ArgProProSerGluHisIleTyrHisSerIleGlu 1269

RESULT 5
T13887
Clr protein - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T13887
R/Chiang, C.; Beachy, P.A.
Mech. Dev. 47, 225-239, 1994
A/Title: Expression of a novel Toll-like gene spans the parasegment boundary and controls
A/Reference number: Z17805; MUID:95151581; PMID:7848870
A/Accession: T13887
A/Status: preliminary; translated from GB/EMBL/DBJ

```

```

A/Molecule type: mRNA
A/Residues: 1-1385 <CHI>
A/Cross-references: UNIPROT:Q24591; EMBL:S76155; NID:g913247; PID:g913248; PION:AA833383
C/Genetics:
A/Cross-references: FlyBase:FBgn0004364
A/Note: Clr

Alignment Scores:
Pred. No.: 1,08e-18 Length: 1385
Score: 371.50 Matches: 250
Percent Similarity: 35.23% Conservative: 170
Best Local Similarity: 20.97% Mismatches: 363
Query Match: 6.25% Indels: 410
DB: 2 Gaps: 54

US-09-396-985b-5 (1-3395) x T13887 (1-1385)

QY 380 GATCAGAAATCTCAGCAAAATCCCTCATGATCCCTTATTTCAACCAAGACCTAGATCTG 439
Db 154 AsnAsnAsnIleArgGlnIleuProGluGlyValTrpCysSerMetProSerLeuGlnLeu 173
QY 440 AGCTTCAACCCCTGAAGATCTTAAAGCTATATGCTTACCAATTTC----- 487
Db 174 LeuAsnLeuThrGlnAsnArgIleArgSerAlaGluPheLeuGlyPheSerGluLeu 193
QY 488 -----TCCAACTTCAG 499
Db 194 CysAlaGlySerAlaLeuSerAsnAlaAsnGlyAlaValSerGlyGlySerGluLeuGln 213
QY 500 TGGCTGATTTATCCAGGTGTAATTTAGACATTTGAGCAAGAGCATGGCATGCG--- 556
Db 214 ThrLeuAspValSerPheAsnGluLeuArgSerLeuProAsp---AlaTrpGlyAlaSer 232
QY 557 ---TTAAACAGCTCTCAACCTTGTGATGACAGAAACCTTATCAAGATTTTCCCA 613
Db 233 ArgLeuArgArgLeuGlnThrLeuSerLeuGlnHisAsnAsnIleSerThrLeuAlaPro 252
QY 614 GGAATTTTCTGGACATCAAAATTTAGAGATCTGTGCTGAGAGACAAATAAGACC 673
Db 253 AsnAlaLeuAlaGlyLeuSerSerLeuArgValLeuAsnIleSerTyrAsnHisLeuVal 272
QY 674 TCTCTAAGAGGTTTCCATTTATGACAGCTTATATCTTAAAGAACTAAATGTGGTCAT 733
Db 273 SerLeuProSerGluAlaPheAlaGlyAsnIleGluLeuArgGluLeuHisLeuGlnGly 292
QY 734 AAT-----CTTATACATTCCTT----- 751
Db 293 AsnAspLeuTyrGluLeuProLysGlyLeuLeuHisIleArgLeuGluGlnLeuValLeu 312
QY 752 -----AAGTTCCTGAATAT-----TTTCTAATCTG 778
Db 313 AspLeuSerGlyAsnGlnLeuThrAspHisIleValaAspAsnSerThrPheAlaGlyLeu 332
QY 779 ACAACCTAGAACATGATGATCTTTCTTATGATCTTATTAACATACTAT-----TCT 829
Db 333 IleArgLeuIleValLeuAsnLeuSerAsnAsnAlaLeuThrArgIleGlySerLeuThr 352
QY 830 GTCAAGACTTACAGTTTCTACGTGAATAATCCCAAGTCATCTCTCTTACAGCTGTCT 889
Db 353 PheIleGluLeuTyrPheLeuGln-----IleLeuAspMetArg 365
QY 890 TTAAACCCATTTGATCTTCATTCAGACCCAGCTTTACAGGAAT-----AGCTTCATGAA 946
Db 366 AsnAsnSerIleGlyHisIleGluGluGlyAlaPheLeuProLeuTyrAsnLeuHisThr 385
QY 947 TTGACTCTAAGAGTAT-----TTTAATAGCTCAAT 979
Db 386 LeuAsnLeuAlaGluAsnArgLeuHisThrLeuAspAsnArgIlePheAsnGlyLeuTyr 405
QY 980 GATGCT---AAAATGCTCTTCAAAACATGACTGGTTTACATGTCCATCGGTGATCTTG 1036
Db 406 ValLeuThrIysLeuThrLeuAsnAsn-----AsnLeuValSerIleValGlu 421

```

QY	1037	GGAGA---TTTAAAAAGAAAGAACTGGAAAGTTTGGACCGTCTC-----	1081
Db	422	SerginalaIpphaeAysnCyserSerapLeuylsgLeuAapLeuSerSerangInleu	441
QY	1082	-----GTCAATGGAAGACATAATGCATGTGAGC-----	1108
Db	442	ThrgIuValProGIuAlaIaGIlaapLeuSerMetLeuylsThrlleuAapLeuGIu	461
QY	1109	-----ATTGATGAGTTCAGGTTAACATATATAAATCATTTTCAGATGATATTATAT	1162
Db	462	AangInIleSergInPheIys-----AasnThlPheArgysn	474
QY	1163	CTCAATTCCTGGCAAAATATTTTCGCATGTCT-----TTCACAGGTGATCATATATAA	1216
Db	475	LeuasnGIuLeuthThgIleuAargLeuIleAapasnAargIleGIaenIleThValGIy	494
QY	1217	CACATAGACAGATGTCTTCAGGCATTTCAAAATGCGCAATCCTTCATCATATGATGATGCAT	1276
Db	495	MetPheGInAapLeuProArg-----LeuSerValLeuasn-----	506
QY	1277	CTTAAGCCTTTCCAAAGCTGATGCTTACCTTTTCTTAAAGTTGGACTTTAACTAACAC	1336
Db	507	-----LeuAlaIyAasnAargIleGInSerIleGIuAargGIyAlaPheAapLeuAysn	523
QY	1337	AGAGAG-----GATATACGCTTTGGTACG	1360
Db	524	ThrgIuIleGIuAlaIleAargLeuAapLysLysPheleuthrAapIleasnGIyIlePhe	543
QY	1361	TTGGCTCTGCCAAGCTCCAGATATGTATGATCTTATGATAAATGGCATGAGCTTAAAGGT	1420
Db	544	AlaThrlleuAlaSerleuLeuthrPheuasnLeuSerGIuAasnIleAValITrp-----	561
QY	1421	TGCTGTCTTATCTGATTTTGGACAACAACCTGAAGCTTACCTAGACCTTCAT	1480
Db	562	---PheAapLysAla---PheIleProSerAenLeuLysTrlPheuAapIleHleGIyAysn	579
QY	1491	GGTGCATCTGCATGATGAGCCCACTTCAATGGCTCTGAAGAG-----CTGGAATAC	1531
Db	580	TyrIleGIuAlaIleu---GIyAasnYrIyLysLeuGInGIuIleAargValThrThr	598
QY	1532	CTGACCTTTCAGCACTCCACTTAAAAAAGGCACAGAATTCAGTGTCTTATCTCTT	1591
Db	599	LeuAapAlaSerIleAasnAargIleThrgIuIleGIyAlaMetSerValProasnSerIle	618
QY	1592	GAATAAATCTTTTACCTTGCATCTCT-----TACACTAATAC-----	1630
Db	619	GIu---LeuLeuPheIleAasnAasnIleIleGIuIleGIuAlaAasnThrPheVal	637
QY	1631	-----AAAATTGACTTTGATGGCATATTTCTTGGCTGATCAGTCTC	1672
Db	638	AapLysThrAargLeuAlaAargValAapLeuLysAlaAenValLeuSerLysIleSerleu	657
QY	1673	AACACTTTAAAAATGGCT-----	1690
Db	658	AasnAlaLeuAargValAlaAProValSerAlaGIuLysProValProGIuPheYtLeuGIy	677
QY	1691	GGCAATTCCTTCAAGACACACCCCTTCAATGTCTTTACAAACACAAACAACTTAACA	1750
Db	678	GIuAenProPheGIuCyAapCySerSerMetGIuTrlPheGIuAargIleAasnAenLeuThr	697
QY	1751	-----TTCCTGATCTTTTCTTAA-----	1768
Db	698	ThlAargInIleAProHleValAlaAapLeuGIuAenIleGIuCyLeuMetProHleSer	717
QY	1768	-----	1768
Db	718	ArgSerAlaAProLeuAargProLeuAlaSerleuSerAlaSerAapPheValCysLysYtr	737
QY	1769	-----TSCCAACTGGAACAG-----	1783
Db	738	GIuSerHleCyAProProThrCyHleAysCySylGIuTrlGIuGInGIuGIuCyGIuGIuVal	757
QY	1783	-----	1783

Dd	758	IlEcySrProGluYanCysSerCyvRheniVaBrAlaThrTrpAlaThrAsnIleValAsp	777
Qy	1784	-----ATATCTAGAGGGGATATTGACACA	1807
Dd	778	CysGluYArgIuInArLeuAlaAlaLeuProAlaRhgIleProGlnArValSerAsp---	796
Qy	1808	CTCTAC-----	1813
Dd	797	LeuYTrLeuArpGluYaEnnMetProGluLeuGluValGluYnIleuThrgIuYArgAsp	816
Qy	1814	AGATCCAGATTATTAACATGAGCACAACAACACTACTGTTTCTGGATCCATCCATATAT	1873
Dd	817	AsnLeuYArgAlaLeuYTrLeuAlaAsnAlaSerAsnLeuMetThrLeuGlnInpGlySerLeu	836
Qy	1874	AAACAGCTGTATCTCCCTCAGAGACTCTGTATGTGCAGTTTCAATCGCATAGAACATCCAA	1933
Dd	837	AlaGlnLeuValaLeuLeuYArgValLeuYnIleuGluYnAsnYnYleuThrAlaLeuGlu	856
Qy	1934	GGA-----ATATCTG	1942
Dd	857	GluYThrgIuRheArgSerLeuGluYleuLeuYArgIuLeuYTrLeuYnIleuYaEnnMetLeu	876
Qy	1943	CAACATTTTCCAAAG-----AGCTAGCCGCTTCAATCTACT	1981
Dd	877	ThrIleIleSerAsnAlaThrRheGluProLeuValSerLeuGluValaLeuYArgLeuAsp	896
Qy	1982	AATATATTCTGT-----	1993
Dd	897	AsnAsnYnYrLeuSerSerLeuProYnIleuGlnYArgIuYnIleuYnIleuGlnYleuThr	916
Qy	1994	-----GCTTGATATGT---GAATATCAGAAATTCTTGACATGGCTC	2032
Dd	917	LeuGluYArgAsnAlaTrpSerCyvArgCyGlnGlnIleuYArgIuLeuYAlaGlnRheVal	936
Qy	2033	AAGGACCAAAAGATCTTGTTGGTGAATGTTGAACAAATGAAGATGCA---TCACTATAT	2089
Dd	937	SerAspRnAlaMetValaValaYArgAspAlaYnIleArpIleYTrCyvLeuYaBrAlaGluYIle	956
Qy	2090	GACATGAAAGGCTCCCTCGTGTGGATTTTACGAATTCC---ACCTGT-----	2134
Dd	957	LyvArGluYnLeuGluLeuIleGluYAsnLeuYAlaAsnGluYProArpCyvSerArpLeuLeu	976
Qy	2135	-----TATATATCAAG	2146
Dd	977	AspAlaSerAlaSerAsnIleSerSerSerGlnArpLeuYAlaGluYTrYArgLeuPro	996
Qy	2147	ACTATCAATCAATGATGAGTGGTGGACAGTGTCTTGATGAGCACTAGATTTCTGATA	2206
Dd	997	LeuLeuAlaAlaValaLeuValLeuIleRheLeuAspValaValLeuIleIleValaRheVal	1016
Qy	2207	TACCACTTCTATTTTCACTGATCTTATTTGCTGGC-----TGTTAA---	2248
Dd	1017	PheArGluSerValaYArgMetTrpLeuRheAlaYnIleYTrGluYAlaYArgValCyvGluPro	1036
Qy	2249	AAGTACAGCAGAGAGAAAGCATATGATGATCTTGTGATCTATCTGAGCCAGATGAG	2308
Dd	1037	ArgRheGluArpAlaGluYleuYTrLeuYAspAlaIleIleLeuYnIleSerGluYAspYTrX	1056
Qy	2309	GACTGGGGTGAAGAAACAGACCTGGTAAAGATTTTGAAGAAGAGTGGCCCGCTTGACACT	2368
Dd	1057	GluYnRheValCyvArGuaEnIleAlaAlaGluLeuGluYnIleYArgYArgProRheArgLeu	1076
Qy	2369	TGCTTCACTTACAGAGCACTTATTTCTCGTGTAGCATTGCTGTCGACATCATCAG---	2425
Dd	1077	CysIleGlnGlnYArgRLeuProPro-----GlnAlaSerYnIleuGlnIleu	1092
Qy	2426	---GAAGCTTCCACAAGACCCGGAAGTTATTTGGTGTGTCTGACATTTATCCAG	2482
Dd	1093	ValGluGluYAlaArGuaIaSerArGluYnIleIleLeuValLeuThrXArgAsnLeuAla	1112
Qy	2483	AGCGTTGTGTATCTTGAATATGAATTTGCTCAGACATGGCAGTTTCTGATAGAGCCG	2542

F:201-224/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR6>
F:220-249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR7>
F:250-273/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR8>
F:279-302/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR9>
F:303-325/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR10>
F:326-349/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR11>
F:351-374/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR12>
F:375-399/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR13>
F:401-424/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR14>
F:428-451/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR15>
F:453-476/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR16>
F:477-500/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR17>
F:502-526/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR18>
F:527-550/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR19>
F:551-574/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR20>
F:577-600/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR21>
F:601-624/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR22>
F:625-648/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR23>
F:649-672/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR24>
F:673-696/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR25>
F:708-731/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR26>
F:733-756/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR27>
F:757-780/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR28>
F:781-804/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR29>
F:805-827/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR30>
F:828-851/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR31>
F:854-877/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR32>
F:879-902/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR33>
F:903-926/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR34>
F:928-948/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR35>
F:949-972/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR36>
F:973-995/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR37>
F:996-1019/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR38>
F:1021-1044/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR39>
F:1056-1080/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR40>

Alignment Scores:

Pred. No.:	Score:	Length:
5.65e-16	1134	
Percent Similarity:	333.50	Matches: 172
	37.42%	Conservative: 112
Best Local Similarity:	22.66%	Mismatches: 244
Query Match:	5.61%	Indels: 231
DB:	1	Gaps: 28

US-09-396-985B-5 (1-3395) x A29944 (1-1134)

```

QY      CTATACCTTACTTCAGATGATGCATGATGCAAAATCTGACAATACTCCCTGATCATCCTTT 416
       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      Lc1Lc1LeuProGlInSlnArLeuValIGluIleProSerTySerLeuArg-His-LeuG 151

QY      ATTCAACCAAGAATCTAGATCTGAGCTTCACACCCCTCGAAGATCTTAAGACGATATAGCT 476
       ::::: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      Lc1Lc1LeuSerAlaArgHisLeuArLeuGlyTyrGlnHisIleThrHisIleGlnHisArSerP 171

QY      TCACCAATTTC---TCACCACTTGAGTGGCTGATTTATTCACAGGTGTGAATTTGAACAA 533
       || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      hcatrgILeuGIuArSerLeuGlnThrLeuIleLeuArgGluAsnCyIleSerGlnIb 191

QY      TTGAAGACCAAGCATGCGATGGCTTAACACAGCTTCACACCTTGATGATGACAGCGAAC 593
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      Lc1Lc1SerHisSerPheSerGlyLeuLeuIleLeuGluThrLeuArLeuSerGlyAsnA 211

QY      CTATCAAGAGTGTTCCTCCACGAGAAGTTTT---TCTGAGACTTAACAAATTTAAGAAATCTG 650
       :: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      Lc1Lc1LeuPheGluIleArProGlnValAlaArLeuIleMetProAdgLeuThrArgLeu 231

QY      TGGCTGTGAGACAAAATACCTCTTAGAGGCTTTCATATTTGACAGCTTATATCTT 710
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      Lc1Lc1LeuThrArPheArIleLeuSerGluIleProTyrArPalaLeuGlyProLeuTySer 251

QY      TTAAGAAATCTTAATGTGGCTCATATCTTAATCTTATTAAGTGGCTGAAATATTTT- 769
       : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      eunArgThrLeuArPileSerHisAsnValIleTrpSerLeuSerGlyAsnGluThrTyG 271

```

Oy	770	-----TCTAATCTGACAAACCTGACAAACATGTCGATCTTCTTATATCAATATATCT	818
Db	271	luu1leuysalSerthrlyuysleuasnleuaspasnleuhsileucluluyrasmhsilleg	291
Oy	819	AAACTATTTCTGCTCAAAAGACTTACAGTTTCTTACAGTAAATCCCCAGTCAATCTCTCT	878
Db	291	luvalleuProProksmsrPheylsryrPhe-----AspThrValasnrlgThr	308
Oy	879	TAGACCTGTCTTTAAACCAATTGACTCCATTTCAAGCCCAAGCCTTTCAGGAATGAGC	938
Db	308	he---PheaspolyasnProileh1sthrleuargluaspAlaphelysProalargi	327
Oy	939	TCGATTAATGACTCTAAGA-----	959
Db	327	leargluuileuymetcargtyrCyrgslyleuthrAsnilleSerProvalalaphesps	347
Oy	960	GTAATTTTAAATAGCTCAAAATGTACTGAAATGTGCTTCAAAACATGACTGTTTACATG	1019
Db	347	erleuValasnsrleuenglilleuaspleserSerglyAsnhsnleuthrlyrsleuhs-	366
Oy	1020	TCCATCGGCTTG-----ACCTTG-----	1043
Db	367	--HislyleuPheasnleuPheaspValleuArgvalilleSermetcargspasnlysr	386
Oy	1044	TTAAATAAAGAAAGATCTGCAAAATGTTTGAACCGTTCGTGATGAGAGATGATGCAATG	1103
Db	386	lelyslleuLysProthrgrluthrPheasn--AlaValHis1rythrleuLeuylsl	405
Oy	1104	TGAGCATTTGATGACGTTCAGCTTAACATATATTAATCATTTTCAGATCATATTAATATC	1163
Db	405	euaspleserSerglyAsnarg-----AsnaspProthrAsnll	417
Oy	1164	TCAATTCGCTGGCAATATATTTCTGCAATG--TCTTTCACAGGTGTACATATTAACAACA	1220
Db	417	euglnlthrleuArgasmethrthrAgmetlArgasmethArgSerleuserlilleSerargl	437
Oy	1221	TAGCAGATGTT-----CCTAGGACATTTCAA--	1256
Db	437	euglySerSerSerValglyProgluaspPheylaspPheglyValgluleuenglualprl	457
Oy	1257	TATCAATCAATTAATGATGTT-----CATCTTAAG	1283
Db	457	euglnlthrArgalaserleuserSerglylleglnSerhlsAlaphelyshsValArgg	477
Oy	1284	CTTTTCCAAAGCTGAGTCTTACTCTTTCTTAAAGTTGACCTTTAATCTAACAACAGAGAG	1343
Db	477	lyleuLysArgleuaspPhe-----SerGluasncllylleserSerlileglua	493
Oy	1344	ATATCAGCTTGGTCAATTG-----	1363
Db	493	snaspAlaphelsgluileglnlaserleuilleserleuysmetSerhlsglyTys	513
Oy	1364	-----GCTTTGGCA-----	1391
Db	513	erSerglySerAlaleuProalagluProleuArghsileuThrSerleuengluleuasp	533
Oy	1392	TTAGTAGAATGCCATGAGCTTTAAGGCTTGCTGTTCTTATCTGATTTT	1441
Db	533	heserAsnhsnhs1sileserSermetSerAspThrSerPhehlsPheleuyluasnleua	553
Oy	1442	-----GGAACA-----	1447
Db	553	rgleuLeuGluleuhs1sleuaspAsnArgllegluInValleuylsolythrPheglngllyA	573
Oy	1448	-----AACACCTGAAGTACTTAAGACTCAGCTTCAATGATGATGATCTCAGATGATG	1495
Db	573	sp1leHiserlyserleuenglulileSerleuArgPheasnhs1leuthrSerlilleSerg	593
Oy	1500	CCAAAC-----	1500
Db	593	lnh1thrPhePheasplesuenglualaleuArglyleuhs1leuaspAsnleuysllea	613

QY 1505 -----TTCATGGCTCTGAAGAAGCTGGAAATCTCGACTTTTCAGC 1544
 Db 613 sPLySIleGluArgArgAlaPheMetAsnLeuAspGluLeuGluTyrLeuSerLeuArg 633
 QY 1545 ACTCCACTTTAAATAAAGGTCACAGAAATCTCAGTGTCTTATCTCTTGAATAACTT----- 1600
 Db 633 LysnLysIleasnAsnLeuAlaAspGluSer---PheGlnAsnLeuProLysLeuGluI 652
 QY 1600 ----- 1600
 Db 652 LeLeuAspMetAlaPheAsnGlnLeuProAsnPheAsnPheAspTyrPheAspGlnValG 672
 QY 672 1yThrLeuSerAsnLeuAsnValAsnValSerHisAsnGlnIleArgGlnLeuMetTyrA 692
 QY 1601 -----CTTAC-----C 1607
 Db 692 snSerSerTyrSerGlyArgAsnGlnHisGlyIleMetTyrHisSerAsnIleLysIleL 712
 QY 1608 TTGACATCTCTTACCACTAATACCAAAATGACTTTGATGCATATTTCTT---GGCTTGA 1664
 Db 712 euAspLeuSerHisAsnAsnIleSerIleIleHisProGlyTyrPheArgProAlaGluI 732
 QY 1665 TCAGTCTCAACACTTAAATAATGGCTGGCAATCTTTCAAGACACACCCCTTCAATG 1724
 Db 732 LeSerLeuThrHisIleuHisIleuGlyTyrAsnSerLeuMet---AsnThrThrArgAspV 751
 QY 1725 TCTTTACAACACACCAAACTTAACATCTCGATCTTTCTTAATGCGCACTGGAAACAGA 1784
 Db 751 alPheGlyAsnMetProHisIleuGlnTyrPheuAspLeuSerTyrAsnTrrPileHisGluL 771
 QY 1785 TATCTAAGGGGGGATTTTGACACACTCTACAGACTCCAGTATTAACATGAGTCACACA 1844
 Db 771 euAspPheAspAlaPheLysAsnThrIlyeGlnLeuGlnLeuValPhePheGlyHisAsnT 791
 QY 1845 ACCTAAGTCTTTGATCCATCCATTAATAACAGCTGTACTCCCTCAGACCTTGATT 1904
 Db 791 yLeuSerAspIleProGlnAspIlePheLysProValGlnGlyLeuArgIleValAsp 811
 QY 1905 GGAGTTTCAT-----C 1916
 Db 811 heSerHisAsnHisIleuArgGlyLeuProAspAsnLeuPheTyrAsnGlyIleMetGluL 831
 QY 1917 GCATAGAGACTCCAAAGAAATACCTGCAACATTTTCCAAAGACT----- 1960
 Db 831 yLeuAspValSerHisAsnMetMetLeuLysIleProSerSerLeuSerSerLeuA 851
 QY 1961 -----CTAGCGCTTTCATCTGACTAATAATCTGTGCTTGATA 2002
 Db 851 laAlaLeuThrLeuCySGluLeuHisLeuSerAsnAsnPheIleSerThrile 868

RESULT 7
 T15864
 hypothetical protein C56B6.6 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T15864
 A:Accession: T15864
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1066 <FNU>
 A:Cross-references: UNIPROT:Q18902; EMBL:U39996; NID:G1055114; PID:G1055120; PIDN:AAA8106
 C:Genetic:
 A:Gene: C5P.C56B6.6
 A:Introns: 62/3; 110/3; 376/3; 432/3; 482/3; 574/2; 649/2; 769/2; 833/3; 892/3; 9-
 Alignment Scores: 8.05e-14 Length: 1066
 Pred. No.:

QY 2036 GACCAAGAAATGTTCTTGCTGTAATGTTGAACAAATGAAATGTCATCCATAGACATG 2035
 Db 527 LeuGluAglLeuTyrPleu--AspAlaSerProTyrAspCysSerCysProLeuLeuAla 545
 QY 2096 AAGGCTTCCTCCGCTGCTTGAT-----TATATATACAGACTATCATCAGTATCGGTGTC 2134
 Db 546 LeuTrgAspPheAlaLeuGlnAsnProGlyValValProArgPheValGlnThrValCys 565
 QY 2135 -----TATATATACAGACTATCATCAGTATCGGTGTC 2170
 Db 566 GluGlyAspAspCysGlnProValTyrThrTyrAsnSerLeuThrCysAlaGlyProAla 585
 QY 2171 AGTGG 2176
 Db 586 AsnVal 587
 RESULT 9
 JCS239
 Insulin-like growth factor acid-labile chain - baboon
 CSpecies: Papio sp. (baboon)
 CDate: 17-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-May-1997
 CAccession: JCS239
 R:Delhanty, P.; Baxter, R.C.
 Biochem. Biophys. Res. Commun. 227, 897-902, 1996
 A>Title: The cloning and expression of the baboon acid-labile subunit of the insulin-like
 A:Reference number: JCS239; MUID:97040714; PMID:8886027
 A:Contents: liver
 A:Accession: JCS239
 A:Molecule type: mRNA
 A:Residues: 1-605
 C:Comment: This factor is structurally related to proinsulin and have insulin-like meta

Alignment Scores:
 Pred. No.: 1.12e-13 Length: 605
 Percent Similarity: 301.00 Matches: 171
 Best Local Similarity: 34.99% Conservative: 90
 Query Match: 5.06% Mismatches: 268
 DB: 2 Indels: 217
 Gaps: 23

US-09-396-985B-5 (1-3195) x JCS239 (1-605)
 QY 85 AAGTTGGACACTCTCATCTTCTCTGCTCTGACCAAGATATACCTTGAATACATATTT 144
 Db 5 LysGlyGlyLeuAlaLeuAlaLeuAlaLeuLeuLeuSerTyrValAlaLeuGlyProArgSer 24
 QY 145 ACAGAGGGGCAACCGCTGGAGAGAGAGGGGAGGGGCCCCAGGAGCTCTGCGCTGCACC 204
 Db 25 LeuGluGlyAlaGluProGlyThrProGlyGluAlaGluGlyProAlaCysProAlaThr 44
 QY 205 ATTACAGATTGTCATGCTTCTTCACAGGCTCCGCTGGTTCAGAAAAATGCGACAGATAT 264
 Db 45 -----CysAlaCysSerTyrAspAsp 51
 QY 265 GCTCTCTTGACATCGCTGGGACTGTGATGATGAGCATTTGTTCTTTCGCTGAGACC 324
 Db 52 GluVal-----AsnGlu-LeuSerValPhe----- 59
 QY 325 AGGAAGCTTGAATCCCTGCATAGAGATACCTTCTTAATATTCATCCATGATGATGATCA 384
 Db 60 -----CysSerSerAr 63
 QY 385 GAATCTCAGCAAAATCCCTCATGACATCCCTTATTTCAACCAAGACCTAGATCTGACTT 444
 Db 63 GAsnLeuThrArgLeuProAspGlyLeuProGlyGlyThrGlnAlaLeuTyrPleuAsp 83
 QY 445 CAACCCCTGAAGATCTTAAGAGCTATAGCTTACCAATTTCTCACAACTTCACTGAGCT 504
 Db 83 rAsnAsnLeuSerLeuProAlaAlaPheArgAsnLeuSerLeuAlaPheLe 103
 QY 505 GGATTTATCCAGGAGGTGAATTTGAGACAAATTGAAGACAAGGCATGAGCATGAGCTTAACA 564

Db	103	uasnleuglnclgylglnleugllyserleuglnp	ProGlnAlaIleuLeugllyleuglnAs	123
Qy	565	GCTCTCAACCTTGGTACTGACAGAAACCCATCATGAGATTTTCC	CGAGAACTTTTC	624
Db	123	nleuCyHeIstleuHlsleuglnuArgamGlnleuArgserleuAlaValGlyThrPheAl		143
Qy	625	TGACATACAAAATTTAGAGATCTGGTGGCTGTGGAGACAAAAT	TGACCTCTTGAGAGG	684
Db	143	aTyThrProAlaIleuAlaIleuLeugllyLeuSerAsnAsnArgleuSerArgleuGlnAs		163
Qy	685	TTTCATATTGACAGCTTATATCTTAAAGAACTAAATGGCTCATATCTTAATCA		744
Db	163	pglyLeuPheuglnleugllyleugllyAsnleuITPAspleuHsleuGlyThrAsnSerleu--		182
Qy	745	TTCTTTAAAGTTGCGCTGAA--TATTTTTCATCTGACAAACCTAGAACCTGGATCT		801
Db	183	---AlaValleuProAspAlaIaIaPheArgGlyleuGlyGlyleuArgGlnleuValle		201
Qy	802	TTCTTTATPAC-----TATATTCAAACTATTTCTGTCAAAAGACTTACAGTTTCTAG		852
Db	201	uAlaGlyAsnArgleuAlaTyrlleuGlnProAlaIleuPheSerGlyleuAlaGlnleuAr		221
Qy	853	TGAAATCCCAAGTCATCTCTTTAGACCTGTCTTAAACCACTTATGACTCATCTCA		912
Db	221	gGln-----leuAspLeuSerArgAsnAlaIleuAlaGlyAlaIlely		234
Qy	913	AGCCCAAGCCCTTCAGGGAAT--AGGCTTCATGAATGTGACTTAAAGTAATTTTAA		969
Db	234	sAlaAsnValPheAlaGlnleuProArgleuGlnlyleuTyrlleu-----		249
Qy	970	TAGCTCAAAATCTACTGAAAAATGTGCTTCAAAAACATGACTGTTTACATGTCACGT		1029
Db	249	-----		249
Qy	1030	GATCTGGAGAAATTTAAATGAAGAGATCTGGAAGTTTTCACGTTCTGTCAATGA		1089
Db	250	-----AspArgAsnleu-----		253
Qy	1090	AGGACTATGCAATGTGACATTTGATGAGTTACAGTTAACATATATATAATCATTTTTCAGA		1149
Db	253	-----		253
Qy	1150	TGATATTATATCTCAATTGCTTGCGCAATTTTCGCAATGCTTTCAACAGGTATCA		1209
Db	254	-----IleAlaIaValAlaProGlyAlaPheleuGlyleu--		265
Qy	1210	TATATAACACATAGACAGATGTTCTTAGACATTTCAAAAGGCAATCTTATCAATCATATAG		1269
Db	266	-----LysAlaIleuArgTyrIleuAsnleuSer-----		274
Qy	1270	ATGTCAATCTTAAGCCTTTCCAAAGCTGAGCTACCTTTTCTTAAAGTTGACCTTAAAC		1329
Db	274	-----		274
Qy	1330	TACCAACAGA-----GAGGATATACAGCTTTGCTCAAGTTGGCTGTCCAGAG		1374
Db	275	-HisAsnArgValaIaGlyleuLeuGlnAspThrPheProGlyleuLeu-----Gln		291
Qy	1375	TCTCAGATATATCATGCTTATAGTAGAAATGCCATAGAGCTTGAAGTTGCTGTCTTATTC		1434
Db	291	ylleuArgValleuArgleuSerHisAsnAlaIaIaIaSerleuArgProAlaGlyThrPheGln		311
Qy	1435	TGATTTTGAACAAACCAACCTGGAAGTACTTAGACCTTACAGCTTCAATGGGTGTC--ATTCCT		1491
Db	311	uAspLeu-----HisPheLeuGlnleuGlnleuGlnleuGlyHisAsnArgIleArgGlnle		329
Qy	1492	GATAGAGTCCCAACTTCATGGGTCTTCAAGAGCTTGGAATACCTGACCTTACGACCTCCAC		1551
Db	329	uAlaGlnArgSerPheGlnleuGlyGlnleuGlnValleuThrIleuAspHisAsnGln		349
Qy	1552	TTTAAAAAGGTACACAAATTCCTAGAGTTCTTATCTTGAAGAAACCTTCTTACCTTCA		1611
Db	349	nleuGlnGlnVal---LysValaGlyAlaPheleuGlyleuThrAsnValaIaValaIaMetAs		368

```

QY      1612 CATCTTACACATAACAAATTGACTTTGATGCAATTTCTGGCTTGATCACTCT 1671
Db      368 nleuSerGlyAsnCySleuArgAsnLeuProGluGlnValPheArgGlyLeuGlyLys 388
QY      1672 CAACACTTTAAATGGCTGGCAATCTCT----- 1699
Db      388 uhiSerLeuHiSleuGluGlySerCySleuGlyArgGLeuArgProHiSerThrPheAlaG 408
QY      1700 -----TTCAAGACACACCTTTCAAAATGTC----- 1726
Db      408 yLeuSerGlyLeuArgArgLeuPheLeuLysAspAsnGlyLeuValGlyIleGluGluG 428
QY      1727 -----TTTAAACAAACACAAACTTAACATTCCTGGATCTTTCTAAAGCCACGGAACA 1782
Db      428 nSerLeuTrpGlyLeuAlaGluLeuGlnLeuAspLeuThrSerAsnGlnLeuThrHi 448
QY      1783 GATATCTAGGGGGGTATTTGACACACTCTACAGACTCCAGTTATTTAAACATGACTCACA 1842
Db      448 sLeuProHiSerGlnLeuPheGlnGlyLeuGlyLysLeuGlnLysLeuLeuLeuSerHiSAs 468
QY      1843 CAACCTACTGTTTGTGATCCATCCCATTTAAACAGCTGTACTCCCTCAGACTCTTGA 1902
Db      468 nArgLeuAlaGluLeuProAlaAspAlaLeuGlyProLeuGlnArgAlaPheTrpLeuAs 488
QY      1903 TTGCACTTCAATCGCATAGACATCCAAAGAAATACCTGCAACATTTTCCAAAGAGTCT 1962
Db      488 pValSerHiAsnArgLeuGlnAlaLeuProGlySerLeuLeuAlaSerLeuGlyAlaGLe 508
QY      1963 AGCGCTCTCAATCTGACTAATAATCTGTGCTGTATATGTAATATGAAATGAAATTTCT 2022
Db      508 uArgTyLeuLeuLeuArgAsnSerLeuArgThrPheThrProGlnProProGlyLe 528
QY      2023 GCAG-----TGGGTCAAGAGCACGAAATATCTTGTGTGATTTGAAACAATGAAAT 2076
Db      528 uGlnArgLeuTrpLeuGluGly-----AsnProTrpAspCy 540
QY      2077 TGCATCACTTATAGAC-----ATGAAGCGCTCCCGTGTTGGA 2115
Db      540 sSerCyProLeuValAlaLeuArgAspPheAlaLeuGlnAsnProSerAlaValAlaProAr 560
QY      2116 TTTTACGAATCCACCTGT-----TATATATCAAGAC 2148
Db      560 gPheValGlnAlaIleCysGluGlyAspAspCysGlnProValTyrThrTyAsnAs 580
QY      2149 TATCATCAGTGTATCG 2164
Db      580 nIleThrCysAlaSer 585

RESULT 10
T10504
disease resistance protein Cf-2.1 - currant tomato
C/Species: Lycopersicon pimpinellifolium (currant tomato)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10504; T10515
R/Dixon, M.S.; Jones, D.A.; Keddie, J.S.; Thomas, C.M.; Harrison, K.; Jones, J.D.
Cell 84, 451-459, 1996
A/Title: The tomato Cf-2 disease resistance locus comprises two functional genes encoding
A/Reference number: Z17062; MUID:96190812; PMID:8608599
A/Accession: T10504
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Cross-references: UNIPROT:Q41397, EMBL:U42444, NID:g1184074, PIDN:AACT5779.1; PID:g118
A/Experimental source: cultivar Cf 2
A/Accession: T10515
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1066, 'I', 1068-1085, 'E', 1087-1110, 'R', 1112 <D12>
A/Cross-references: EMBL:U42445, NID:g1184076; PIDN:AACT5780.1; PID:g1184077
A/Experimental source: cultivar Cf 2
Alignment Scores:

```

```

Pred. No.: 3,91e-13 Length: 1112
Score: 294.00 Matches: 185
Percent Similarity: 35.43% Conservative: 108
Best Local Similarity: 22.37% Mismatches: 270
Query Match: 4.95% Indels: 264
DB: Gaps: 32

US-09-396-985b-5 (1-3395) x T10504 (1-1112)

QY      326 GAAAGCTTGAATCCCTGCATAGAGGTATCTCTAATATTAC-----TACCAATGCATG 379
Db      397 GlySerIleProAlaSerLeuGlyAsnLeuAsnLeuSerArgLeuTyLeuTyAsn 416
QY      380 GATCAGAAATCTGCAAAATCCCTCAATGATCCCTAT-----TCAACCAAGAACCTA 433
Db      417 AsnGlnLeuSerGlySerIleProGluGluIleGlyTyLeuSerSerLeuThrTyLeu 436
QY      434 GATCTGAGCTTCAACCCCTGAAGATCTTAAAGAGTATAGCTTCAACATTTCTGACAA 493
Db      437 AspLeuSerAsnAsnSerIleAsnGlyPheIleProAlaSerPheGlyAsnMetSerAsn 456
QY      494 CTTCAGTGGCTGATTTATTCAGAGGTGAATTAAGACAAATGGAACAAAGCATGGCAT 553
Db      457 LeuAlaPheLeuPheLeuTyArgIuAsnGlnLeuAlaSerSerValProGluGluIleGly 476
QY      554 GGCTTAAACCAAGCTCTCAACCTTGATAGTACAGAAACCTATCAAGAGTTTCCCA 613
Db      477 TyLeuArgSerLeuAsnValIleAspLeuSerGluAsnAlaLeuAsnGlySerIlePro 496
QY      614 GGAAGTTTTCTGACTAACAATTTAGAAATCTGTGTGCTGTGAGACAAAAATGACC 673
Db      497 AlSerPheGlyAsnLeuAsnLeuSerArgLeuAsnLeuValAsnAsnGlnLeuSer 516
QY      674 TCTCTAGAGGTTCCATATTTGACAGACTTATATCTTAAAGAAATGAATGTGGCTCAT 733
Db      517 GlySerIleProGluGluIleGlyTyLeuArgSerLeuAsnValIleuAspLeuSerGlu 536
QY      734 AATCTTACATTCCTTTAAGTCCGGAATATTTTCTAATCTGACAAACCTAGAACAT 793
Db      537 AsnAlaLeuAsnGly---SerIleProAlaSerPheGlyAsnLeuAsnLeuSerArg 555
QY      794 GTGATCTTCTTATATCTAATATTTCAACTATTTCTGTCAAGACTTACAGTTTCACT 853
Db      556 LeuAsnLeuValAsnAsnGlnLeuSerGlySerIleProGluGluIleGlyTyLeuArg 575
QY      854 GAAATCCCAAGTCAATCTCTCT----- 877
Db      576 SerLeuAsnAspLeuGlyLeuSerGluAsnAlaLeuAsnGlySerIleProAlaSerLeu 595
QY      877 ----- 877
Db      596 GlyAsnLeuAsnLeuSerMetLeuTyLeuTyAsnAsnGlnLeuSerGlySerIle 615
QY      878 -----TTAGACCTGTCTTTAAACCAATT 901
Db      616 ProGluGluIleGlyTyLeuSerSerLeuThrTyLeuSerLeuGlyAsnAsnSerLeu 635
QY      902 GACTCCATTCAAGCCCAAGCTTTCAAGGAAATTAG---CTCATGTAATTGACTCTTACA 958
Db      636 AsnGlyLeuIleProAlaSerPheGlyAsnMetArgAsnLeuGlnAlaLeuIleLeuAsn 655
QY      959 AGT-----AATTTTAATAGCTCAAAATGTA 982
Db      656 AspAsnAsnLeuIleGlyIleProSerSerValCysAsnLeuThrSerLeuGluVal 675
QY      983 CTGAAATG-----TGCTTCAAAACATGACT 1009
Db      676 LeuTyThrProArgAsnLeuLysGlyLeuValProGlnCysLeuGlyAsnIleSer 695
QY      1010 GGTTCATATCCATCGCTTGATCTGGGAGAAATTTAAAAATGAA----- 1054
Db      696 AsnLeuGlnValLeuSerMetSerSerAsnSerPheSerGlyIleuLeuProSerSerIle 715

```


DB: 2 Gaps: 34

US-09-396-985B-5 (1-3395) x T13174 (1-1051)

QY 503 CTGATTTATCCAGGTGGAATTTGACAAATTGAGACAAAGCATGGCATGGCTTAAC 562

DB 297 ILeuysIleAlaAsnCythrLeuGluThrLeuHISalaglualPheHISglYleuAsn 316

QY 563 CAGCTTCAGCTGGTACGTGACAGAAACCCATCAAGAGTTTCCCGAAGAGTTT 622

DB 317 GluLeuYrAlaValAsnLeuThrAspValGlyLeuAlaIleIleAsnProAspThrPhe 336

QY 623 TCTGACTACAAATTTAGAGATCTGGTGGCTGGAGACAAATATACCTCTAGAG 682

DB 337 ValGlyAsnLysLysLeuArgMetLeuThrIleSerGlyAsnAspLeuSerValMetSer 356

QY 683 GGTTCAT---ATTGACAGCTTATATCTTAAAGAACTPAAAGTGGCTCATATCTT 739

DB 357 SerIleHisYrLeuLeuLysSerSerIleGluGluLeuAspPheSerArgAsn 376

QY 740 ATACATTCCTTAATGCTGCAATTTCTTATCTGACAAACCTGAACATGTGAT 799

DB 377 LeuMetGluLeuAsn---ProLysAlaPheSerHisIleuSerAsnValValYrIleAsn 395

QY 800 CTTTCTTAACTATATCAAACTATTTCTGCAAGACTTACAGTTTCTACGTGAAT 859

DB 396 LeuSerArgIleAsnSerLeuLysLysLeuProGluLysAlaPheGlu----- 410

QY 860 CCCCAAGTCAATCTC-----TCTTAAAGCTGTCTTAAACCAATGACTCCATTC 913

DB 411 ---LysValThrLeuGluGluGluLeuAspLeuSerYrAsnSerLeuThrGluLeuPro 429

QY 914 GCCCAAGCTTTCAGGAATTAGCTCCATGATGATGATCAAGATGAT----- 964

DB 430 ArgAspIlePheAsnGlyThrThrLeuSerIleLeuHISleuLysYrAsnThrPheAsn 449

QY 965 -----TTTAAATGCTCAATATGATCAATGATGCTTCAAAACATGACTGCT 1012

DB 450 GlyAspLeuHisPheGlyThrLysAspLeuGlnGlnLeuAspLeuSerPheAsnSerIle 469

QY 1013 TTACATGCTCATCGGTGATCTTGGAGAAATTTAAATGAAAGAAATCTGAAAGTTT 1072

DB 470 ValGlnValHisHis-----SerMetPhe 477

QY 1073 GACCGTTCTGCATGAGACATGATGAGACAT----- 1111

DB 478 AspLys-----MetProGlyLeuThrAsnLeuAsnLeuLysGlyAsnGlyIleLysLys 495

QY 1112 -----GATGAGTTCAAGTTACATATATTAATCATTTTTCAGATGATATTATAT 1162

DB 496 IleGlnProAspSerPhe---LeuThrLeuLysAsnLeuArgHisIleAspLeu---Ser 513

QY 1163 CTCATTTGCTTGGCAATATTTCTGCAATGCTTCTTCAAGGTGATCATATTAACACATA 1222

DB 514 IleAsnAspLeuAspGlnIleSerGlyMetLeuPhe----- 525

QY 1223 GCAATGTCTTCAAGCATTTCAATGCAATCTTATCATATCATATGATCTTAAAG 1282

DB 526 -----PheLysAsnSerGluLeuAspValIleArg-----LeuAsn 537

QY 1283 CCTTTTCCAAAGCTAGT---CTACCT-----TTTCTTAAAGTTGGACCTTAAT 1330

DB 538 AspAsnProArgLeuSerGlnLeuProThrAspGlyPheLeu---SerTyrSer----- 554

QY 1331 ACCAAGAGAGATATCAGCTTTGGTCAAGTTGGCTTGCAGAGCTCAGATATCTAGAT 1390

DB 555 -----GlyGluPhe-----ThrValYrTyrLeuAsp 563

QY 1391 CTTAGTAAATGCCATGAGCTTGAAGTGGCTCTTATCTGATTTTGAACA--- 1447

DB 564 IleSerAsnCyValIle-----GlyProLeuGlnGlyHisLysAlaPheSerThrMet 580

QY 1448 AACAACTGAAGTACTTAGACTCAGCTTCAATGATGATGATGATGATGATGATGATGAT 1507

DB 581 ProHisLeuThrThrLeuLysLeuAlaIleAsnAsnIle-----AsnHis 595

QY 1508 ATGGGTCTAGAAAGCTGGATATACCTGACCTTTCAGACATCCACTTTAAAGGTCA 1567

DB 596 LeuProArgGlu----- 599

QY 1568 GAATTCACAGTCTTATCTCTGAAAAACTCTTACCTTGAACATCTTACACT--- 1624

DB 600 -----IlePheThrGlyLeuHisLysLeuIleAspLeuAspLeuSerAsnLeu 616

QY 1625 AATACAAATTTGACTTGTATGAGCATATTTCTGGCTTGTATGACCTTCAACATTTAAA 1684

DB 617 IleThrArgMetAsp---AspLeuIlePheMetAspAsnGlyGluLeuThrLysLeuSer 635

QY 1685 ATGGCTGCAATTTCTTCAAGACAAACCTTTCA---AATGCTTTCAAAACACAA 1741

DB 636 LeuAlaGlyAsnProIle-----SerArgLeuSerValArgLeuPheLeuProLeuHis 653

QY 1742 AACTTAACATTCCTGATCTTCTTAAATGCCACCTGGAACAGATATCTAGGGGGTATTT 1801

DB 654 GlnLeuArgCysLeuAspValAsnAspCysGluLeuThrThrLeu----- 668

QY 1802 GACACACTCTACAGACTCCAGTTATTAACATGATGCAACAAACCTACTGTTCTGAT 1861

DB 669 -----LeuSerAspArgAspLeu----- 674

QY 1862 CCATCCCATTTTAAACAGCTTACTCCCTCAGACCTCTTGAATGACATTCATGACATA 1921

DB 675 GlyAlaGlyYrLysIlePheAspSerLeuArgSerPheAsnAlaSerGlyAsnLeuIle 694

QY 1922 ---GAGACATCAAGAAATCTGCACAACTTTTCCAAAGAGCTAGCCGTCTCAATCTG 1978

DB 695 LysLysIleSerSerGluAspValLysSerPhe---LysAsnLeuArgSerLeuAspIle 713

QY 1979 ACTATATTTCTGCTGCTTGTATATGTAATATGCAATTTCTTGAAGTGGTCAAGAC 2038

DB 714 ThrAsnAspProLeuLysCysThrProAspPheGlnGluPheIleSerYr----- 730

QY 2039 CAGAAATGTTCTTGGATGTTGAACAATGAAATGATGATCACTATGACATGAAG 2098

DB 731 -----ValThrLeuGlnMetGlnMetThrProLysArgLeuProValLeu 745

QY 2099 GCTCCCTGCTGCTGATTTTATGAAATTCACCTGTTATATATCAAGCATATCATGAT 2158

DB 746 AlaAsnLeuGluAspAspAlaThr----- 753

QY 2159 GTATCGGTGCTCAGTGGCTTGTGTAGCCACTGTAGCATTTCTGATATACACTTCTAT 2218

DB 754 -----IleValGlnLeuGlnThrLeuAlaGlnAlaGlyTyrPheSerSerLeu 768

QY 2219 TTTCACCTGATCTTATTTGCTGCTGTAAAGATGACAGAGAGAGAAAGCATCTATGAT 2278

DB 769 AlaHisGluVal-----Cys---LysHisAlaGluGlySerAspLeuLeuAsp 783

QY 2279 GCATTTGTGATCTACGAGCAGAGATGAGACCTGGGTGAGAAAGAGCTGTAAAGAT 2338

DB 784 -----GluLysLysAlaAspSerAlaGluAlaLysLeuGluLysArg 797

QY 2339 TTAGAGAGAGAGTGGCCCGC 2359

DB 798 LeuLysGluSerValLysLys 804

RESULT 13

B3665

slit protein 2 precursor - fruit fly (Drosophila melanogaster)

C1:Species: Drosophila melanogaster

C1:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 02-Aug-2002

C1:Accession: B3665

R1:Rocheberg, J.M.; Jacob, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.

Gene Dev. 4, 2169-2187, 1990

A1:Title: slit: an extracellular protein necessary for development of midline glia and co

A1:Reference number: A3665; MUID:91099665; PMID:2176636


```

QY 1708 ----- 1708
Db 700 LysCysSerSerGluAenSerGluGlyCysLeuGlyAspGlyTyrCysProProSerCys 719
QY 1709 -----AACCCCTTCAATGTC----- 1726
Db 720 ThrCysThrGlyThrValAlaCysSerArgAenGlnLeuGlyGluIleProArgGly 739
QY 1726 ----- 1726
Db 740 IleProAlaGluThrSerGluLeuTyrLeuGluSerAenGluIleGluGlnIleHisTyr 759
QY 1727 -----TTTACAAACACAACTTAACATTCCTGATCTTTGTAATGCCAATGGAA 1780
Db 760 GluArgIleArgHisLeuArgSerLeuThrArgLeuAspLeuSerAenAenGlnIleThr 779
QY 1781 CAGATATCTAGGGGGGATTTTGACACACTCTACAGACTCCAGTTATTAACATGATGAC 1840
Db 780 IleLeuSerAenTyrThrPheAlaAsnLeuThrTyrLeuSerThrLeuIleLeuSerTyr 799
QY 1841 AACCACTACTCTGTTCTGGATCCATCCATTAATAACAGCTGTACTCCCTCAGAGACTCTT 1900
Db 800 AsnLysLeuGlnCysLeuGlnArgHisAlaLeuSerGlyLeuAenAsnLeuArgVal 819
QY 1901 GATTGACGTTTCATTCGATAGAG--ACATCCAAAGGAATATCGCAACATTTCCAAAG 1957
Db 820 SerLeuHisGlyAenArgIleSerMetLeuProGluGlySerPheGluAspLeu--Lys 838
QY 1958 AGCTGACCGCTCTTCAATCTGACTAATTAATCTGTCTGTTGATATGTAATATCAGAT 2017
Db 839 SerLeuThrHisIleAlaLeuGlySerAenProLeuTyrCysAspArgGlyLeuLeuTyr 858
QY 2018 TTCTTGCAATGGGTCACAGAGACCAAAATGTTCTTGGAATGTTGAACAATGAATGT 2077
Db 859 PheSerAspTyrPheLysLeuAspTyrValGluProGlyIleAlaArgCys 875
QY 2078 GCATCACCATTATAGACGAAGGCTCCCTGGTGTGGATTTTACGAATTCACAC----- 2131
Db 876 AlaGluProGluGlnMetLysAspLysLeuIleLeuSerThrProSerSerSerPheVal 895
QY 2132 -----TGTATAT----- 2139
Db 896 CysArgGlyArgValArgAsnAspIleLeuAlaLysCysAenAlaCysPheGluGlnPro 915
QY 2140 ATACAGACTATCTCAGTGTATCGGT-----GGTCAGTGCTTGT-- 2181
Db 916 CysGlnAenGlnAlaGlnCysValAlaLeuProGlnArgGluTyrGlnCysLeuGln 935
QY 2182 -----GGTAGCACTGT 2193
Db 936 ProGlyTyrHisGlyLysHisCys 943

RESULT 14
A36665
slit protein 1 precursor - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 30-Apr-1991 #sequence revision 30-Apr-1991 #text change 02-Aug-2002
C/Accession: A36665; A31640; S13523
R/Rochberg, J.M.; Jacobs, J.R.; Goodman, C.S.; Artavanis-Tsakonas, S.
Genes Dev. 4, 2169-2187, 1990
A/Title: slit: an extracellular protein necessary for development of midline glia and cc
A/Reference number: A36665; MUID:91099665; PMID:2176636
A/Accession: A36665
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1480 <ROT>
A/Cross-references: GB:X53959; NID:98614; PIDN:CAA37910.1; PID:98615
Cell 55, 1047-1059, 1988
R/Rochberg, J.M.; Hartley, D.A.; Walther, Z.; Artavanis-Tsakonas, S.
A/Title: slit: An EGF-homologous locus of D. melanogaster involved in the development of
A/Reference number: A31640; MUID:89077533; PMID:314436
A/Accession: A31640

```

```

A/Molecule type: DNA
A/Residues: 881-1182, 'G', 1185-1404, 'GT', 1463-1464, 'YHA' <RO2>
A/Cross-references: GB:M23543; NID:9340939; PID:9514357
C/GeneticCB:
A/Gene: FlyBase:slit
A/Cross-references: FlyBase:FBgn0003425
A/Introns: 1351/3
C/Superfamily: fruit fly slit protein; EGF homology; Leucine-rich alpha-2-glycoprotein x
C/Keywords: alternative splicing; growth factor
F/66-91/Domain: proteoglycan amino-terminal homology <PAH1>
F/101-124/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F/125-148/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F/149-172/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F/173-196/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F/197-220/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
F/228-272/Domain: proteoglycan carboxyl-terminal homology <PCS1>
F/288-313/Domain: proteoglycan amino-terminal homology <PAH2>
F/323-346/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
F/347-370/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
F/371-394/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR8>
F/395-418/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR9>
F/419-442/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR10>
F/450-494/Domain: proteoglycan carboxyl-terminal homology <PCS2>
F/512-537/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR11>
F/547-571/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR12>
F/572-595/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR13>
F/596-619/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR14>
F/620-643/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR15>
F/651-695/Domain: proteoglycan carboxyl-terminal homology <PCS3>
F/708-733/Domain: proteoglycan amino-terminal homology <PAH4>
F/743-766/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR16>
F/767-790/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR17>
F/791-814/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR18>
F/815-838/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR19>
F/846-890/Domain: proteoglycan carboxyl-terminal homology <PCS4>
F/1028-1061/Domain: EGF homology <EGF>
F/1068-1099/Domain: EGF homology <EGF2>
F/1115-1148/Domain: EGF homology <EGF1>

Alignment Scores:
Pred. No.: 2,74e-12 Length: 1480
Score: 282.50 Matches: 161
Percent Similarity: 33.29% Conservative: 88
Best local Similarity: 21.52% Mismatches: 246
Query Match: 4.75% Indels: 254
DB: 2 Gaps: 25

US-09-396-985b-5 (1-3395) x A36665 (1-1480)
QY 374 TGCATGATGAGATCTCAGACAAATGCCCTCATGACATCCCTTATTCACCAAGACTTA 433
Db 308 CysArgGluLysSerLeuThrSerValProValThrLeuProAspAspThrThrAspVal 327
QY 434 GATCTGAGCTTCAACCCCTGAAGATCTTAAGAAGCTTATGCTTACCAATTTCTCAAA 493
Db 328 ArgLeuGlnLysnPhelIleThrGluLeuProLysSerPheSerPheArgArg 347
QY 494 CTTCAGTGGCTGATTTATTCAGGTGTGAATTTGAGCAATTTGAAAGCAAGCATGGCAT 553
Db 348 LeuArgArgIleAspLeuSerAenAenAenIleSerArgIleAlaHisAspAlaLeuSer 367
QY 554 GCGTTAAACAGATCTTCACCTTGATCTGACAGAAACCTTATTCAGATTTTCCCA 613
Db 368 GlyLeuLysGlnLeuThrThrLeuValLeuTyrGlyAsnLysIleLysAspLeuProSer 387
QY 614 GGAAGTTTCTGCACTAACAATTTAGAAATCTGGTGGCTGTGGAGCAAAATGACC 673
Db 388 GlyValPheLysGlyLeuGlySerLeuArgLeuLeuLeuLeuLeuAlaGlnIleSer 407
QY 674 TCTCTAGAGGGTTTCCATATTTGACAGCTTATATCTTAAAGAACTAAATGTGGCTCAT 733
Db 408 CysIleArgLysAspAlaPheArgAspLeuHisSerLeuSerLeuLeuSerLeuTyrAsp 427

```


C; Superfamily: fruit fly slit protein; EGF homology; leucine-rich alpha-2-glycoprotein

Alignment Scores:

2.76e-12	Length:	1523
----------	---------	------

Score:	282.50	Matches:	202
Percent Correct:	33.33%	Concentration:	115

Percent similarity:	32.32%	Conservative:	117
Best local similarity:	20.47%	Mismatches:	325

Query Match:	4.75%	Indels:	344
Mismatches:	20.37%	Mismatches:	323

DB:	2	Gaps:	44
-----	---	-------	----

[illegible]

US-09-396-985B-5 (1-3395) x T13953 (1-1523)

[illegible]

Dd	434	-----		1066
Qy	1010	GGTTTACATGTCATCGGTTGATCTTGAGAAATTTTAAAAATGAAGAAATCGAA---		1066
Dd	440	ValCysAspCysHisLeuLysETTPLeuValAspYrLeuGlnAspProIleGluThr		459
Qy	1067	-----AGTTTGACCGTTCTGTCTGACGGAAGACTATGCAATGTGAC		1108
Dd	460	SerGlyAlaArgCysSerSerProArgArgLeuAlaAsnYsArgIleSerGlnIleLys		479
Qy	1109	ATTGATGAGTTCAGATTAAACA-----TATTAATATCTTTTCAGATGATTT		1156
Dd	480	SerIlybSphPheArgCysSerGlySerGlnAspYrArgAsnArgPheSerSerGluCys		499
Qy	1157	TAT---AATCTCAATGGCTTGGCAAAATATTTCTGCAATGTCTTTACAGGTGTACATATA		1213
Dd	500	PheMetAspLeuValCysProGluLysCysArgCysGluGly-----		513
Qy	1214	AAACACATAGACAGATGTTCTTACGAGCATTTCAAAATGGCAATCCTTATCATCATTAAGTGT		1273
Dd	514	---ThrIleValAspCysSerAsn-----GlnYsLeuSerArgIleProSer		528
Qy	1274	CATCTTAAAGCTTTTCCAAAGCTGACGTACCTTTCTTAAAGTGTGACCTTTACTACAC		1333
Dd	529	HisLeuProGluYr-----ThrThrAspLeuArgLeu		539
Qy	1334	AACAGAGAGATATCAGCTTTGTGACGTGGCT-----CTGCCAAGTCTC		1378
Dd	540	AsnAspAsnAspIleAlaValLeuGluAlaThrGlyIlePheYsLysLeuProAsnLeu		559
Qy	1379	AGATATCATGATCTTACTAGAAAATGCCATG-----ACCTTAGAGGT		1420
Dd	560	ArgYsIleAsnLeuSerAsnAsnArgIleLysGluValArgGluGlyAlaPheAspGly		579
Qy	1421	TGCTGTTCTTATTTCTGATTTTGGAAACAACAACCTGAAGTACTTAGACCTCAGCTTCAAT		1480
Dd	580	AlaIleGlyValGlnGlu-----LeuMetLeuThrGlyAsn		591
Qy	1481	GGTGTCATCTGATGAGTCCAC--TTCATGGGCTTTAGAGAGCTGGAATATCTGGAC		1537
Dd	592	GlnLeuGlnThrMetHisGlyArgMetPheArgGlyLeuSerGlyLeuYsThrLeuMet		611
Qy	1538	TTTAGACATCCACTTTAAAAAAGCTGACAGAAATTCACATGTTCTTATCTTTGAAAAA		1597
Dd	612	LeuArgSerAsnLeuIleSerCysValAsnAsn--AspThrPheAlaGlyLeuSerSer		630
Qy	1598	CTTCTTACCTTGCATCTCTTACACTTAAT-----ACCAAAATTTGACTTTGATGGCATA		1651
Dd	631	ValArgLeuLeuSerLeu---TyrAspAsnArgIleThrThrIleSer---ProGlyAla		648
Qy	1652	TTTCTTGAGCTGATCAGTCTCAACACTTTAAAAATGGCTGGCAATCTTCTTC		1702
Dd	649	PheThrThrLeuValSerLeuSerThrIleAsnLeuLeuSerAsnProPheAsnCysAsn		668
Qy	1702	-----		1702
Dd	669	CysHisMetAlaTrpLeuGlyArgTrpLeuArgLysArgIleValSerGlyAsnPro		688
Qy	1703	-----AAAGACAACACCTTTCAATGTC-----		1726
Dd	689	ArgCysGlnYsProPhePheLeuYsGluIleProIleGlnAspValAlaIleGlnAsp		708
Qy	1727	TTTTCACAAACACACAACTTAACATTTCTGGATCTTTCTAAATGCCAATG-----		1777
Dd	709	PheThrCysGluGlyAsn-----GluGlnAsnSerCysGlnLeuSerProArg		724
Qy	1778	-----GAACAGATA-----CTTAGGGGGGATA-----		1798
Dd	725	CysProGluGlnCysThrCysValGluThrValValArgCysSerAsnArgIleLeuHis		744
Qy	1798	-----		1798

```
Db 745 ThrIleuProIysGlyMetProIysAspValThrGluLeuValGluGlyAsnHisIleu 764
QY 1799 -----TTGACACACTCTACAGACTCCAGTTATTATAACATAGTCAAC 1840
Db 765 ThrAlaValProIysGluLeuSerThrPheArgGlnLeuThrIleAspLeuSerAsn 784
QY 1841 AACAACTTACTGTTCTGATTCATCCATTATTAACAGCTGACTCCCTCAGGACTCTT 1900
Db 785 AsnSerIleSerMetLeuThrAsnHisThrPheSerAsnMetSerHisIleuSerThrIleu 804
QY 1901 GATTGACGTTTCAATCGC-----ATAGACATCCAAAGGAATACTGCA 1945
Db 805 IleuSerThrAsnArgLeuArgCysIleProValHisAlaPheAsnGlyLeu----- 822
QY 1946 CATTTCCAAAGACTCTAGCCGCTTCAATCTGACTAATAATTCTGTGCT----- 1996
Db 823 -----ArgSerLeuArgValLeuThrIleuHisGlyAsnAspIleSerSerValPro 839
QY 1996 ----- 1996
Db 840 GluGlySerPheAsnAspLeuThrSerLeuSerHisIleuAlaIleuGlyIleAsnProIeu 859
QY 1997 ---TGATATGTGAATATCAGAAATTCTTGCACTGGGTCAAG----- 2035
Db 860 HisCysAspCysSerLeuArgTrpLeuSerGluTrpIleuValArgIleuValGlyLeuPro 879
QY 2036 -----GACCAGAAATGTTCTTGTAAT 2059
Db 880 GlyIleAlaArgCysSerSerProGluSerMetAlaAspArgLeuLeuThrPro 899
QY 2060 GTTGACAAATGAATGTGCATCATTAGACATG-----AAGGCTCCCTG 2107
Db 900 ThrHisArgPheGlnCysIysGlyProValAspIleAsnIleValAlaIysCysAsnAla 919
QY 2108 GTGTGGATTT-----ACGAATTCACTGT----- 2134
Db 920 CysLeuSerSerProCysIysAsnAsnGlyThrCysSerGlnAspProValGluGlnTyr 939
QY 2135 -----TATATATACAGAC-----TATCATCAGTGT 2160
Db 940 ArgCysThrCysProIySerTyrIysGlyLysAspCysThrValProIleAsnThrCys 959
QY 2161 ATCGGTGTCAGTGTGCTTGTGTAGCCACTGTAGCAATTTCTGATATACCACTTCTATT 2220
Db 960 ValGlnAsnProCysGlnHisGlyGlyThrCysHisIleuSer----- 973
QY 2221 TCACCTGATCTTATTGCTGCTGCTGTAAGATACAGACAGAGAAAGCATATGATGC 2280
Db 974 -----GluSerHisArgAspGlyPheSerCys 982
QY 2281 ATTTGTGATCTA-----CTCGAGCCAGAAATGAGACTGGGT 2316
Db 983 SerCysProIeuGlyPheGluGlyGlnArgCysGlnIleAsnProAsp----- 998
QY 2317 GAGAAACGAGCTGTAAGATTAGAAAGAGAGTCCCGCTTTCAGCTTTCCTTCA 2376
Db 999 -----AspCysGlnAspAsnAspCysGlnAsnSerAla---ThrCys 1011
QY 2377 TTACAGGAGACTTATTCCTGTGTAGCCATTGCTCCAAACATCATCCAGAAAGCTTCCA 2436
Db 1012 ValAspGlyIleAsnAsnTyrAlaCysValCysProProAsnTyrThrGlyGluLeuCys 1031
QY 2437 CAAGAGCCGGAAGTATTGT 2457
Db 1032 AspGluValIleAspTyrCys 1038
```


QY 1460 TACTTAGACCTCAGCTTCATGTCATCCGTGATGAGTGCACCTTCATGCTGAGAA 1519
 DB 401 TyrlenuapleuSerPhehansnGlyValIleleuMetSerAlaahnpheMeGlyleuGlu 420
 QY 1520 GAGCTGAAATACCTGAGCTTCAGACCTCACTTAAAAAGTCAAGAAATTCAGTG 1579
 DB 421 GluleuGluTyrlleuAapPheGlnHiserThrleuTySylsValThnGluPheSerVal 440
 QY 1580 TTCTTATCTCTGAAAAAATCTTCTTACCTTCAGATCTCTTACATTAACCAAAATTCAC 1639
 DB 441 PheleuSerleuGluTyrlleuTyrlleuAapPheSerThrleuTySylsValThnGluPheSerVal 460
 QY 1640 TTGATGAGCATATTTCTGAGCTTCAGCTCACTTAAACCTTAAAGTGCAGATTCCT 1699
 DB 461 PheapGlyIlePheleuGlyleuIleSerleuAanthrleuTySylsValThnGluPheSerVal 480
 QY 1700 TTCAAGACCAACACCTTTCATGCTTCATTAACCAACCAACCTTAACTTCCTGAT 1759
 DB 481 PheTySylsPheThrleuSerAapValPheThrAanthrThrAanthrThrPheleuAap 500
 QY 1760 CTTTCTTAAATGCGAATGCGAATATATCTGAGGGGATTTGACACCTTCAGACTC 1819
 DB 501 leuSerTySylsGlnleuGluGlnIleSerAapGlyValPheAapThrleuTySylsVal 520
 QY 1820 CAGTTATTAACATGAGTCAACAACCTTACTGTTTCTGATCCATCCATTTATAACAG 1879
 DB 521 GlnleuAanthrMetSerHisAapAanthrleuPheleuAapProSerHisTyrlleGln 540
 QY 1880 CTGACTCTCCCTCAGACTCTTGTATGATGAGTTTCAATGCAATGCAATGCAACCAAGAAATA 1939
 DB 541 leuTySylsSerleuAapGlnThrleuAapPheSerPheAanthrIleGlnThrSerTySylle 560
 QY 1940 CTGGAACATTTTCCAAAGCTCAGCTCCCTCTTCAATCTGATTAATTAATCTGCTGCTGT 1999
 DB 561 leuGlnHisPheProTySylSerleuAlaValPheAanthrThrAanthrThrAanthrThrAanthr 580
 QY 2000 ATATGTAATATCAAAATTTCTGAGTGGTCAAGACCAAGAAATTTCTGCTGAT 2059
 DB 581 IleTySylGluTyrlleuAanthrPheleuGlnThrValTySylAapGlnTySylMetPheleuValAap 600
 QY 2060 GTTGAACAATGAATGTGATCACTTATGACATGAAGGCTCCCTGCTGCTGATTTT 2119
 DB 601 ValGlnGlnMetTySylAapSerProIleAapMetTySylAapSerleuValleuAapPhe 620
 QY 2120 ACGAATTCACCTGTTATATATCAAGACTATCATCACTGATGCTGCTGCTGCTGCTT 2179
 DB 621 ThrAanthrThrTySylTyrlleTyrlleThrIleleuSerValSerValSerValSerValleu 640
 QY 2180 GTGGAGCCTGAGCATTTCTGATATACCACTTCTTATTCACCTGATCTTATTCCT 2239
 DB 641 ValValAlaThrValAlaPheleuIleTyrllePheTyrllePheHisleuIleleuAla 660
 QY 2240 GGGCTGTAATAAAGTACAGAGAGAGAGAAAGCATATGATGATTTGATCTACTCAGC 2299
 DB 661 GlyTySylTySylTySylSerAapGlyGlnSerIleTyrlleAapAlaPheValIleTySylSer 680
 QY 2300 CAGAAATGAGCTGGGTGAGAAAGAGCTGGTAAAGATTTTGAAGAAGAGAGTCCCGCC 2359
 DB 681 GlnAanthrAapThrValAapAapGlnleuValTySylAanthrGlnGluGluValAapProAap 700
 QY 2360 TTTGAGCTTCTGCTTATTAAGGAGCTTATTCCTGCTGATGAGCTTCTGCGCAATC 2419
 DB 701 PheGlnleuTySylleuHisTyrlleAapPheIleProGlyValAlaIleAlaAanthrIle 720
 QY 2420 ATCCAGAGAGGCTTCCACAGAGCCGGAAGATTTATGCTGCTGCTGCTGCTGCTGCTTATC 2479
 DB 721 IleGlnGlnGluTyrllePheHisTySylSerAapGlyValIleValIleValIleSerAapHisPheIle 740
 QY 2480 CAGAGCCCTGCTGATCTTTGAATATGAGATGCTCAAGATGCAATTTCTGAGTAC 2539
 DB 741 GlnSerAapTyrllePheGlnTyrlleGlnIleAapGlnThrTyrllePheleuSer 760
 QY 2540 CGCTCTGCGATCATCTTCTGAGAAAGTGAAGAGTCTTCTGAGGAGCAG 2599

DB 761 ArgSerGlyIleIlePheIleValleuGluTySylValGluTySylSerleuAapGlnGln 780
 QY 2600 GTCAATTTGATGCGCTTCTTATGAGAAACACCACTTCAGTGGGAGGCAATGCTCTG 2659
 DB 781 ValGluTyrllePheThrAapGlnleuSerAapAanthrThrleuGlnTyrlleAapAanthrleu 800
 QY 2660 GGGAGGACATCTTCTGAGAGACTCAAAAAAGCCCTGTTGATGAGAAAAAGCTTGAAT 2719
 DB 801 GlyAapHisIlePheThrAapGlnleuTySylValAlaAanthrAapGlyValIleleuAap 820
 QY 2720 CCAGATGAACATCAGAGAGAAACCAAGAGCAACCACTTGAAC 2764
 DB 821 ProAapGlnThrSerGlnGluGlnGluValAanthrThrleuThr 835
 RESULT 2
 ID Q8K2T5 PREDIMINARY; PRT; 835 AA.
 AC Q8K2T5;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Toll-like receptor 4.
 GN Name="Tlr4";
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor; DOI=10.1073/pnas.242603899;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Mariani K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadlton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skaleks U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029856; AA429856.1; -;
 DR HSSP; O60603; 1077.
 DR MGD; MGI:96824; Tlr4.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0004872; F:receptor activity; IDA.
 DR GO; GO:0007249; F:1-kappab kinase/NF-kappab cascade; IDA.
 DR GO; GO:0008063; P:Toll signaling pathway; IDA.
 DR InterPro; IPR000887; Aldlee_KDPG_KHG.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00560; LRR_1; 10.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO0019; LEURICHRPT.
 DR SMART; SM00082; LRRT; 1.

DR SMART; SM00255; TIR; 1.
DR PROSITE; PS00159; ALDOLASE_XDPG_KHG_1; UNKNOWN_1.
KM RECEPTOR; PS50104; TIR; 1.
SQ SEQUENCE 835 AA; 95488 MW; A103C3997A59CF5B CRC64;

Alignment Scores:

	1.81e-263	Length:	835
Pred. No.:	3748.00	Matches:	715
Score:	91.86%	Conservative:	52
Percent Similarity:	85.63%	Mismatches:	68
Best Local Similarity:	63.07%	Indels:	0
Query Match:	2	Gaps:	0

US-09-396-985b-5 (1-3395) x Q8KZT5 (1-835)

```
QY 260 ATGATGCGCTCTTGCAATCTGGCTGGAGACTGTGATCATGGCATTTGCTTCTGCTG 319
Db 1 MetMetProProIleuLeuAlaArgThrLeuIleMetAlaLeuPhePheSerCysLeu 20
QY 320 AGACGAGAGCTTGAATCCCTGCATAGAGCTACTTCTTAATATTAACCTTAAGCATG 379
Db 21 ThrProGlySerLeuAsnProCysIleGluValAlaProAsnIleThrTyGlnCysMet 40
QY 380 GATCAGAACTCAGCAAAATCCCTCATGACATCCCTATTCAACCAAGAACTAGATCTG 439
Db 41 AspGlnIysLeuSerIysValProAspAspIleProSerSerThrIysAsnIleAspLeu 60
QY 440 AGCTTCAACCCCTGAAAGATTAGAAGCTAAGCTTACCAAAATTTCTCACACTTCAG 499
Db 61 SerPheAsnProLeuIysIleLeuIysSerIysSerPheSerAsnPheSerGluLeuGln 80
QY 500 TGGCTGATTTATTCAGAGTGTGAATTTGAGCAATTTGAACAAGAGCATGGCATGGCTTA 559
Db 81 TrpLeuAspLeuSerIargCysGlnIleGlnThrIleGlnAspIysAlaItrpHisGlyLeu 100
QY 560 AACGAGCTCTCAACCTTGATGACTGACAGAAACCTTACAAAGATTTTCCCGCAGAACT 619
Db 101 HisIleIleuSerAsnLeuIleLeuThrGlyAsnProIleGlnSerPheSerProGlySer 120
QY 620 TTTTCTGACTAACAAATTTNAGAAATCTGGTGGCTGTGAGACAAAAATGACCTTCTTA 679
Db 121 PheSerGlyLeuThrSerLeuGluAsnLeuValAlaValGluThrIysLeuAlaSerLeu 140
QY 680 GAGGCTTCCATATTTGACAGCTTATATCCCTTAAGAACTTAATGGTGGCTCAATCTT 739
Db 141 GluSerPheProIleGlyGlnLeuIleThrLeuIysIysLeuAsnValAlaHisAsnPhe 160
QY 740 ATACATTCCTTTAAGTGCCTGAATATTTTCTAATCTGACAAACCTAGAAACATGTGAT 799
Db 161 IleHisSerCysIysLeuProIaItyrPheSerAsnLeuThrAsnLeuValHisValAsp 180
QY 800 CTTTCTTATACTATATTTCAAACTAATTTCTGTCAAAGACTTACAGTTTCTTACGTAAAT 859
Db 181 LeuSerIysAsnTyrlleGlnThrIleThrValAsnAspLeuGlnPheLeuArgGluAsn 200
QY 860 CCCCAGATCATCTCTTTAGACCTGTGCTTTAAACCAATGACTCCATTCAGCCCAA 919
Db 201 ProGlnValAsnLeuSerLeuAspIleSerLeuAsnProIleAspPheIleGlnAspGln 220
QY 920 GCGTTTACAGGAAATTAAGCTCCATGAAATGACTCTAAGAAATTAATTTAATAGCTCAAT 979
Db 221 AlaPheGlnGlyIleIysIysLeuHisGlnLeuThrLeuArgGlyAsnAsnAsnSerSerAsn 240
QY 980 GTACTGAAATATGTCCTTCAAAACATGACTGGTTTACATGTCTCAGGTGATCTGGGA 1039
Db 241 IleMetIysThrCysLeuGlnAsnLeuAlaGlyLeuHisValHisArgLeuIleLeuGly 260
QY 1040 GAATTTAAAAATGAAGAATCTGAAAAGTTTGAACGCTTGTGCATGGAAGAACTATGC 1099
Db 261 GluPheIysAspGluArgAsnLeuGlnIlePheGlyProSerIleMetGluGlyLeuCys 280
QY 1100 AATGTGACATGATGATTCAGGTTAACATATATAATATCATTTTTCAGATGATATTAT 1159
```

```
Db 281 AspValThrIleAspGluPheArgLeuThrHisThrAsnAspPheSerAspIleVal 300
QY 1160 AATCTCAATTTGCTGGCAAAATATTTCTGCATATCTTTACAGGTGATATATAAACAC 1219
Db 301 LysPheIleCysLeuAlaAsnValSerIleAsnSerLeuAlaGlyValSerIleIysTy 320
QY 1220 ATAGCAGATGTCCTTGGCAGTTTCAATGAGCAATCTTATTCATCACTTATAGATGCTCTT 1279
Db 321 LeuGluAspValProIysHisPheIysTrpGlnSerLeuSerIleIleArgCysGlnLeu 340
QY 1280 AACGCTTTTCCAAAGCTGAGTCTACCTTTTCTTAAAGTTGACCTTTAACTACCAACAG 1339
Db 341 LysGlnPheProThrLeuAspLeuProPheLeuIysSerIleuThrLeuThrMetAsnIys 360
QY 1340 GAGGATATCAGCTTTTGCTCAGTTGGCTGCGCCAAAGCTCAGATATCTAATCTTATTA 1399
Db 361 GlySerIleSerPheIysIysValAlaLeuProSerLeuSerIysIysLeuAspLeuSerIarg 380
QY 1400 AATGCCATGAGCTTTAGAGTGTGCTGTCTTATCTGATTTTGAACAAACACTGAAG 1459
Db 381 AsnAlaLeuSerPheSerGlyCysCysSerIysSerAspLeuGlyThrAsnSerLeuArg 400
QY 1460 TACTTAGACCTCAGCTTCAATGCTGTGCATCTGATGAGTGCACCACTTCAATGGCTTAGAA 1519
Db 401 HisLeuAspLeuSerPheAsnGlyAlaIleIleMetSerAlaAsnPheMetGlyLeuGln 420
QY 1520 GAGCTGGAATCCTGACCTTTCAGCACTCCACTTTAAAAAGCTCAGAGATTTCTAGTG 1579
Db 421 GluLeuGlnHisLeuAspPheGlnHisSerThrLeuIysArgValHisGluPheSerAla 440
QY 1580 TTCTTATCTCTTAAAACTCTTCTTACATCTGACATCTTACCTAATACCAAAATTGAC 1639
Db 441 PheLeuSerLeuGlnIysLeuLeuIysLeuAspIleSerIysThrAsnThrIysIleAsp 460
QY 1640 TTTGATGCAATATTTCTTGCTTATGATCAGTCTCAACACTTTAAAAATGGCTGCAATTC 1699
Db 461 PheAspGlyIlePheLeuGlyLeuThrSerLeuAsnThrLeuIysMetAlaGlyAsnSer 480
QY 1700 TTCAAGACCAACCCCTTTCAAAATGCTTTTCAAAACAAACAACTTAATCTTCGTGAT 1759
Db 481 PheIysAspAsnThrIleuSerAsnValPheAlaAsnThrIysAsnLeuThrPheLeuAsp 500
QY 1760 CTTTCTTAATAGCAACCTGGAACAGATATCTAGGGGGGTATTTGACACACTCTACAGATC 1819
Db 501 LeuSerIysCysGlnLeuGlnGlnIleSerTrpGlyValPheAspThrLeuHisArgLeu 520
QY 1820 CAGTTATTAACATGAGTCACAACAACTAATGTTTCTGATTCATCCCATTTAATAACAG 1879
Db 521 GlnLeuLeuAsnMetSerHisAsnAsnLeuLeuPheLeuAspSerSerHisTyraGln 540
QY 1880 CTGTACTCCCTCAGAGACTGTGATTTGACGTTTAAATCGCATAGACATCCAAAGAAAT 1939
Db 541 LeuIysSerIleuSerThrIleuAspCysSerPheAsnArgIleGlnThrSerIysGlyIle 560
QY 1940 CTGCAACATTTTCCAAAGAGCTAGGCGTCTTCAACTGACTAATTAATCTGTGCTGT 1999
Db 561 LeuGlnHisPheProIysSerLeuAlaPhePheAsnLeuThrAsnAsnSerValAlaCys 580
QY 2000 ATATGTGAATATGCAATTTCTTGACGTGGGTCAAGAGCCAGAAAATGTTCTGTGTAAT 2059
Db 581 IleCysGlnHisGlnIysPheLeuGlnTrpValIysAspGlnIysGlnPheLeuValAsn 600
QY 2060 GTTGAACAAATGAATGTGCATCACTATAGACATGAAGGCTCCCTGCTGTGTAATTT 2119
Db 601 ValGlnGlnMetThrCysAlaIthrProValGlnMetAsnThrSerLeuValIleuAspPhe 620
QY 2120 ACGAATTCACCTGTATATATACAGACATATGATAGCTATACGGTGTGCTGCTGCT 2179
Db 621 AsnAsnSerThrCysIysTyMetIysIysThrIleIleSerValIleSerValIleSerValIle 640
QY 2180 GTGTAGCCACTGATCATTTCTGATATACACTTCTAATTTCACTGATTAATTTGCT 2239
```

RC STRAIN=C57BL/6J;
RX MEDLINE=99145502; PubMed=9998976;
RA Qureshi S.T., Lavieliere U., Leveque G., Clermont S., Moore K.J.,
RA Gros P., Malo D.;
RA "Endotoxin-colerant mice have mutations in Toll-like receptor 4
RT (TLR4).";
RL J. Exp. Med. 189:615-625(1999).
RN [4]
RN SEQUENCE FROM N.A.
RP TISSUE=Macrophage;
RX MEDLINE=20014145; PubMed=10548109; DOI=10.1038/44605;
RA Underhill D.M., Ozinsky A., Hajjar A.M., Stevens A., Wilson C.B.,
RA Bassetti M., Adorem A.;
RA "the Toll-like receptor 2 is recruited to macrophage phagosomes and
RT discriminates between pathogens.";
RL Nature 401:811-815(1999).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANTS ASN-94; ILE-209; GLY-219; ILE-254;
RP ILE-423; SER-477; ALA-516; ASP-593; ILE-600; VAL-607; ILE-637; HIS-761;
RP AND LYS-811.
RC STRAIN=Various strains;
RX MEDLINE=20558910; PubMed=11104518;
RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
RA "Phylogenetic variation and polymorphism at the Toll-like receptor 4
RT locus (TLR4).";
RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
RN [6]
RN SEQUENCE OF 1-154 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,
RA Nikiado I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirral L.M., Kanapin A., Matsuda H., Batalov S., Beisiel K.W.,
RA Blake J.A., Bradt D., Bruste V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmerond S., Gustlich S., Hirokawa C., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petrea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sanderlin A., Schneider C., Sempke C.A., Secou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wymshaw-Borle A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,
RA Hitroze-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocenti K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yamunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [7]
RN FUNCTION.
RP MEDLINE=20507837; PubMed=10952994; DOI=10.1074/jbc.M007386200;
RA Rhee S.H., Hwang D.;
RT "Murine Toll-like receptor 4 confers lipopolysaccharide responsiveness
RT as determined by activation of NF kappa B and expression of the
RT inducible cyclooxygenase.";
RL J. Biol. Chem. 275:34035-34040(2000).
CC -I- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -I- SUBUNIT:Belongs to the lipopolysaccharate (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TLR4.

CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAP via
 CC their respective TIR domains.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- TISSUE SPECIFICITY: Highly expressed in heart, spleen, lung and
 CC muscle. Lower levels are found in liver and kidney.
 CC -1- POLYMORPHISM: Interstrain analyses reveals that TLR4 is a
 CC polymorphic protein and that the extracellular domain is far more
 CC variable than the cytoplasmic domain, which is variable at the C-
 CC terminal.
 CC -1- DISEASE: The protein is encoded by the Lps locus, an important
 CC susceptibility locus, influencing the propensity to develop a
 CC disseminated Gram-negative infection.
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).

DR EMBL; AF095353; AAC99411.1; -
 DR EMBL; AF185285; AAF04278.1; -
 DR EMBL; AF110133; AAD29272.1; -
 DR EMBL; AF177677; AAF05317.1; -
 DR EMBL; AK014533; -; NOT_ANNOTATED_CDS.
 DR HSSP; Q15399; 1FV.
 DR MGI; MGI:96824; Tlr4.
 DR GO; GO:0046666; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; NAS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0045116; P:macrophage activation; NAS.
 DR GO; GO:0045576; P:macrophage activation; NAS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; NAS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-12 biosyn. . . ; NAS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; NAS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR_Cterm.
 DR InterPro; IPR00483; LRR_Cterm.
 DR InterPro; IPR00157; TIR.
 DR Pfam; PF00560; LRR; 10.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KW Disease mutation; Glycoprotein; Immune response;
 KW Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 25 Potential.
 FT CHAIN 26 835 Toll-like receptor 4.
 FT DOMAIN 26 638 Extracellular (Potential).
 FT TRANSMEM 639 659 Potential.
 FT DOMAIN 660 835 Cytoplasmic (Potential).
 FT REPEAT 29 52 LRR 1.
 FT REPEAT 53 75 LRR 2.
 FT REPEAT 76 99 LRR 3.
 FT REPEAT 100 123 LRR 4.
 FT REPEAT 127 148 LRR 5.
 FT REPEAT 149 172 LRR 6.
 FT REPEAT 173 196 LRR 7.
 FT REPEAT 201 224 LRR 8.
 FT REPEAT 227 251 LRR 9.
 FT REPEAT 305 330 LRR 10.
 FT REPEAT 348 370 LRR 11.

FT REPEAT 371 393 LRR 12.
 FT REPEAT 396 419 LRR 13.
 FT REPEAT 420 443 LRR 14.
 FT REPEAT 468 492 LRR 15.
 FT REPEAT 494 516 LRR 16.
 FT REPEAT 517 540 LRR 17.
 FT REPEAT 542 563 LRR 18.
 FT REPEAT 565 589 LRR 19.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 34 75 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 75 172 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 172 204 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 204 237 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 237 307 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 307 492 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 492 495 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 495 524 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 524 572 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 572 575 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 575 613 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 613 613 N-linked (GlcNAc. . .) (Potential).

Alignment Scores:
 Pred. No.: 3e-263 Length: 835
 Score: 3745.00 Matches: 715
 Percent Similarity: 91.74% Conservative: 51
 Best Local Similarity: 85.63% Mismatches: 69
 Query Match: 63.02% Indels: 0
 DB: 1 Gaps: 0

US-09-396-985b-5 (1-3395) x TLR4_MOUSE (1-835)

OY 260 ATGATGCGCTCTTGATCGATCGGAGCTGATCATGGCATTTGCTTCTGCGCTG 319
 1 MecMechProctRtrpleuenualaargThleuilemechaleuPheSerCysleu 20
 320 AGACCAAGAGCTTGAATCCCTCATAGAGTACTTCTTAATATTAACCAATGCATG 379
 21 ThrProglySerleuenuenProCysilegluValValProbsnlethrTrgIncysmec 40
 OY 380 GATCAGAAATTCAGCAAAATCCTCATGACATCCCTTATTCAACCAAGAACTTATG 439
 41 AspGlnlySerleuenuenValProaspAspIleProSerSerThrlysaenIleaspleu 60
 OY 440 AGCTTCAACCCCGTGAAGTCTTAAGAGTCAAGTCAACCAATTCGACAACTCAG 499
 61 SerPheasnProleuysileuulysertySerPheSerasnPheSerGluLeuGln 80
 OY 500 TGGCTGATTATTCAGGTGTGAAATTTAGACAAATTTGACCAAGCATGGCTTGA 559
 81 TrpleuasnpleuSerThrCysgluilegluThrIlegluasnlysaIatpHisGlyleu 100
 OY 560 AACCAAGCTTCAACCTTGATCTGACAGCAAACTTCAAGCTTTTCCCGAGGAAT 619
 101 HisHisleuSerasnleuIleleuThrGlyasnProIleGlnSerPheSerProGlySer 120
 OY 620 TTTTGTGACATCAATTTAGAAATCTGTGAGTGTGAGCAAAATGACCTCTCTA 679
 121 PheSerGlyleuThrSerleuGluasnleuValAlaValGluThrlysaIeulaseleu 140
 OY 680 GAGGCTTCCATATTTGACAGCTTATATCTTAAGAACTTAATATGCTGCTTAT 739
 141 GluSerPheProIleGlyGlnleuIleThrleuylSerleuasnValAlaHisasnPhe 160
 OY 740 ATACATTCCTTTAAGTTCCTGAAATTTTCTTAATCTGACAAACTTGAACATTTGGAT 799
 161 IleHisSerCyslysaSerProAlaTrpPheSerAsnleuThrAsnleuValHisValasp 180
 OY 800 CTTTCTATATCAATATTTCAACTTTCTGTGCAAGACTTACAGTTTTCAGCGTGAAT 859
 181 LeuSerTyraenlyrIleGlnThrIleThrValasnpleuGlnPheleuAlaGlylaen 200
 OY 860 CCCAAGTCAATCTCTTTAGACTGTCTTTAAACCAATGATGATCCATTCAGCCCA 919

```

|||||
Db 201 ProGlnValAsnLeuSerLeuAspMetSerLeuAsnProIleAspPheIleGlnAspGln 220
Qy 920 GCCTTCAGGGAATTAAGCTCCATGAAATGACTTAAGAACTAATTTTAATAGCTCAAT 979
Db 221 AlAphGlnGlyIleLysLeuHisIleIleuThrLeuAlaGlyAsnPheAsnSerSerAsn 240
Qy 980 GTACTGAATATGCTTCAAAACATGACTGTTTACATGCTCAATCGGTGATCTTGGA 1039
Db 241 IleLeuLysThrCysLeuGlnAsnLeuAlaGlyLeuHisValHisArgLeuIleLeuGly 260
Qy 1040 GAATTTAAATGAAAGAAATCTGGAAATTTGACCTTGTGCATGGAAGAAGCTATGC 1099
Db 261 GluPheLysAspGluArgAsnLeuGluIlePheGluProSerIleMetGluGlyLeuCys 280
Qy 1100 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1159
Db 281 AspValThrIleAspGluPheArgLeuThrIleThrAsnAspPheSerAspIleVal 300
Qy 1160 AATCTCAATGCTTGGCAATATTTTGTCAATGCTTTCACAGGCTGATCATATAAAC 1219
Db 301 LysPheHisCysLeuAlaAsnValSerIleMetSerLeuAlaGlyValSerIleLysThr 320
Qy 1220 ATAGCAGATGTTCTTACGCAATTTCAATGCAATCTTATGCAATCATTAATGATGAT 1279
Db 321 LeuGluAspValProLysHisPheLysThrPheIleSerLeuSerIleIleArgCysGlnLeu 340
Qy 1280 AAGCTTTCCAAAGCTGAGCTACCTTTTAAAGTTGAGCTTTTAACTTAACTTAACT 1339
Db 341 LysGlnPheProThrLeuAspPheLeuPheLeuLysSerLeuThrLeuThrMetAsnLys 360
Qy 1340 GAGGATATACAGCTTGTGCTGAGCTGCTGCAAGTCCAGATATAGATCTTATAGTA 1399
Db 361 GlySerIleSerPheLysValAlaLeuProSerLeuSerIleLysLeuAspLeuSerArg 380
Qy 1400 AATGCCATGAGCTTTAAGGTTGCTGTTTATTTGATTTGGAACAACAACCTGAAG 1459
Db 381 AsnAlaLeuSerPheSerGlyCysCysSerIleSerAspLeuGlyThrAsnSerLeuArg 400
Qy 1460 TACTTAACTCAGCTTCAATGCTGATCTGATGATGATGATGATGATGATGATGATGAT 1519
Db 401 HisLeuAspLeuSerPheAsnGlyAlaIleIleMetSerAlaAsnPheMetGlyLeuGln 420
Qy 1520 GAGCTGGAATACCTGAGCTTTCAGACTCCACTTAAAGAAAGTCAAGAAATTTCAAG 1579
Db 421 GluLeuGlnHisLeuAspPheGlnHisSerThrLeuLysArgValThrGluPheSerAla 440
Qy 1580 TTCTTATCTTGAAGAACTTTTACCTTGAATCTTCACTTAACTTAACTTAACTTAACT 1639
Db 441 PheLeuSerLeuGluLysLeuLeuThrLeuAspIleSerIleThrAsnThrLysIleAsp 460
Qy 1640 TTTCATGAGCAATTTCTTGGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1699
Db 461 PheAspGlyIlePheLeuGlyLeuThrSerLeuAsnThrLeuLysMetAlaGlyAsnSer 480
Qy 1700 TTCAAGACACACCTTTTCAATGCTTCTTCAACACACCAACCACTTAACTTCTGAT 1759
Db 481 PheLysAspAsnThrLeuSerAsnValPheAlaAsnThrThrAsnLeuThrPheLeuAsp 500
Qy 1760 CTTTCTTAATGCAACTGGAACAGATATCTAGGGGGGTATTTGACACACTCTTACAGATC 1819
Db 501 LeuSerLysCysGlnLeuGluGlnIleSerThrPciLysAlaPheAspThrLeuHisArgLeu 520
Qy 1820 CAGTTATTAACAGATGATCAACAACTTACTTCTTGTGATGATGATGATGATGATGATGAT 1879
Db 521 GlnLeuLeuAsnMetSerHisAsnAsnLeuLeuPheLeuAspSerSerHisIleLysArgGln 540
Qy 1880 CTGACTACCTCAGAGCTCTGATGCTGATGCTTCAATGCAATGAGATGAGATGAGATGAT 1939
Db 541 LeuLysSerLeuSerThrLeuAspCysSerPheAsnArgIleGluThrSerLysGlyIle 560
Qy 1940 CTGACACATTTCCAAAGAGCTAGCGGCTTCAATGATGATGATGATGATGATGATGAT 1999

```

```

Db 561 LeuGlnHisPheProLysSerLeuAlaPhePheAsnLeuThrAsnAsnSerValAlaCys 580
Qy 2000 ATATGATATATACGAATTTCTTGCAGTGGGTCAAGACCGAAGAAATGTTCTTGATGAT 2059
Db 581 IleCysGlnHisGlnLysPheLeuGlnThrValLysGlnGlnLysGlnPheLeuValAsn 600
Qy 2060 GTTGAACAAATGAATGTGATCACCATTATGACATGAAAGGCTCCGTGTGTGATTTT 2119
Db 601 ValGluGlnMetThrCysAlaThrProValGluMetAsnThrSerLeuValLeuAspPhe 620
Qy 2120 ACGAATTCACCTGTATATATACAGACTATCATCTGATGTATGGTGTGATGCTGCTT 2179
Db 621 AsnAsnSerThrCysIleMetIleLysThrIleIleSerValSerValIleSerValIle 640
Qy 2180 GTGCTGACCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2239
Db 641 ValValSerThrValAlaPheLeuIleLysThrHisPheThrLeuHisLeuIleValAla 660
Qy 2240 GGTGTGTAAGTAAGTACACAGACAGAGGAAAGCATCTATGATGATGATGATGATGATGAT 2299
Db 661 GlyCysLysLysThrSerArgGlyGluSerIleLysThrAspAlaPheValIleLysSer 680
Qy 2300 CAGATGAGACCTGGGTGAGAAACGAGCTGTAAAGATTTAGAAAGAGATGCCCGC 2359
Db 681 GlnAsnGluAspTrpValArgAsnGluLeuValLysAsnLeuGluGlyValProArg 700
Qy 2360 TTTCAGCTTCCCTTCACTTACAGGACTTATTCCTGCTGATGATGATGATGATGATGATGAT 2419
Db 701 PheHisLeuCysLeuHisIleLysThrArgAspPheIleProIleAlaIleAlaAlaAsnIle 720
Qy 2420 ATCCAGGAAAGCTTCCACAAAGACCGGAAAGTTATTTGCTGCTGATGATGATGATGATGAT 2479
Db 721 IleGlnGluGlyPheHisLysSerArgLysValIleValValValSerArgHisPheIle 740
Qy 2480 CAGAGCGGTGGTGTATCTTTGAATATGAGATGCTCAGACATGCGACTTCTGATGATG 2539
Db 741 GlnSerArgTrpCysIlePheGlyGlyGluIleAlaGlnThrTrpGlnPheLeuSerSer 760
Qy 2540 CGCTGCTGCAATCTTCACTTATGCTTGAAGAGTGAAGAGTCTTGCAGGACACAG 2599
Db 761 ArgSerGlyIleIlePheIleValLeuGlnLysValGluLysSerLeuLeuArgGln 780
Qy 2600 GTGCAATGATGATGCTTCTTACAGAAACACTTACCTCGAGTGGAGAGCAATGCTCTG 2659
Db 781 ValGluLeuThrArgLeuLeuSerArgAsnThrIleLeuGluThrPheLysAsnProLeu 800
Qy 2660 GGAAGCAGATCTTGTGAGAGACCTCAAAAGCCCTGTTGATGAGAAAGCTTGAAT 2719
Db 801 GlyArgHisIlePheTrpArgLeuLysAsnAlaLeuLeuAspGlyLysAlaSerAsn 820
Qy 2720 CCAAGTGAACATCAAGAGAAAGAAAGAAAGCAACACTTGAAC 2764
Db 821 ProGluGlnThrAlaGluGlnGluGlnThrAlaThrTrpThr 835

RESULT 4
TLR4 CRIGR STANDARD; PRT; 838 AA.
AC G9W82;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-1-like receptor 4 precursor.
GN Name-TLR4;
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Macrophage;
RX MEDLINE=2014868; PubMed=1068379;
RA Lien E., Means T.K., Heine H., Yoshimura A., Kusumoto S., Fukase K.,

```

RA Panton M.J., Oikawa M., Qureshi N., Monks B., Finberg R.W.,
RA Ingalls R.R., Golenbock D.T.:
RT "Toll-like receptor 4 imparts ligand-specific recognition of bacterial
lipopolysaccharide.";
RL J. Clin. Invest. 105:497-504(2000).
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
immune response to bacterial lipopolysaccharide (LPS). Acts via
MYD88, TRAP and TRAF6, leading to NF-kappa-B activation, cytokine
secretion and the inflammatory response (by similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
multi-protein complex containing at least CD14, LY96 and TRAF4.
CC Binds LY96 via the extracellular domain. Binds MYD88 and TRAP via
their respective TIR domains.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC hamster ovary fibroblast cell line.
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See [http://www.ebi.ac.uk/announcements/](http://www.ebi.ac.uk/announcements)
or send an email to license@ebi.ac.uk).

CC -----
DR EMBL; AF153676; AAD41891.1; -.
DR HSBP; Q15399; LFV.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR003591; LRR_cyp.
DR InterPro; IPR001571; TIR.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF01582; TIR; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR SMART; SM00082; LRCT; 1.
DR SMART; SM00369; LRR_Typ; 1.
DR SMART; SM00255; TIR; 1.
DR PROSITE; PS50104; TIR; 1.
KW Glycoprotein; Immune response; Inflammatory response;
KW Leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 25 Potential.
FT CHAIN 26 838 Extracellular (Potential).
FT DOMAIN 26 629 Toll-like receptor 4.
FT TRANSMEM 630 650 Extracellular (Potential).
FT DOMAIN 651 838 Cytoplasmic (Potential).
FT REPEAT 31 52 LRR 1.
FT REPEAT 53 75 LRR 2.
FT REPEAT 76 99 LRR 3.
FT REPEAT 100 123 LRR 4.
FT REPEAT 127 148 LRR 5.
FT REPEAT 149 172 LRR 6.
FT REPEAT 173 196 LRR 7.
FT REPEAT 200 224 LRR 8.
FT REPEAT 227 251 LRR 9.
FT REPEAT 251 275 LRR 10.
FT REPEAT 275 300 LRR 11.
FT REPEAT 300 324 LRR 12.
FT REPEAT 324 348 LRR 13.
FT REPEAT 348 372 LRR 14.
FT REPEAT 372 396 LRR 15.
FT REPEAT 396 420 LRR 16.
FT REPEAT 420 444 LRR 17.
FT REPEAT 444 468 LRR 18.
FT REPEAT 468 492 LRR 19.
FT REPEAT 492 516 LRR 20.
FT REPEAT 516 540 LRR 21.
FT REPEAT 540 564 LRR 22.
FT REPEAT 564 588 LRR 23.
FT DOMAIN 588 612 LRR 24.
FT CARBOHD 612 636 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 636 660 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 660 684 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 684 708 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 708 732 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 732 756 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 756 780 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 780 804 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 804 828 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 828 852 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 852 876 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 876 900 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 900 924 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 924 948 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 948 972 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 972 996 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 996 1020 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1020 1044 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1044 1068 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1068 1092 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1092 1116 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1116 1140 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1140 1164 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1164 1188 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1188 1212 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1212 1236 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1236 1260 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1260 1284 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1284 1308 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1308 1332 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1332 1356 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1356 1380 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1380 1404 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1404 1428 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1428 1452 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1452 1476 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1476 1500 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1500 1524 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1524 1548 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1548 1572 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1572 1596 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1596 1620 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1620 1644 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1644 1668 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1668 1692 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1692 1716 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1716 1740 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1740 1764 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1764 1788 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1788 1812 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1812 1836 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1836 1860 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1860 1884 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1884 1908 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1908 1932 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1932 1956 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1956 1980 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 1980 2004 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2004 2028 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2028 2052 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2052 2076 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2076 2100 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2100 2124 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2124 2148 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2148 2172 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2172 2196 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2196 2220 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2220 2244 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2244 2268 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2268 2292 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2292 2316 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2316 2340 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2340 2364 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2364 2388 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2388 2412 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2412 2436 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2436 2460 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2460 2484 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2484 2508 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2508 2532 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2532 2556 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2556 2580 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2580 2604 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2604 2628 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2628 2652 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2652 2676 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2676 2700 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2700 2724 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2724 2748 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2748 2772 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2772 2796 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2796 2820 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2820 2844 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2844 2868 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2868 2892 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2892 2916 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2916 2940 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2940 2964 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2964 2988 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 2988 3012 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3012 3036 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3036 3060 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3060 3084 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3084 3108 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3108 3132 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3132 3156 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3156 3180 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3180 3204 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3204 3228 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3228 3252 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3252 3276 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3276 3300 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3300 3324 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3324 3348 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3348 3372 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3372 3396 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3396 3420 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3420 3444 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3444 3468 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3468 3492 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3492 3516 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3516 3540 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3540 3564 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3564 3588 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3588 3612 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3612 3636 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3636 3660 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3660 3684 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3684 3708 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3708 3732 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3732 3756 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3756 3780 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3780 3804 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3804 3828 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3828 3852 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3852 3876 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3876 3900 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3900 3924 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3924 3948 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3948 3972 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3972 3996 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 3996 4020 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4020 4044 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4044 4068 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4068 4092 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4092 4116 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4116 4140 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4140 4164 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4164 4188 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4188 4212 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4212 4236 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4236 4260 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4260 4284 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4284 4308 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4308 4332 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4332 4356 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4356 4380 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4380 4404 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4404 4428 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4428 4452 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4452 4476 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4476 4500 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4500 4524 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4524 4548 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4548 4572 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4572 4596 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4596 4620 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4620 4644 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4644 4668 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4668 4692 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4692 4716 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4716 4740 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4740 4764 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4764 4788 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4788 4812 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4812 4836 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4836 4860 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4860 4884 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4884 4908 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4908 4932 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4932 4956 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4956 4980 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 4980 5004 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5004 5028 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5028 5052 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5052 5076 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5076 5100 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5100 5124 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5124 5148 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5148 5172 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5172 5196 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5196 5220 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5220 5244 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5244 5268 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5268 5292 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5292 5316 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5316 5340 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5340 5364 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5364 5388 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5388 5412 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5412 5436 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5436 5460 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5460 5484 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5484 5508 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5508 5532 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5532 5556 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5556 5580 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5580 5604 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5604 5628 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5628 5652 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5652 5676 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5676 5700 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5700 5724 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5724 5748 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5748 5772 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5772 5796 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5796 5820 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5820 5844 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5844 5868 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5868 5892 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5892 5916 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5916 5940 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5940 5964 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5964 5988 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 5988 6012 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6012 6036 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6036 6060 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6060 6084 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6084 6108 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6108 6132 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6132 6156 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6156 6180 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6180 6204 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6204 6228 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6228 6252 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6252 6276 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6276 6300 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6300 6324 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6324 6348 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6348 6372 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6372 6396 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6396 6420 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6420 6444 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6444 6468 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6468 6492 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6492 6516 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6516 6540 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6540 6564 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6564 6588 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6588 6612 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6612 6636 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6636 6660 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6660 6684 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6684 6708 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6708 6732 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6732 6756 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6756 6780 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6780 6804 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6804 6828 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6828 6852 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6852 6876 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6876 6900 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6900 6924 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6924 6948 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6948 6972 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6972 6996 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 6996 7020 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7020 7044 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7044 7068 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7068 7092 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7092 7116 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7116 7140 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7140 7164 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7164 7188 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7188 7212 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7212 7236 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7236 7260 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7260 7284 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7284 7308 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7308 7332 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7332 7356 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7356 7380 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7380 7404 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7404 7428 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7428 7452 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7452 7476 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7476 7500 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7500 7524 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7524 7548 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7548 7572 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7572 7596 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7596 7620 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7620 7644 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7644 7668 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7668 7692 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7692 7716 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7716 7740 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7740 7764 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7764 7788 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7788 7812 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7812 7836 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7836 7860 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7860 7884 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7884 7908 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7908 7932 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7932 7956 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7956 7980 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 7980 8004 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8004 8028 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8028 8052 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8052 8076 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8076 8100 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8100 8124 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8124 8148 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8148 8172 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8172 8196 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8196 8220 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8220 8244 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8244 8268 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8268 8292 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8292 8316 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8316 8340 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8340 8364 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8364 8388 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8388 8412 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8412 8436 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8436 8460 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8460 8484 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8484 8508 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8508 8532 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8532 8556 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8556 8580 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8580 8604 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8604 8628 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8628 8652 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8652 8676 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8676 8700 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8700 8724 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8724 8748 N-linked (GlcNAc. . .) (Potential).
FT CARBOHD 8748


```

Db      321 LeuGIysenLeuLysAspPheProLysGlyPheGlyTrpGlnAspPheGlnLeuValAsn      340
Qy      1271 TGTCATCTTAAGCCTTTTCCAAAGCTAGTCTACCTTTCTTAAAGTTGAGCTTAACT      1330
Db      341 CysArgIleGlyLysPheProThrLeuGlnLeuThrSerLeuLysArgLeuValPheThr      360
Qy      1331 ACCAAGAGAGAGATATCATGCTTGTGTCAGTGGCTGCGCAAGTCTCAGATATCTAGAT      1390
Db      361 SerAsnLysAspMetLysSerPheAsnGlnValLysLeuPheProSerLeuGlnPheLeuAsp      380
Qy      1391 CTTAGTGAATAATGCCATGAGCTTTAGAGGTTGCTGTTCTTATCTGATTTGGAACAAC      1450
Db      381 LeuSerArgPheAsnArgLeuSerPheLysSerCysCysSerGlnValAspLeuLysThr      400
Qy      1451 AACTGTAAGTACTTAAGACCTTCAATGTCATCTCCATGAGAGCGCAACTTCAATG      1510
Db      401 ArgLeuLysHisLeuAspLeuSerPheAsnAspValIleSerMetSerSerAspPheMet      420
Qy      1511 GGTCGTAAGAGCTGGAATACCTGAACTTTCAGACCTCACTTAAAGGATGACAGAA      1570
Db      421 GlyLeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLysGlnAlaSerAsp      440
Qy      1571 TTCTCAGTGTCTTATCTCTTGAATAAATTCTTACCTTGAACATCTCTTACACTAATACC      1630
Db      441 PheProValPheLeuSerLeuLysAsnLeuArgTrpLeuAspIleSerTrpThrAsnThr      460
Qy      1631 AAAATTGACTTGAATGGCATTTCTTGGCTTGAATCAGTCTCAACACTTAAAGGCT      1690
Db      461 ArgValAlaPheHisGlyIlePheAspGlyLeuValSerLeuGlnValLeuLysMetGlnAla      480
Qy      1691 GGCAATTCCTTCAAGAGCAACACCCCTTCAATGCTTCAACAAACAACAACTTAA      1750
Db      481 GlyAsnSerPheLysAspAsnPheLeuProAsnIlePheArgGlnMetThrAsnLeuThr      500
Qy      1751 TTCCTGATCTTTCTTAAATGCCAACTGGAACAGATATCTAGGGGAGTATTTGACACATC      1810
Db      501 ThrLeuAspLeuSerLysCysAsnLeuGlnValSerGlnGlnAlaPheCysLeuLeu      520
Qy      1811 TACGAGCTCCAGTTATTAACATGATGATCAACAACACTACTGTTCTTGGATCCATCCCAT      1870
Db      521 ProArgLeuArgValLeuAsnMetSerHisAsnAsnLeuPheLeuAspMetLeuPro      540
Qy      1871 TATAAAGCTGTATCCTCCAGACTCTGATTTGAGCTTCAATGCGATGAGACATCC      1930
Db      541 TyrLysProLeuHisSerLeuGlnHisLeuAspCysSerPheAsnArgIleValAlaPhe      560
Qy      1931 AAA---GGAAATACGCAACATTTTCCAAAGAGCTAGCGCTTCAATCTGACTAATAT      1987
Db      561 LysTrpGlnGlnLeuGlnHisPheProSerSerLeuHisSerLeuAsnLeuThrGlnAsn      580
Qy      1988 TCTGTTGCTGTATATGTAATATCAATATCAATTTCTGAGTGGGTCAAGAGACGAAATG      2047
Db      581 AspPheAlaCysValCysGlyLysGlnSerPheLeuGlnTrpValLysAspGlnArgGln      600
Qy      2048 TTCTGGAATGTTGAACAATGAATGTCATCACCCTAATAGACATGAAGAGCGCTCCCTG      2107
Db      601 LeuLeuValGlnValGlnHisLeuValCysAlaIleProLeuGlnMetArgGlyMetPro      620
Qy      2108 GTGTGGAATTTTGAATTCACCTGTTATATATATATATATATATATATATATATATATAT      2167
Db      621 ValLeuGlyPheAsnAlaHisCysGlnHisSerLysThrIleValGlyGlySerVal      640
Qy      2168 GTCAAGTGTCTGTGGTGAAGCACTGTAGATTTCTGATATACCACTTATTTTCACTG      2227
Db      641 PheSerIleLeuMetValSerValIleAlaValLeuValLysPheTyrPheHisLeu      660
Qy      2228 ATACTTATGCTGCTGTAAAGATGACGAGAGAGAAACATCTATGAGCACTTGTG      2287
Db      661 MetLeuLeuAlaGlyCysLysLysTrpValArgGlyGlnSerIleTyrAspAlaPheAla      680
Qy      2288 ATCTACTGACGACGAGATGAGAGCTGGGTGAGAAACGAGCTGTAAAGATTTGAGAA      2347

```

```

Db      681 IleTyrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGln      700
Qy      2248 GAGATGCCCGGCTTTCAGCTTTGCTGCTTATTAACAGGAGCTTATTCGGGTAGGCACTT      2407
Db      701 GlyValProProPheGlnLeuCysValHisTrpArgAspPheIleProGlyValAlaIle      720
Qy      2408 GCTGCCAATCATATCCAGAAAGGCTTCCACAAAGCCGGAAGATTAATGTTGGTGGTCT      2467
Db      721 AlaAlaMetIleIleGlnGlnLysPheHisLysSerArgValIleValValSer      740
Qy      2468 AGACACTTTATCCAGACCGGTGGTGTATCTTGAATATGAGATGCTCAGACATGCGAG      2527
Db      741 GlnHisPheIleGlnSerArgTrpCysIlePheGlnLysGlnIleAlaGlnThrTrpGln      760
Qy      2528 TTTCGAGTATGCGCTGCGATCATGTTGATGCTTGAAGAGGAGAGGAGAGTCCCTG      2587
Db      761 PheLeuSerSerArgAlaGlyIleIlePheIleValLeuHisLysLysGlnLysSerLeu      780
Qy      2588 CTGAGCAGAGAGCTGGAATGTATCGCTTCTTACAGAAACACTTCACTGAGTGGAG      2647
Db      781 LeuArgGlnGlnValGlnLeuTyrArgLeuLeuAsnArgAsnThrTrpLeuGlnTrpGln      800
Qy      2648 GACAACTCTTGGGAGGACACATCTTGGAGAAAGACTCAAAAAGCCCTGTTGATGGA      2707
Db      801 AspSerValLeuGlyArgHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGly      820
Qy      2708 AAGGCTTGATGCA-----GATGAACATCAGAGAGAAACAAGAGCAACA      2755
Db      821 LysProTrpSerProAlaGlyThrAlaAspAlaAlaGlnSerArgGlnHisAspAlaGln      840
Qy      2756 ACTTGGAC      2764
Db      841 ThrSerThr      843

RESULT 6
TLR4_PAPAN STANDARD; PRT; 826 AA.
ID TL4_PAPAN
AC 09TSP2;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TLR4;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Carnivora; Cercopithecoidea;
OC Cercopithecoidea; Papio.
NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20558910; PubMed=11104518;
RA Smirnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;
RT "Phylogenetic variation and polymorphism at the Toll-like receptor 4
RT locus (TLR4).";
RL Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).
CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
CC immune response to bacterial lipopolysaccharide (LPS). Acts via
CC MyD88, TRAF6 and TRAF6, leading to NF-kappa-B activation, cytokine
CC secretion and the inflammatory response (By similarity).
CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
CC multi-protein complex containing at least CD14, LY96 and TLR4.
CC Binds LY96 via the extracellular domain. Binds MyD88 and TRAF6 via
CC their respective TIR domains (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
CC -1- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.
CC -1- SIMILARITY: Contains 1 TIR domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

```


RT "TLR4 mutations are associated with endotoxin hyporesponsiveness in humans".
 RT Nat. Genet. 25:187-191(2000).
 RL [5]
 RN SEQUENCE OF 24-38.
 RP PubMed=15340161; DOI=10.1110/ps.04682504;
 RA Zhang Z., Henzel W.J.;
 RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites".
 RT Protein Sci. 13:2819-2824(2004).
 RL Nature 408:111-115(2000).
 RN [6]
 RP MUTAGENESIS OF GLU-697, ARG-710, ASP-711 AND PRO-714.
 RX MEDLINE=20531768; PubMed=11081518; DOI=10.1038/35040600;
 RA Xu Y., Tao X., Shen B., Horng T., Medzhitov R., Manley J.L., Tong L.;
 RT "Structural basis for signal transduction by the Toll/interleukin-1 receptor domain".
 RT Nature 408:111-115(2000).
 RL [7]
 RN CARBOHYDRATE-LINKAGE SITES, AND MUTAGENESIS OF ASN-526 AND ASN-575.
 RP MEDLINE=21648731; PubMed=11706042; DOI=10.1074/jbc.M109910200;
 RA da Silva Correia J., Ulevitch R.J.;
 RT "MD-2 and TLR4 N-linked glycosylations are important for a functional lipopolysaccharide receptor".
 RT J. Biol. Chem. 277:1845-1854(2002).
 RN [8]
 RP VARIANTS ARG-188; SER-246; GLY-293; SER-329; ILE-399; LEU-443;
 RX LYS-474; HIS-510; ARG-694; HIS-763 AND HIS-834.
 RA MEDLINE=21405531; PubMed=11514453;
 RA Smirnova I., Hamblin M.T., Webster C., Beutler B., Di Rienzo A.;
 RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4 in humans".
 RT Genetics 158:1657-1664(2001).
 RL [9]
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate immune response to bacterial lipopolysaccharide (LPS). Acts via MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response.
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via their respective TIR domains.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in placenta, spleen and peripheral blood leukocytes. Detected in monocytes, macrophages, dendritic cells and several types of T-cells.
 CC -1- PTM: N-glycosylated. Glycosylation of Asn-526 and Asn-575 seems to be necessary for the expression of TLR4 on the cell surface and the LPS-response. Likewise, mutants lacking two or more of the other N-glycosylation sites were deficient in interaction with LPS.
 CC -1- POLYMORPHISM: Allele TLR4*B (GLY-299, ILE-399) is associated with a blunted response to inhaled LPS.
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
 CC -1- SIMILARITY: Contains 1 TIR domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; U93091; AAC80227.1; -;
 DR EMBL; U88880; AAC34135.1; -;
 DR EMBL; AF177765; AAF05316.1; -;
 DR EMBL; AF177766; AAF07823.1; -;
 DR EMBL; AF172171; AAF89753.1; -;
 DR EMBL; AF172169; AAF89753.1; JOINED.
 DR EMBL; AF172170; AAF89753.1; JOINED.
 DR HSSP; O60603; 1FTW.
 DR Genew; HGNC:11850; TLR4.
 DR MIM; 603030; -.

DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0046596; C: lipopolysaccharide receptor complex; NAS.
 DR GO; GO:0001530; C: lipopolysaccharide binding; NAS.
 DR GO; GO:0004888; F: transmembrane receptor activity; NAS.
 DR GO; GO:0007250; F: activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; F: detection of fungi; NAS.
 DR GO; GO:0009598; F: detection of pathogenic bacteria; NAS.
 DR GO; GO:0006955; P: immune response; TAS.
 DR GO; GO:0042116; P: macrophage activation; IMP.
 DR GO; GO:0045576; P: mast cell activation; ISS.
 DR GO; GO:0045671; P: negative regulation of osteoclast different. . .; NAS.
 DR GO; GO:0045362; P: positive regulation of interleukin-1 biosyn. . .; ISS.
 DR GO; GO:0045084; P: positive regulation of interleukin-12 biosyn. . .; NAS.
 DR GO; GO:0045368; P: positive regulation of interleukin-13 biosyn. . .; ISS.
 DR GO; GO:0045410; P: positive regulation of interleukin-6 biosyn. . .; ISS.
 DR GO; GO:0007165; P: signal transduction; TAS.
 DR GO; GO:0042088; P: T-helper 1 type immune response; NAS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003591; LRR_typ.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF00550; LRR; 12.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00369; LRR_TYP; 2.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KW Direct protein sequencing; Glycoprotein; Immune response;
 KW Inflammatory response; Leucine-rich repeat; Polymorphism; Receptor;
 KW Repeat; Signal; Transmembrane.
 FT SIGNAL 1 23
 FT CHAIN 24 839
 FT DOMAIN 24 631
 FT TRANSMEM 632 652
 FT DOMAIN 653 839
 FT REPEAT 52 76
 FT REPEAT 77 100
 FT REPEAT 101 124
 FT REPEAT 128 149
 FT REPEAT 150 173
 FT REPEAT 174 197
 FT REPEAT 203 225
 FT REPEAT 228 252
 FT REPEAT 277 303
 FT REPEAT 307 330
 FT REPEAT 332 350
 FT REPEAT 351 372
 FT REPEAT 373 398
 FT REPEAT 400 421
 FT REPEAT 422 445
 FT REPEAT 447 469
 FT REPEAT 470 494
 FT REPEAT 495 518
 FT REPEAT 520 541
 FT REPEAT 543 566
 FT REPEAT 568 592
 FT DOMAIN 672 818
 FT CARBOHYD 35 35
 FT CARBOHYD 173 173
 FT CARBOHYD 205 205
 FT CARBOHYD 282 282
 FT CARBOHYD 309 309
 FT CARBOHYD 497 497
 FT CARBOHYD 526 526
 FT CARBOHYD 575 575
 FT CARBOHYD 624 624
 FT CARBOHYD 630 630
 FT VARIANT 188 188
 FT VARIANT 246 246
 FT VARIANT 246 246
 O -> R.
 /FTId=VAR_018729.
 C -> S.
 /FTId=VAR_018730.

FT VARIANT 299 299 D -> G (in allele TLR4*B; reduced LPS-
 response; dbSNP:4986790).
 FT /Frid=VAR_012739.
 FT VARIANT 329 329 N -> S.
 FT /Frid=VAR_018731.
 FT VARIANT 399 399 T -> I (in allele TLR4*B; reduced LPS-
 response; dbSNP:4986791).
 FT /Frid=VAR_012740.
 FT VARIANT 443 443 F -> L.
 FT /Frid=VAR_018732.
 FT VARIANT 474 474 E -> K.
 FT /Frid=VAR_018733.
 FT VARIANT 510 510 Q -> H.
 FT /Frid=VAR_018734.
 FT VARIANT 694 694 K -> R.
 Alignment Scores:
 Pred. No.: 5,31e-199 Length: 839
 Score: 2860.50 Matches: 559
 Percent Similarity: 80.24% Conservative: 115
 Best Local Similarity: 66.55% Mismatches: 159
 Query Match: 48.13% Indels: 7
 DB: Gaps: 5
 US-09-396-985b-5 (1-3395) x TLR4_HUMAN (1-839)
 QY 260 ATGATGCTCTTGCATCTGGGCTGGAGCTGTGATCATGCGATG---TTCTTTCTGCG 316
 DB 1 Metceteralaseratglenalaglythrleuileproalawetalaipheleusercys 20
 QY 317 CTGAGACGAGGAACTTGAATCCCTGCATAGAGGACTTCTTAATATTAATCTTACCAATGC 376
 DB 21 ValargproglusertrpgluProCyvalgluValalProamniethrlyGlnCys 40
 QY 377 ATGATCAGAACTCTCAGCAAAATCCCTGCATGACATCCCTTATTAACCAAGACTTATGAT 436
 DB 41 MetgluleuasnphetrylyslleProapasnleuPropheserthrlysaenleuasp 60
 QY 437 CTGAGCTTCAACCCCTGAGATCTTAAGAACTGTATGCTTCAACATTTCTCAACTT 496
 DB 61 LeuserheasnProleuarghislenglysertryserPhepserPheProgluLeu 80
 QY 497 CAGTGGCTGATTTATTCAGGTGTGAATTTGAGACAATTTGAACAAGCATGGCATGCG 556
 DB 81 GlnValleuasnpheserargCysgluileglnhrilegluasnrglyalatyGlnSer 100
 QY 557 TTAACACAGCTCTCAACCTTGTGATGACAGAAACCTTATCAAGATTTTCCCAAGA 616
 DB 101 LeuserhisleuserThrleuileleuthrglyasnProileglnserleuAlaleugly 120
 QY 617 AGTTTTCTGACCTAACAATTTTGAAGATCTGGTGGCTGGAGACAAAATGACCTCT 676
 DB 121 AlapheaserglyleuserSerleuglnlyleuValalavalglutrhAsnleuAlaser 140
 QY 677 CTAGAGGGTTTCCATATTTGACAGCTTATATCTTAAAGAACTAAATGGCTCATAT 736
 DB 141 LeuglnasnherproileglnhislleuylserthreuleuylguleuasnValalasn 160
 QY 737 CTATATCATCTTTAAGTGGCTGAATATTTTCTATGCAAACTGAACATGATG 796
 DB 161 LeuileglnserPheylsleuProglutryrPheaserasnleuThrAsnleuGlnhislleu 180
 QY 797 GATCTTTCTATATCATATTTGAAGATCTTGTCTCAAGACTTACAGTTTCTACGTGAA 856
 DB 181 AspleuseraserasnlyslleGlnseriletryCysThrAspleuargValleuAsn 200
 QY 857 AATCCCAAGATCATCTCTTTTGAACCTGTCTTAAACCAATTTGATGCTCAAGCC 916
 DB 201 MetProleuasnleuasnleuSerleuasnleuSerleuasnPrometAsnphelileglnPro 220
 QY 917 CAAGCTTTTCAAGGAATTTAGGCTCCATGATTTGACTTGAAGAACTTAATTTATAGTCA 976
 DB 221 GlnAlapheylsergluileargleuinhislleuylserthreuleuargleuasnpheserleu 240

QY 977 AATGTAAGAAATGTCCTTCAAAACATGACTGGTTTACATGCTACCGGTGATCTTG 1036
 DB 241 AsnValmetylserthrCysilleglnslglnleuAlaglyleuGlnValhlsargleuValleu 260
 QY 1037 GGAGAAATTTAAATGAAGAATCTGAAAAGTTTGAACCGTCTGTGCATGAAGAAGCTA 1096
 DB 261 GlyClnupheargangnglgllyAsnleuGlnlylupheAspysSerAlaleuGlnlyleu 280
 QY 1097 TGCAATGTGAGCAATGATGATGAGTTCAACATATTAATCATTTTTCAGATGATTT 1156
 DB 281 CysasnleuthrileglnslglnleuargleuAlatyrlleuAsptryltyrleuAspAspIle 300
 QY 1157 TATATCTC---AATTCCTTGGCAAAATATTTTTCGCAATGTCTTTCACAGGTGTCATATA 1213
 DB 301 IleaspleuasnleuSerleuThrAsnValaserSerleuValserValThrIle 320
 QY 1214 AACACATPACAGATGTCTTCCATGAGCATTTGCAATGGCAATCTTATCATATTAGATGT 1273
 DB 321 GlnargVallylAsnphesertryrAsnPhelglyTrrpGlnhislleuGlnleuValAsnCy 340
 QY 1274 CATCTTAAGCTTTTCCAAAGCTGACGTCTACCTTTTCTTAAAGTTGAGCTTAACTACC 1333
 DB 341 LyasPhegllylnPheProthrleuylsleuylserleuylsargleuThrphethrSer 360
 QY 1334 AACAGAGAGATATCACCTTGGTCACTTGGCTGCGCAAGTCTCAGATATCTAGATCTT 1393
 DB 361 AsnlyselglylAsnAlapheaserGluValaspleuProserleuGlnupheleuAspIleu 380
 QY 1394 AGTGAATATGCAATGACCTTTAGAGTGTCTTATTTCTGATTTTGAACAACAAC 1453
 DB 381 SertrgasnnglyleuserPheylsglyCysCysserGlnserAspPhegllyThrThrSer 400
 QY 1454 CTGAAGTACTTAAAGCTCACCTTCAATGCTGTATCTGTAGATGAGCAACTTATAGGT 1513
 DB 401 leuylsertryleuasnleuSerPheasnnglyValillethmetSerSerAsnphelengly 420
 QY 1514 CTGAAGACCTGGAATATCTGAGCTTCCAGACTTCCACTTAAATAAAGTCAAGAAATTC 1573
 DB 421 leuGlnleuGlnleuGlnleuAsnphelGlnhislserAsnleuylsGlnmetSerGlnPhe 440
 QY 1574 TCAAGTCTTATCTCTTGAACAACTTCTTACCTTGAACATCTTCACTAATATACCAA 1633
 DB 441 SerValrPheleuserleuAsnleuAlletyrlleuAsnprileserhslthrhlsthrArg 460
 QY 1634 ATTGACTTTGATGCAATTTTCTGGCTTGAATGATCTCAACACTTAAATAATGGCTGGC 1693
 DB 461 ValAlapheasnnglyllepheasnnglyleuserSerleuGlnValleuylsMetAlagly 480
 QY 1694 AATTCCTTCAAGAACACACCTTCAATGTCCTTCAACAAACAACTTAACATTC 1753
 DB 481 AsnSerPheGlnsluasnPheleuProAspIlePhehrthrGlnleuArgAsnleuThrPhe 500
 QY 1754 CTGATCTTTTAAATGCAACTGGAACAGATATCTGAGGGGGATTTTGAACACACTGTAC 1813
 DB 501 leuAspleuserGlnCysGlnleuGlnleuSerProthrAlapheasnleuSer 520
 QY 1814 AAGCTCAAGTTATTAACATGAGTACACAAACACTTACTGTTCTGATCCATTCAT 1873
 DB 521 SerleuGlnValleuasnMetSerhslAsnAsnpheserleuAspTrnPherProtyr 540
 QY 1874 AACAGGTATCTCCCTCAAGACTCTTGAATTTGAGCTTCAAGCAATGAGACATCC--- 1930
 DB 541 LyasCysleuasnberleuGlnValleuAsptryrSerleuAsnlyslleMetThrSerlys 560
 QY 1931 AAAGATATCTGCAACATTTTCCAAAGAGTCTAGCCGTCTTCAATCTGATCAATATATCTT 1990
 DB 561 LyeglsluGlnleuGlnhislPheProserSerleuAlapheleuasnleuthrGlnAsnAsp 580
 QY 1991 GTTCTGTATATGTGAATATCAGAATTTCTTGCAGTGGGTCAAGACCAAGAAATGTTTC 2050
 DB 581 PheAlaCysThrCysgluInslglnserPheleuGlntrpIlelyAspGlnargGlnleu 600

QY	2051	TTGGTGAATGTTTGAACAAATGAATATGGACATACCTATAGCATGAAGAGCTCCCTGGT	2110
Db	601	LeuValGluValAGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal	620
QY	2111	TTGGATTTTACGAATTCCACCTGGTTATCTTATACAAAGATATATCATCAGTGATCGGTGCT	2170
Db	621	LeuSerLeu---AsnIleThrCysGlnMetCasnIlyThrIleIleGlyValSerValLeu	639
QY	2171	AGTGTGCTTGTGGTAGGACCTGTAGACATTTTGTATATACCATTTTATTTTCCACTGATA	2230
Db	640	SeValIleLeuValSerValSerValAlaValLeuValTyrLysPheTyrPheIleLeuMet	659
QY	2231	CTTATTTGCTGGCTGTAAAAAAGTATACAGCAGAGAGAAAGACATCTATAGATGATTTGTATC	2290
Db	660	LeuLeuValAGLysCysIleTyrTolYArgGlyGluMetIleTyrAspAlaPheValIle	679
QY	2291	TACTGAGACCGAAGATGAGACCTGGGTGAAGAAACGAGCTGTAAAGATTTAGAGAAAGGA	2350
Db	680	TyrSerSerGlnAspGlnAspTrrValATrGanGlnLeuValIlyAsnIleGlnGlnGly	699
QY	2351	GTGGCCCGCTTTCAGCTTTGGCTTCATATACAGGAGCATTTATTTCTGTGTAGCCATTGCT	2410
Db	700	ValProProPheGlnLeuCysLeuIleStrylTrGAspPheIleProGlyValAlaIleLeuA	719
QY	2411	GCCAAATCATATCCAGAAAGCTTCCACAAGACCGGAAAGTTATTTGTGTGGTGTCTAGA	2470
Db	720	AlaAsnIleIleIleGlnGlyPheIleIlySerAspArgLysValIleValValSerGln	739
QY	2471	CACTTTATTCAGAGCGCTTGATGATCTTTAAATATGAGATTTGCTCGACATATGGCAGTTT	2530
Db	740	HisPheIleGlnSerAspArgTrrCysIlePheGlnTyrGlnIleAlaGlnThrTrrPheIle	759
QY	2531	CTGAGTAGCCGCTGTGAGCATATCTTCATTTGCTTCTTGTGAAGAAAGTGAAGATCCTTGTCTG	2590
Db	760	LeuSerSerATrGAlaGlyIleIlePheIleValLeuGlnIlyValGlnIlyThrLeuLeu	779
QY	2591	AGGCAGCAGGTGCAATTGTATGCGCTTCTTAGCAGAAACACTTACTTGAGTGGAGGAC	2650
Db	780	ArgGlnGlnValAGluLeuTyrATrGLeuLeuSerATrGAsnThrTyrLeuGlnTrrPgluAsp	799
QY	2651	AATGCTCTGGGGAGGACATCTTCTCGAGAGAGCTCAAAAAAGCCCTTGTGAATGGAAAA	2710
Db	800	SerValIleuGlyATrGHisIlePheThrATrGAspLeuATrGValAlaLeuIlyAspIlyLys	819
QY	2711	GCTTGAATCCAGAT-----GAAACATCAGAGAAAGAAAGAAAGCAACACTTTG	2761
Db	820	SerTrrPanProGlnGlyThrValGlyThrGlyCysAsnTrrPgluIlyAlaIleThrSerIle	839
RESULT 8			
ID	TLR4_PANPA	STANDARD;	PRT; 839 AA.
AC	Q9TNN0;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Toll-1ike receptor 4 precursor.		
GN	Name=TLR4;		
OS	Pan paniscus (Pygmy chimpanzee) (Bonobo).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.		
OX	NCBI_TaxId=9597;		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=20558910; PubMed=11104518;		
RX	Smitnova I., Poltorak A., Chan E.K.L., McBride C., Beutler B.;		
RA	"Phylogenetic variation and polymorphism at the Toll-1ike receptor 4		
RT	locus (TLR4)." ;		
RL	Genome Biol. 1:RESEARCH002.1-RESEARCH002.10(2000).		
CC	-1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate		
CC	immune response to bacterial lipopolysaccharide (LPS). Acts via		
CC	MyD88, TRAF6 and TRAF6, leading to NF-kappa-B activation, cytokine		
CC	secretion and the inflammatory response (By similarity).		
CC	-1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a		

CC	multi-protein complex containing at least CD14, LY96 and TLR4.
CC	Binds LY96 via the extracellular domain. Binds MYD88 and TRAP via
CC	their respective TIR domains (By similarity).
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC	-1- SIMILARITY: Belongs to the Toll-like receptor family.
CC	-1- SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
CC	-1- SIMILARITY: Contains 1 TIR domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; AF179220; AAF05320.1; -.
DR	EMBL; AF179218; AAF05320.1; JOINED.
DR	EMBL; AF179219; AAF05320.1; JOINED.
DR	HSSBP; Q15399; IFFV.
DR	GO; GO:0046666; C:lipopolysaccharide receptor complex; ISS.
DR	GO; GO:0001530; F:lipopolysaccharide binding; ISS.
DR	GO; GO:0004888; P:transmembrane receptor activity; ISS.
DR	GO; GO:0007250; P:activation of NF-kappaB-inducing kinase; ISS.
DR	GO; GO:0016046; P:detection of fungi; ISS.
DR	GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
DR	GO; GO:0045216; P:macrophage activation; ISS.
DR	GO; GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.
DR	GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
DR	GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
DR	GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
DR	GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
DR	GO; GO:0042088; P:T-helper 1 type immune response; ISS.
DR	InterPro; IPR001611; LRR.
DR	InterPro; IPR000483; LRR_Cterm.
DR	InterPro; IPR003591; LRR_Cyp.
DR	InterPro; IPR00157; TIR.
DR	Pfam; PF00560; LRR; 12.
DR	Pfam; PF01463; LRRCT; 1.
DR	Pfam; PF01582; TIR; 1.
DR	PRINTS; PR00019; LEURICHRPT.
DR	SMART; SM00369; LRR_TYR; 2.
DR	SMART; SM00082; LRRCT; 1.
DR	SMART; SM00255; TIR; 1.
DR	PROSITE; PS50104; TIR; 1.
KW	Glycoprotein; Immune response; Inflammatory response;
KW	leucine-rich repeat; Receptor; Repeat; Signal; Transmembrane.
FT	SIGNAL 1 23 Potential.
FT	CHAIN 24 839 Toll-like receptor 4.
FT	DOMAIN 24 631 Extracellular (Potential).
FT	TRANSMEM 632 652 Potential.
FT	DOMAIN 653 839 Cytoplasmic (Potential).
FT	REPEAT 52 76 LRR 1.
FT	REPEAT 77 100 LRR 2.
FT	REPEAT 101 124 LRR 3.
FT	REPEAT 128 149 LRR 4.
FT	REPEAT 150 173 LRR 5.
FT	REPEAT 174 197 LRR 6.
FT	REPEAT 203 225 LRR 7.
FT	REPEAT 228 252 LRR 8.
FT	REPEAT 277 303 LRR 9.
FT	REPEAT 307 330 LRR 10.
FT	REPEAT 332 350 LRR 11.
FT	REPEAT 351 372 LRR 12.
FT	REPEAT 373 398 LRR 13.
FT	REPEAT 400 421 LRR 14.
FT	REPEAT 422 445 LRR 15.
FT	REPEAT 447 469 LRR 16.
FT	REPEAT 470 494 LRR 17.
FT	REPEAT 495 518 LRR 18.
FT	REPEAT 520 541 LRR 19.
FT	REPEAT 543 566 LRR 20.

FT REPEAT 568 592 LRR 21.
 FT DOMAIN 672 818 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 282 282 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 624 624 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 630 630 N-linked (GlcNAc . . .) (Potential).
 SQ SEQUENCE 839 AA; 95637 MW; 3B328C5682127D37 CRC64;

Alignment Scores:
 Pred. No.: 6,28e-199 Length: 839
 Score: 2859.50 Matches: 559
 Percent Similarity: 80.24% Conservative: 115
 Best Local Similarity: 66.55% Mismatches: 159
 Query Match: 48.12% Indels: 7
 DB: 1 Gaps: 5

US-09-396-985B-5 (1-3395) x TLR4_PANRA (1-839)

QY 260 ATGATGCTCTTTCATCTGGTGGGACTGTGATCATGCGATTG--TTCCTTTCTGC 316
 Db 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 317 CTGAGCAGGAACTTGAATCCCTGCTAGAGGACTCTTATATTTACTTACCATTGC 376
 Db 21 ValArgProGluSerTrpGluProCysValGluValAlaProAlaIleThrTyrGlnCys 40
 QY 377 ATGATGAGATCTCAGGAAATCCCTCATGACATCCCTTATGACCAAGAACCTTATGAT 436
 Db 41 MetCgluLeuAsnProMetTyrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 60
 QY 437 CTGAGCTTCAACCCCTGAGAGATTTAAGAGCTATAGCTTACCAATTCTTCAACAATT 496
 Db 61 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 80
 QY 497 CAGTGGTGGATTTATTCAGGTGTGAATTTGAGCAATTTGAGCAAGGCAATGGCATGGC 556
 Db 81 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnIleAspGlyAlaTyrGlnSer 100
 QY 557 TTAACAGAGCTCTCAACCTTGTACTGTAGAGAAACCTTATCAAGATTTTCCCAAGA 616
 Db 101 LeuSerIleLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 120
 QY 617 AGTTTTCGTGACTTACAAATTTAGAGATCTGTGCTGTGAGAGCAAAATGACCTCT 676
 Db 121 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValAlaGluThrAsnLeuAlaSer 140
 QY 677 CTGAGGAGTTTCCATATTGACAGCTTATATCTTAAAGAACTAAATGTGGCTCATAT 736
 Db 141 LeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 160
 QY 737 CTATATCATCTCTTAAGTGGCTGAAATATTTTCTATGTCAGAAACCTAGAACATGTC 796
 Db 161 LeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeu 180
 QY 797 GATCTTCTTATTAATCTATTTCAAACTATTTCTGCAAGACTTACAGTTTCTACGTAA 856
 Db 181 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGln 200
 QY 857 AATCCCCAATCATCTCTCTTATGACCTGTCTTAAACCAATGATCATGATCAAGCC 916
 Db 201 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 220
 QY 917 CAAGCCTTTAGGGAATTAGGCTCATGAATGACTTAAAGAGTAATATTTAATAGTCA 976
 Db 221 GlnAlaPheLysGluIleArgLeuHisLysLeuThrLeuLysGlnAsnProPheAspSerLeu 240
 QY 977 AATGTACTGAATAATGTCTTCAAAACATGACTGTGTATACATGTCATCGATTGATCTTG 1036

Db 241 AsnValMetLysThrCysIleGlnGlyLeuValAlaGlyLeuValHisArgLeuValLeu 260
 QY 1037 GGAATAATTTAAATGAAGAAATCTGGAAGATTGACCTTCTGTCATGGAAGACTA 1096
 Db 261 GlyIlePheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 280
 QY 1097 TGCATGTGAGCATTTGATGAGTTACAGTTTAACTATATTAATCTTTTTCAGATGATTT 1156
 Db 281 CysAsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspLysTyrTyrLeuAspAsnLys 300
 QY 1157 TATTAATCTC--AATTCCTTGGCAAAATATTTCTGCAATGTCTTTCACAGGTGTACATTA 1213
 Db 301 IleAspLeuPheAsnGlySerLeuThrAsnValSerSerPheSerLeuValSerValThrIle 320
 QY 1214 AAACATACATGACATGATTTCTTACGACTTTCAAATGCAATCTTATCATATTAAGATGT 1273
 Db 321 LysSerValLysAspPheSerTyrAsnPheGlyTyrGlnHisLeuGluLeuValAsnCys 340
 QY 1274 CATCTTAAGCCTTTCCAAAGCTGACGTACCTTTCTTAAAGTTGAGACTTAACTTAC 1333
 Db 341 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 360
 QY 1334 AACAGAGAGATATACACTTTTGTCACTTGTGCTGTCGCAAGTCTCAGATATCTGATCTT 1393
 Db 361 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 380
 QY 1394 AGTTGAATGCCATGACCTTATGAGTGTGCTGTTCTTATTTCTGATTTTGGAAACAAAC 1453
 Db 381 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 400
 QY 1454 CTGAAGTACTTAAAGCTCAGCTTCAATGAGTGTCACTCTGATGATGAGCAACTTATGAGGT 1513
 Db 401 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheGlnGly 420
 QY 1514 CTAGAGAGCTGAAATCTGTGACTTTCAGACTTCCACTTCACTTAAAGAAAGTCAAGAAATTC 1573
 Db 421 LeuGlnIleGlnGluHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 440
 QY 1574 TCACTGTTCTTATCTCTGAAAACTCTTATCTTACATCTCTTACATATATCAATA 1633
 Db 441 SerValPheLeuSerLeuAspAsnLeuIleTyrLeuAspIleSerHisIleThrHisArg 460
 QY 1634 ATTGACTTGTATGGAATATTTCTTGTGATGATGATGATGATGATGATGATGATGATGAT 1693
 Db 461 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLysLysMetAlaGly 480
 QY 1694 AATTTCTTCAAGAACAAACACTTTTCAATGTCTTTTCAAAACAAACAACTTAAACATTC 1753
 Db 481 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 500
 QY 1754 CTGATCTTTTCTAAATCCCACTGGAACAGATATCTAGGGGGGATTTTGAACAACCTTAC 1813
 Db 501 LeuAspLeuSerGlnCysGlnIleGlnGluLeuSerProThrAlaPheAsnSerLeuSer 520
 QY 1814 AGATCCAGTTTAAACATGAGTCAACAAACCTATGTTTCTGATCCATGCCATTTAT 1873
 Db 521 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 540
 QY 1874 AAACAGCTTACTCCCTCAGAGCTTGTGATGAGATTTCAATGACATAGACATCC--- 1930
 Db 541 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetClnHisLys 560
 QY 1931 AAAGAAATATGGAACATTTTCCAAAGAGTCAAGCTGCTTCAATGCTGATTAATATCT 1990
 Db 561 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 580
 QY 1991 GTTCTTGTATATGTAATATGAAATTTCTTCAAGTGGTCAAGGACGAATAATGTTTC 2050
 Db 581 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleLysAspGlnHisGlnLeu 600
 QY 2051 TTGGAATGTTGAACAAATGAATGTGATCACTTATGACATGAAGGCTCCCTGGTG 2110

Db 601 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 620
 QY 2111 TTGGATTTTGAATTCACCTGTTATATATACAAAGCTATTCATGATGGTGGTC 2170
 Db 621 LeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 639
 QY 2171 AGTGTGCTTGGTAGACCTGTAGCATTTCTGTATATACCACTTCTATTTTCACTGATA 2230
 Db 640 SerValLeuValValSerValValAlaValLeuValLysLysPheThrPheHisLeuMet 659
 QY 2231 CTATATGCTGCTGTATAAAGATACAGACAGAGAAAGCATCTATATGATGATTTGTATC 2290
 Db 660 LeuLeuValGlyCysIleLysIleYrGlyArgGlyGlnAsnIleLysIleYrAspAlaPheValIle 679
 QY 2291 TACTCGACGACATGAGCATGGGTGAGAAACGAGCTGGTAAAGATTTAGAGAAAGGA 2350
 Db 680 TyrSerSerGlnAspGlnAspIleTrpValArgAsnGlnLeuValLysAsnLeuGlnGly 699
 QY 2351 GTGCCCCGCTTTCAGCTTTGCTTCATTTACAGAGCATTTATTCCTGTGTAGCCATTGCT 2410
 Db 700 ValProProPheGlnLeuLeuValValValValValValValValValValValValVal 719
 QY 2411 GCCAATCATCTCCAGAGAGGCTTCCAGAAAGCCGAGAAAGTTATTTGGTGGTCTAGA 2470
 Db 720 AlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValIleValIleValIle 739
 QY 2471 CACTTTATCCAGAGCGCTGTGTATCTTGAATATAGATGTCGATGGCAGACTTT 2530
 Db 740 HisPheIleGlnIleAsnIleArgTrpCysIlePheGlnIleValIleValIleValIleValIle 759
 QY 2531 CTGAGTAGCCGCTTTCAGCATCTTTCATTTGCTTCCTGTTGAGAAAGTGGAAAGTCTTGG 2590
 Db 760 LeuSerSerArgLysGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeu 779
 QY 2591 AGGACAGAGGCTGCAATGTTATTCGCTTTCAGAGAAACCTTACGAGTGGAGAGAC 2650
 Db 780 ArgArgGlnValGlnLeuLysArgLeuLeuSerArgAsnThrLysLeuGlnIleTrpGlnAsp 799
 QY 2651 AATGCTCTGGGAGGACATCTTCTGAGAGAACTCAAAAAGCCCTGTGGATGGAAA 2710
 Db 800 SerValLeuGlyArgHisIlePheTrpArgTrpLeuArgLysAlaLeuLeuAspGlyLys 819
 QY 2711 GCCTTGATCCAGAT-----GAAACATCAGAGAGAAAGCAAGAACAACTTTG 2761
 Db 820 SerTrpAsnProGlnGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle 839
 RESULT 9
 Q8SPB8 PRELIMINARY; PRT; 837 AA.
 AC Q8SPB8; (1)
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP MEDLINE=2140531; PubMed=11514453;
 RA Smitrova I., Hamblin M.T., McBride C., Beutler B., Di Rienzo A.;
 RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
 in humans";
 RL Genetics 158:1657-1664 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Beutler B., Smitrova I., Hamblin M.T., McBride C., Di Rienzo A.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF497565; AAM18617.1; -
 DR EMBL; AF497563; AAM18617.1; JOINED.
 DR EMBL; AF497564; AAM18617.1; JOINED.

DR HSP; 060603; 1077.
 DR GO; GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO; GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO; GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO; GO:0007250; F:activation of NF-kappaB-inducing kinase; ISS.
 DR GO; GO:0016046; P:detection of fungi; ISS.
 DR GO; GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO; GO:0042116; P:macrophage activation; ISS.
 DR GO; GO:0045576; P:mast cell activation; ISS.
 DR GO; GO:0045671; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO; GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO; GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO; GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO; GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 DR GO; GO:0042088; P:T-helper 1 type immune response; ISS.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000463; LRR_Cterm.
 DR InterPro; IPR003591; LRR_Cyp.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF0560; LRR_1; 10.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PRO0019; LEURICHRPT.
 DR SMART; SM00082; LRRCT; 1.
 DR SMART; SM00369; LRR_TYP; 2.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 DR Receptor.
 KW Receptor.
 SQ SEQUENCE 837 AA; 95497 MW; 5A177BAB341396DD CRC64;
 Alignment Scores:
 Pred. No.: 1,12e-196 Length: 837
 Score: 2828.50 Matches: 556
 Percent Similarity: 79.76% Conservative: 114
 Best Local Similarity: 66.19% Mismatches: 161
 Query Match: 47.59% Gaps: 9
 DB: 2 Gaps: 6
 US-09-396-985b-5 (1-3395) x Q8SPB8 (1-837)
 QY 260 ATGATGCTTCTTTCAGTCTGCTGGAGCTCTGATCATGGCATG--TTCCTTTCTGTC 316
 Db 1 MetMetSerLaseArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 317 CTGAGACCAAGAGCTTGAATCCCTGATAGAGTACTCTTATATTAACCAATGTC 376
 Db 21 ValArgProGlnSerTrpGlnProCys-----ValValProAsnIleThrLysGlnCys 38
 QY 377 ATGATCAGATCTCAGCAAAATCCCTCATGATCATCCCTTATTAACCAAGAACTAGAT 436
 Db 39 MetGlnLeuAsnPheThrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 58
 QY 437 CTGAGCTTCAACCCCTGGAAGATCTTAAGAAGCTATAGCTTTCACCAATTTCTACAATT 496
 Db 59 LeuSerPheAsnProLeuArgHisLeuGlySerLysSerPhePheSerPheProGlnLeu 78
 QY 497 CAGTGTGATTTATCCAGAGTGAATGAGACATTTGAAGACAAAGGATGGATGGC 556
 Db 79 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaLysGlnSer 98
 QY 557 TTAACCAAGCTTCAACCTTGTACTGACAGAAACCTTATCAAGAGTTTTCACCAAGA 616
 Db 99 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 118
 QY 617 AGTTTCTGAGCTTAACAAATTTAGAGATCTGTGCTGTGAGACAAATAGACTCT 676
 Db 119 AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSer 138
 QY 677 CTAGAGGCTTTCATATTTGACAGCTATATCTTAAAGAACTTAATGAGCTCATTAAT 736
 Db 139 LeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGlnLeuAsnValAlaHisAsn 158
 QY 737 CTATATCATTCCTTAAAGTTGCTGGAATATTTTCTATCTGACAAACCTAGAACATGTG 796


```

Db      159 Leu1Leu1SerPheLysLeuProGluLysPheSerSerLeuThrAsnLeuGluLysLeu 178
Qy      797 GATCTTCTTATATATATCAACTATTTCTGTCAAAAGACTTACAGTTTCTACGGTAA 856
Db      179 AsnLeuSerSerAsnLysIleGlnSerIleLysCysThrAspLeuValLeuIleGln 198
Qy      857 AATCCCAAGTCAATCTCTTTAGACCTGTCTTTAAACCAATGATGATCCATCAAGCC 916
Db      199 MetProLeuLeuAsnLeuSerLeuAspSerLeuAsnProMetThrPheIleGlnPro 218
Qy      917 CAAGCTTTAGGGAATTTAGGCTCCATGAATGATCTAGAGATTAATTTAATAGCTCA 976
Db      219 GlyAlaPheLysGluIleArgLeuH1bLysLeuThrLeuArgAsnAsnPheAspSerLeu 238
Qy      977 AATGTATCAAAATGTGCTTCAAAACATGATGCTTTTACATGTCATCGGTGATATCTG 1036
Db      239 AsnValMetLysThrCysIleGlnIleLeuH1aGluLeuValAlaArgArgLeuValLeu 258
Qy      1037 GGAATTTTAAATAAGGAATCTGAAAGTTTGAACGTTGTCTGATGGAAGACTA 1096
Db      259 GlyGluPheArgAsnGluLysAsnLeuGluLysPheAspLysSerAlaLeuGluLysLeu 278
Qy      1097 TGCATGTGAGCATTTGATGATGATGATGATTAATATATTAATCAATTTTTCAGATGAT 1156
Db      279 CysAsnLeuThrIleGluGluPheArgLeuH1aLysLeuAspLysThrLysLeuAspAspIle 298
Qy      1157 TATATATCTC---AATGCTGGGCAATATATTTCTGCATATGCTTTTCAACAGGTGATAT 1213
Db      299 IleAspLeuPheAsnLysCysLeuThrAsnValSerSerSerLeuValSerValThrIle 318
Qy      1214 AATCACTATGACAGATGTTCTTACAGTTCATTAATGATGATCTTATCATCATTAAGAT 1273
Db      319 GluArgValLysAspPheSerLysAsnPheGlyThrGlnH1bLeuGluLeuValAsnCys 338
Qy      1274 CATTTAAGCTTTTCCAAAGCTGATGTCATCTTTTAAAGTTGATGATTAATCACTAC 1333
Db      339 LysPheGlyGluPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 358
Qy      1334 AACAGACAGATATACAGCTTTGTCAGTGGCTGTGCAAGTCTCAATATCATAGATCT 1393
Db      359 AsnLysLeuGlyLysAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 378
Qy      1394 AGTGAATATCCATGACCTTATAGAGTGTGCTGTTCTTATCTGATTTTGAACAACAAC 1453
Db      379 SerArgAsnLysLeuSerPheLysGlyCysCysSerLysSerAspPheGlyThrThrSer 398
Qy      1454 CTGAAGTACTTGAACCTCAGCTTCAATGTGTCTCATCTGATGATGCAACTTCATGGGT 1513
Db      399 LeuLysThrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 418
Qy      1514 CTGAAGAGCTGGAATATCCTGGACTTTCAGACCTCCACTTAAAGGTCACAGATTC 1573
Db      419 LeuGluGlnLeuGlnH1bLeuAspPheGlnH1bSerAsnLeuLysGlnMetSerGluPhe 438
Qy      1574 TCAGTGTCTTATCTCTTGAAGAACTCTTACCTTCAACATCTTCACTTAATACCAA 1633
Db      439 SerValPheLeuSerLeuArgAsnLeuIleLysLeuAspIleSerH1bStrH1bStrH1bArg 458
Qy      1634 ATTGACTTGTATGATATTTCTTGCTGTGATGATGATCAACTTAAATATGAGCTGGC 1693
Db      459 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 478
Qy      1694 AATTTCTTCAAAACAACACCTTTCAAATGTCTTTCACAAACAACAACAACTTAACATTC 1753
Db      479 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrIleLeuArgAsnLeuThrPhe 498
Qy      1754 CTGATCTTCTTAAATGCAACTGGAACAGATATCTAGGGGGATTTTGAACACTGTAC 1813
Db      499 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 518
Qy      1814 AGACTCAGTTATTAACATGAGTCACACAACCTACTGTTTGTGATTCATCCATTAAT 1873

```

```

Db      519 SerLeuGlnValLeuAsnMetSerH1aAsnAsnPhePheSerLeuAspThrPheProLys 538
Qy      1874 AAACAGCTGATCTCCACAGACCTTGATTTGATGATTCATGCGATGACATGACATCC--- 1930
Db      539 LysCysLeuAsnSerLeuArgValLeuAspLysSerLeuAsnH1bIleMetThrSerLys 558
Qy      1931 AAAGAACTACTGCAACATTTTCCAAAGACTTACCCGCTTTCATCTGACTAATTAATCTCT 1990
Db      559 LysGlnGluLeuGlnH1bPheProSerSerLeuH1aPheLeuAsnLeuThrGlnAsnAsp 578
Qy      1991 GTTGCTGTATATGTGAATATCAGAAATTTCTTGACGTGGCTCAAGAACACAGAAAATGTC 2050
Db      579 PheAlaCysThrCysGlnH1bGlnSerPheLeuGlnIntrPheLysAspGlnArgGlnLeu 598
Qy      2051 TTGGTGAATGTGAACAATGCAATGCAATGCACTTATGACATGAAAGGCTCCCTGGTG 2110
Db      599 LeuValGluValGluValGluMetGluCysValThrProSerAspLysGlnLysMetProVal 618
Qy      2111 TTGATTTTACGAATTCACCTGTTATATATACAAAGACTATCATCAGTGTATCGGTGTC 2170
Db      619 LeuSerLeu---AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 637
Qy      2171 AGTGTCTGTGTAGGCACTGTAGCATTTCTGATATATCAACTTATTTTACCTGTATA 2230
Db      638 SerValLeuValLysSerValAlaValLeuValLysPheLysPheThrIleLeuMet 657
Qy      2231 CTATATGCTGCTGTAAAGTACAGACAGAGAAAGCATCTATGATGATTTGTGATC 2290
Db      658 LeuLeuH1aGlyCysIleLysLysGlyArgGlyGluAsnValLysAspAlaPheValIle 677
Qy      2291 TACTGACGACAGATGAGACTGAGTGAGAAACAGCTGTGAAAGATTTAGAAAGAGA 2350
Db      678 TyrSerSerLysPheGluAspThrValArgAsnGluLeuValLysAsnLeuGluGlnGly 697
Qy      2351 GTGCGCCGCTTACGCTTTCCTTATACAGGACTTATATTCCTGCTGATGCCATTTGCT 2410
Db      698 ValProProPheGlnLeuCysLeuH1bLysThrArgAspPheIleProGlyValAlaIleAla 717
Qy      2411 GCCAACAATCAAGAGAGGCTCCACAAGCCGGAATTTATGAGTGAGTGTCTAGA 2470
Db      718 AlaAsnIleIleH1bGluGlyPheH1bLysSerArgLysValIleValAlaValSerGln 737
Qy      2471 CACTTATCCAGAGCCGTTGATCTTATCTTGAATATGAGATTTGCTCAGATGACAGATTT 2530
Db      738 HisPheIleGlnSerArgLysPheGlyThrGluIleAlaGlnThrTrpGlnPhe 757
Qy      2531 CTGATGAGCCGCTGTGACATCTTCTATTTGCTTGAAGAAGTGAAGAGTCTTGCTG 2590
Db      758 LeuSerSerArgLysGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLeu 777
Qy      2591 AGGCACAGATCGAATTTGATGCTTCTTGAAGAAACAACCTTACCTCAGAGTGGAGAGAC 2650
Db      778 ArgGlnGlnValGluLeuLysArgLeuLeuSerArgAsnThrLysLeuGluLysTrpGluAsp 797
Qy      2651 AATGCTGTGGGAGGACACTCTCTGAGAGAAGCTCAAAAAGCCCTGTTGATGAGAAA 2710
Db      798 SerValLeuGlyArgHisIlePheThrPheArgLysLeuGlyAlaLeuLysAspGlyLys 817
Qy      2711 GCCTGAATTCAGAT-----GAAACATCAGAGGAAGAAACAAGAACACACTTTC 2761
Db      818 SerTrpAsnProGluGlyThrValGlyThrGlyCysAsnTrpGlnGluAlaThrSerIle 837

```

```

RESULT 10
TUR4_FELCA STANDARD; PRT; 833 AA.
AC P58727;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-like receptor 4 precursor.
GN Name=TUR4;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_Taxid=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yoshioka N., Kano R.;
 RL "Felis catus Toll like receptor 4.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate
 CC immune response to bacterial lipopolysaccharide (LPS). Acts via
 CC MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine
 CC secretion and the inflammatory response (By similarity).
 CC -1- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a
 CC multi-protein complex containing at least CD14, LY96 and TIRAP.
 CC Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via
 CC their respective TIR domains (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Toll-like receptor family.
 CC -1- SIMILARITY: Contains 19 leucine-rich (LRR) repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: AB060687; BAB3947.1; -.
 CC HSP: O60603; IFTX.
 DR GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 DR GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 DR GO: GO:0004888; F:transmembrane receptor activity; ISS.
 DR GO: GO:0007250; P:activation of NF-kappa-B-inducing kinase; ISS.
 DR GO: GO:0016046; P:detection of fungi; ISS.
 DR GO: GO:0009598; P:detection of pathogenic bacteria; ISS.
 DR GO: GO:0042116; P:macrophage activation; ISS.
 DR GO: GO:0045576; P:macrophage activation; ISS.
 DR GO: GO:0045561; P:negative regulation of osteoclast different. . . ; ISS.
 DR GO: GO:0045584; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 DR GO: GO:0045584; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 DR GO: GO:0045584; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 DR GO: GO:0045510; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 DR GO: GO:0004288; P:T-helper 1 type immune response; ISS.
 DR InterPro: IPR001631; LRR.
 DR InterPro: IPR000483; LRR_Cterm.
 DR InterPro: IPR003591; LRR_Typ.
 DR InterPro: IPR00157; TIR.
 DR Pfam: PF00560; LRR_12.
 DR Pfam: PF01463; LRRCT_1.
 DR Pfam: PF01582; TIR_1.
 DR PRINTS: PR00019; LEURICHRPT.
 DR SMART: SM00369; LRR_Typ; 1.
 DR SMART: SM00082; LRRCT_1.
 DR SMART: SM00255; TIR_1.
 DR PROSITE: PS50104; TIR_1.
 DR GlycoProtein: Immune response; Inflammatory response;
 KM Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 833 Toll-like receptor 4.
 FT DOMAIN 24 632 Extracellular (Potential).
 FT TRANSMEM 633 653 Potential.
 FT DOMAIN 654 833 Cytoplasmic (Potential).
 FT REPEAT 53 76 LRR 1.
 FT REPEAT 77 100 LRR 2.
 FT REPEAT 101 124 LRR 3.
 FT REPEAT 128 149 LRR 4.
 FT REPEAT 150 173 LRR 5.
 FT REPEAT 174 197 LRR 6.
 FT REPEAT 203 225 LRR 7.
 FT REPEAT 228 252 LRR 8.
 FT REPEAT 310 334 LRR 9.
 FT REPEAT 350 372 LRR 10.

FT REPEAT 373 398 LRR 11.
 FT REPEAT 399 421 LRR 12.
 FT REPEAT 422 445 LRR 13.
 FT REPEAT 447 469 LRR 14.
 FT REPEAT 470 494 LRR 15.
 FT REPEAT 495 518 LRR 16.
 FT REPEAT 520 542 LRR 17.
 FT REPEAT 544 566 LRR 18.
 FT REPEAT 568 592 LRR 19.
 FT DOMAIN 673 819 TIR.
 FT CARBOHYD 35 35 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 173 173 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 205 205 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 238 238 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 309 309 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 497 497 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 526 526 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 570 570 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 575 575 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 625 625 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 833 AA; 95592 MW; 3E3A84F2BEBA55EA CRC64;
 Alignment Scores:
 Pred. No.: 1,85e-196 Length: 833
 Score: 2825.50 Matches: 545
 Percent Similarity: 65.14% Conservative: 121
 Best Local Similarity: 47.54% Mismatches: 162
 Query Match: 1 Indels: 3
 DB: Gaps: 3
 US-09-396-985b-5 (1-3395) x TLR4_FELCA (1-833)
 QY 260 ATGATGCTCTCTGATGATCGGTGGAGCTGATCATGGCATG---TTCCCTTCTGCG 316
 1 MetMetProProThrArgLeuAlaGlyThrLeuLeuProAlaMetAlaPheLeuSerCys 20
 QY 317 CTGAGACCAAGAACTTGAATCCCTGCATGAGAGTCTTCTTAATATTACCAATGC 376
 21 LeuArgProGluSerTrpAspProCysValGluValAlaProSerIleThrTrpGlnCys 40
 QY 377 ATGATGATGAAATTTCAAGCAAAATCCCTCATGACATCCCTTATTCAACCAAGAACTTGAAT 436
 41 MetAspLeuSerLeuIleHisIleProAspAsnIleProSerSerThrIlyAspLeuAsp 60
 QY 437 CTGAGCTTCAACCCCTGAAGATCTTAAAGAGTAAAGCTTAAAGCTTCAACAACTT 496
 61 MetSerPheAsnProLeuArgAsnLeuGlySerHisSerPheSerAsnProGluLeu 80
 QY 497 CAGTGCCTGATTTATTCAGAGTGTGAATTTGAAGACAAATTGAAGACAGCATGGCATGGC 556
 81 GluValLeuAspLeuSerArgCysGluIleGlnIleIleGluAspAlaIleTrpGlnGly 100
 QY 557 TTAACCAAGCTTCAACCTTGTGACTGACAGGAACCTTCAAGAGTTTCCCAAGGA 616
 101 LeuAsnHisLeuSerIleLeuIleThrGlyAsnProIleGlnArgLeuPheProGly 120
 QY 617 AGTTTTCGAGATCAAAATTTAGAGAAATCTGCTGCTGGAGCAAAAGAAAGCTCT 676
 121 AlaPheSerGlyLeuSerIleLeuIleThrValAlaValIleThrAsnIleAlaSer 140
 QY 677 CTAGAGGGTTTCATATTTGACAGCTTATCTTAAAGAACTTAAATGAGTGCATTAAT 736
 141 LeuGluAspPheProIleGlyHisLeuGlyThrLeuGlySerLeuValAlaHisAsn 160
 QY 737 CTATTAACATTCCTTTAAGTTCCTGAATATTTTCTTAATCTGAACAACCTTAAGCATGG 796
 161 LeuIleHisSerPheLeuSerProGluTrpPheSerAsnMetSerAsnLeuGluTrpLeu 180
 QY 797 GATCTTCTTATTAACATTAATTTCAATTTCTGCAAGACTTAAAGCTTCAAGCTGAA 856
 181 AspLeuSerAsnAsnGlyIleGlnAsnIleTrpHisIlyAspLeuGlnValLeuHisGln 200
 QY 857 AATCCCAAGTCAATCTCTTTAAGACCTGCTTTAAACCAATGATCTCATTAAGCC 916

```

Db      201  LysProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAspPheIleGlnPro 220
Qy      917  CAAGCTTTCAAGGATATAGGCTCCATGAATATGACTCAAGAACTAATTTTAAATAGCTCA 976
Db      221  G1ValAlaPheLysG1ValAlaLysLeuArgL1LeuThrLeuArgSerAspAspSerThr 240
Qy      977  AATGACTGAAATGTCCTTCAAAACATGACTGGTTTACATGTCATCCGTTGATCTTG 1036
Db      241  AspValMetLysAlaSerIleGlnGlyLeuAlaGlyLeuGlnIleHisGlnLeuValLeu 260
Qy      1037  GGAGAAATTTAAATGAAAGAAATCTGGAAAGTTTGAACGCTTGTCATGAAAGACTA 1096
Db      261  G1GlyLysPheLysAsnG1LysArgAsnLeuG1LysPheAspLysSerIleLeuGlnGlyLeu 280
Qy      1097  TGCAGATGAGCATGATGATGAGTTTACATATATATATATATATATATATATATATATAT 1153
Db      281  CysAsnLeuIleIleGlnLysPheArgL1LeuAlaLysPheAspLysPheSerGlnAspAla 300
Qy      1154  ATTATATATCTCAATTCCTTGGCAAAATATTTCTGCAATGTCCTTCAACAGGTGATATA 1213
Db      301  IleAspSerPheAsnGlyLeuAlaAsnValSerThrIleSerLeuValHisLeuTyrPhe 320
Qy      1214  AAACACATGACAGATGTTCTTAGGCATTTCAATGGCAATCCTTATCAATCATTAAGATGT 1273
Db      321  LysG1LysLeuLysGlnLeuProLysAsnLeuG1LysGlnArgLeuGlnLeuValAsnGly 340
Qy      1274  CATCTTGAAGCTTTCCAAAGCTGAGTCACTCTTTCTTAAAGTTTGAAGCTTAACTAAC 1333
Db      341  GluPheGlnGlnPheProLysPheLysAspProLysLysGlnLeuValPheSerAla 360
Qy      1334  AACACAGAGATATACACTTGTGCTGAGTGGCTGGCAAGTCTCAGATATCTAGATCTT 1393
Db      361  AsnGlnValArgAsnAlaPheThrGlnValLysLeuGlnLysSerLeuGlnPheLeuAspLeu 380
Qy      1394  AGTGAATGCGCATGAGCTTGAAGGTGCTGTTCTTATCTGATTTTGAACAAACAAAC 1453
Db      381  SerArgAsnAspPheSerLeuLysSerCysSerGlnArgAspLeuG1LysThrArg 400
Qy      1454  CTGAGATCACTTGAAGCTCAGTTCATGATGCTCATCTGATGATGATGATGATGATGATG 1513
Db      401  LeuLysHisLeuAspLeuSerPheAsnAsnIleIleThrIleSerSerAspPheLeuGly 420
Qy      1514  CTGAAGAGCTGGAATACCTGACTTCAAGCATTCACATTTTAAAGTACAGAAATTC 1573
Db      421  LeuGlnGlnLeuGlnLysLeuAspPheGlnHisSerSerLeuLysGlnValSerAspPhe 440
Qy      1574  TCAAGTCTTATATCTTGAAGAACTTCTTACCTTGAACATCTCTTACATATATACCAA 1633
Db      441  SerValPheLeuProLeuLysAsnLeuArgTyrLeuAspIleSerTyrThrHisIleThrGln 460
Qy      1634  ATTGACTTGAATGAGCATATTTCTGGCTTGAATGATGATGATGATGATGATGATGATG 1693
Db      461  ValAlaIleHisGlyIlePheAsnGlyLeuIleSerLeuGlnIleLeuLysMetAlaGly 480
Qy      1694  AATCTTTCAAGACACACCCCTTCAATGCTTCAAAACAAACAAACCTTAAACATTC 1753
Db      481  AsnSerPheGlnPheAsnPheLeuProAsnIlePheIleGlnLeuThrAsnLeuThrIle 500
Qy      1754  CTGAGTCTTCTTAAATGCCAATGGAACAGATATCTAGGGGGATTTTGAACACTGTAC 1813
Db      501  LeuAspLeuSerAspCysGlnLeuGlnGlnValSerGlnValAlaPheAsnSerLeuPro 520
Qy      1814  AGACTCCAGTTTAAATCATGAGTCAACAACAACCTACTGTTCTGATCCATCCCATAT 1873
Db      521  LysLeuGlnLeuLeuAsnMetSerHisAsnHisLeuLeuSerLeuAspThrLeuProTyr 540
Qy      1874  AAACAGCTGATCTCCCTCAGACTCTGATGAGTTCAGTTTCAATGCGCATAGAGACATCC 1933
Db      541  GluProLeuHisSerLeuGlnThrLeuAspCysSerPheAsnHisGlyIleValAlaSerLys 560
Qy      1934  ---GAAATCTGCAACATTTTCCAAAGTCTAGCCGCTTTCATCTGACTAATATATCT 1990

```

```

Db      561  GlnGlnGlnLeuArgHisPheProSerAsnLeuSerLeuAsnLeuThrArgAsnAsp 580
Qy      1991  GTTCTGTGATATGATGATATACAGATTTCTTGCAGTGGGTCAGAACCAAAATGTTTC 2050
Db      581  PheAlaCysValCysGlnHisGlnSerPheLeuGlnIleValLysAspGlnArgGlnLeu 600
Qy      2051  TTGGTGAATGTTGAACAATGAAATGTCATGACTATAGACATGAAGCCCTCCCTGGTG 2110
Db      601  LeuValGlnValGlnGlnMetValCysAlaLysProLeuAspMetGlnLysMetProMet 620
Qy      2111  TTGATTTTACGAATTCACCTGTTATATATATACAAAGCTATCATCAGTGTATCGGTGTC 2170
Db      621  LeuAsnPheArgAsnAlaThrCysGlnValArgLysThrIleIleThrGlySerValPhe 640
Qy      2171  AGTGTCTGTGAGGACACGTGATGATTCATGATACCACTCTTATTTTCACTGATA 2230
Db      641  ThrValLeuLeuValPheLeuValValValLeuValLysPheTyrPheHisLeuMet 660
Qy      2231  CTATTTCTGGCTGTAAAGATACAGACAGAGAGAAAGCATCTATGATGATTTGTGATC 2290
Db      661  LeuLeuAlaGlyCysLysLysTyrSerArgGlyLysSerThrTyrAspAlaPheValIle 680
Qy      2291  TACTGAGCCGAAATGAGACTGGGTGAGAAACAGACTCGTGAAGATTTTGAAGAAAGA 2350
Db      681  TyrSerSerGlnAspGlnAspIlePheValArgAsnGlnLeuValLysAsnLeuGlnGly 700
Qy      2351  GTGCCCGCTTTCAGCTTTCCTTGCATTAACAGGAGCTTATCTCGGTGAGCCATGCT 2410
Db      701  ValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 720
Qy      2411  GCCAATCATTCACAGAGAGCTTCCAAAGCCGAGAAAGTATATGATGATGATGATGATG 2470
Db      721  AlaAsnIleIleGlnGlnGlnPheHisLysSerArgLysValIleValIleValSerGln 740
Qy      2471  CACTTTTCCAGACCCGTGGTGTATCTTGAATATGAGATGCTCAGACATGCGCATTT 2530
Db      741  HisPheIleGlnSerArgTyrCysIlePheGlnLysGlyIleAlaGlnThrThrGlnPhe 760
Qy      2531  CTGAGTACCGCTTGCATCATCTTCAATGCTTGTGAAGAAAGGAGAACTCTGTGCTG 2590
Db      761  LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeuGlnLysSerLeuLeu 780
Qy      2591  AGGACAGAGCTGCAATGTATCGCTTCTTGAAGAAACACTTCACTGAGTGGAGAGAC 2650
Db      781  ArgGlnGlnValGlnLeuTyrArgLeuLeuAsnArgSerHisThrTyrLeuGlnIlePheLys 800
Qy      2651  AATGCTTGGAGGAGCAGCATCTTCTGAGAGAACTCAAAAAGCCCTGTTGATGAGAAA 2710
Db      801  SerValLeuGlnLysArgHisIlePheThrArgArgLeuArgLysAlaLeuAspGlyLys 820
Qy      2711  GCCTTGAATCCAGATGAAACATCAGAGAGAA 2743
Db      821  ProArgCysProGlnGlyMetAlaAspAlaGln 831

RESULT 11
TLR4_PONPY STANDARD; PRT; 828 AA.
AC Q8SP89;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toll-1ike receptor 4 precursor.
GN Name=TLR4;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pongo.
OX NCBI_Taxid=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21405531; Pubmed=11514453;
RA Smirnova I., Hamblin W.T., McBride C., Beutler B., Di Rienzo A.;
RT "Excess of rare amino acid polymorphisms in the Toll-like receptor 4
in humans."

```

Genetics 158:1657-1664 (2001).

- FUNCTION: Cooperates with LY96 and CD14 to mediate the innate immune response to bacterial lipopolysaccharide (LPS). Acts via MyD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response (by similarity).

- SUBUNIT: Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TIR4. Binds LY96 via the extracellular domain. Binds MyD88 and TIRAP via their respective TIR domains (by similarity).

- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).

- SIMILARITY: Belongs to the Toll-like receptor family.

- SIMILARITY: Contains 20 leucine-rich (LRR) repeats.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL; AF497562; AAM18616.1; .
 EMBL; AF497560; AAM18616.1; JOINED.
 EMBL; AF497561; AAM18616.1; JOINED.
 HSSP; O60603; 1PYM.
 GO: GO:0046696; C:lipopolysaccharide receptor complex; ISS.
 GO: GO:0001530; F:lipopolysaccharide binding; ISS.
 GO: GO:0004888; F:transmembrane receptor activity; ISS.
 GO: GO:0007250; P:activation of NF-kappa-B-inducing kinase; ISS.
 GO: GO:0016046; P:detection of fungi; ISS.
 GO: GO:0009598; P:detection of pathogenic bacteria; ISS.
 GO: GO:0042116; P:macrophage activation; ISS.
 GO: GO:0045576; P:osteoclast activation; ISS.
 GO: GO:0045571; P:negative regulation of osteoclast different. . . ; ISS.
 GO: GO:0045362; P:positive regulation of interleukin-1 biosyn. . . ; ISS.
 GO: GO:0045084; P:positive regulation of interleukin-12 biosyn. . . ; ISS.
 GO: GO:0045368; P:positive regulation of interleukin-13 biosyn. . . ; ISS.
 GO: GO:0045410; P:positive regulation of interleukin-6 biosyn. . . ; ISS.
 GO: GO:0042088; P:T-helper 1 type immune response; ISS.
 InterPro: IPR001611; LRR.
 InterPro: IPR000483; LRR_Cterm.
 InterPro: IPR003591; LRR_Typ.
 InterPro: IPR001517; TIR.
 Pfam; PF00560; LRR; 12.
 Pfam; PF01463; LRRCT; 1.
 Pfam; PF01582; TIR; 1.
 PRINTS; PR00019; LEURICHRPT.
 SMART; SM00369; LRR_Typ; 1.
 SMART; SM00082; LRRCT; 1.
 SMART; SM00255; TIR; 1.
 PROSITE; PS50104; TIR; 1.
 Glycoprotein; Immune response; Inflammatory response; Leucine-rich repeat; Receptor; Signal; Transmembrane.
 KEGG; Leucine-rich repeat; Receptor; Signal; Transmembrane.
 FT SIGINL 1 23
 FT CHAIN 24 828
 FT DOMAIN 24 629
 FT TRANSMEM 630 650
 FT DOMAIN 651 828
 FT REPEAT 50 74
 FT REPEAT 75 98
 FT REPEAT 99 122
 FT REPEAT 126 147
 FT REPEAT 148 171
 FT REPEAT 172 195
 FT REPEAT 201 223
 FT REPEAT 226 250
 FT REPEAT 275 301
 FT REPEAT 325 348
 FT REPEAT 349 370
 FT REPEAT 371 396
 FT REPEAT 398 419
 FT REPEAT 420 443
 LRR 1.
 LRR 2.
 LRR 3.
 LRR 4.
 LRR 5.
 LRR 6.
 LRR 7.
 LRR 8.
 LRR 9.
 LRR 10.
 LRR 11.
 LRR 12.
 LRR 13.
 LRR 14.

FT REPEAT 445 467 LRR 15.
 FT REPEAT 468 492 LRR 16.
 FT REPEAT 493 516 LRR 17.
 FT REPEAT 518 539 LRR 18.
 FT REPEAT 541 564 LRR 19.
 FT REPEAT 566 590 LRR 20.
 FT DOMAIN 670 816 TIR.
 FT CARBOHYD 33 33 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 171 171 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 203 203 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 280 280 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 307 307 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 524 524 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 573 573 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 622 622 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 628 628 N-linked (GlcNAc...) (potential).
 SQ SEQUENCE 828 AA; 94340 MW; 51AC0984B5970DFD CRC64;

Alignment Scores:

Pred. No.: 9, 05e-196 Length: 828
 Score: 2816.00 Matches: 550
 Percent Similarity: 79.93% Conservative: 111
 Best Local Similarity: 66.51% Mismatches: 160
 Query Match: 47.38% Indels: 6
 DB: 1 Gaps: 5

US-09-396-985b-5 (1-3395) x TIR4_PONRY (1-828)

QY 260 ATGATGCGCTCTTGATCTGCTGGAGCTGATCATGGCATG--TTCCTTCTCTGC 316
 1 MetMetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCys 20
 QY 317 CTGAGACCGAGAGCTTGAATCCCTGCATGAGTACTTCTTAATATTACTTCCATGCG 376
 21 ValArgProGluSerTrpGluProCys-----ValValProAsnIleTrpYrGlnCys 38
 QY 377 ATGATCAGAACTCATGCAAAATCCCTCATGATCCCTTATTCACCAAGAACTGAT 436
 39 MetGluLeuAsnIleThrYrIleProAsnLeuProPheSerThrIleAsnLeuAsp 58
 QY 437 CTGAGCTTCAACCCCTGAAGATCTTAAGAAGCTTATAGCTTCAACATTTCTCAACACTT 496
 59 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 78
 QY 497 CAGTGCCTGATTTATCCAGCTGTGAATGAACATTTGAACAAGCATGGCATGGCG 556
 79 GlnValLeuAsnProLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyrGlnSer 98
 QY 557 TTAACACAGCTCAACCTTGTAGTACAGAAACCTTCAAGATTTTCCACAGA 616
 99 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnAsnLeuAlaLeuGly 118
 QY 617 AGTTTCTGAGTAACAATTTAGAAATCTGTGTGGCTGTGAGACAAATAAGACTCT 676
 119 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGluThrAsnLeuAlaSer 138
 QY 677 CTGAGAGGTTCCATATGACAGCTTATTCCTTAAGAACTTAATGTGGCTCATAT 736
 139 LeuGluAsnIleProIleGlyHisLeuLeuYrThrLeuYrGluLeuAsnValAlaAsn 158
 QY 737 CTATATCATCTCTTAAGTGGCTGAATATTTCTTAATCTGACAAACCTAGAACTGTG 796
 159 LeuIleGlnSerPheLeuValProGluTyrPheSerAsnLeuThrAsnLeuGluHisLeu 178
 QY 797 GATCTTCTTATATCAATATTTCAACTATTTCTGTCAAGACTTACAGTTTCTAGCTGAA 856
 179 AsnLeuSerSerAsnYrIleGlnSerIleTyrCysValAspArgLeuGlnValHisGln 198
 QY 857 AATGCCAATCAATCTCTTTAGACCTGTCTTAAACCAATGACATTCATCAAGCC 916
 199 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnAlaMetAsnPheIleGlnPro 218

QY	917	CAAGCTTTGGGGAAATTAGGCTGCATTAATTGATCTTAAGAAGTAATTTTAAATGGCTCA	976
Db	219	GlYalApeHySgLuIleArgLeuH1sYsLeuInTrLbYdAsnSerPheAspSerLeu	238
QY	977	AATGTACTGAATAATGTGCTTCAAAACAATGACTGGTATTACATGTCACATCGGTGAATCTTG	1036
Db	239	AsnValMetLysElnHrCysIleGlnIlyeulAaGlyLeuGluValH1sH1leValLeu	258
QY	1037	GGAGAAATTAAAAATGAAGAATTTGGAAAGTTTGAACCGTTCTGTCAATGAAGACTA	1096
Db	259	GlyIuPheArgAsnGluLysAsnLeuGluLysPheAspTrnSerAlaLeuGluLysLeu	278
QY	1097	TGCATGAGCAATGATGAGTTCAGGTTCATCATATATTAATTCATTTTTCAGATGATATTT	1155
Db	279	CysAsnNeutrInrIleGluGluPheArgLeuAlaTyLeuAspTyArgTyLeuAspSerIle	298
QY	1157	TATATATCTC---AATTGCTTGGCAAAATATTTCTGCAGAAATGCTTTCACAGGTGATCATATA	1213
Db	299	IleAspLeuPheAsnCysLeuAlaAsnValSerSerPheSerLeuValSerValThrIle	318
QY	1214	AAACACATAGACGATGTTCTTAGCGATTTCAAATGGCAATCCCTTATCAATCATAGATGT	1273
Db	319	LysSerValLysAspPheSerTyArgAsnHegIyTrpGlnH1sLeuGluLysValAsnCys	338
QY	1274	CATCTTAAGCCTTTTCCAAAGCTAGGTACTCTTTCTTAAAGTTGAGCTTTAACTACACC	1333
Db	339	LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrAla	358
QY	1334	AACGAGAGATATTCAGCTTTGGTACGTGGGTCTGCCAAGTCTCAGATATCTATGATCTT	1393
Db	359	AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu	378
QY	1394	AGTAGAAATGCCATGACGCTTTAGAGGTTCTGTTCTTATTTGATTTTGGAAACAACAC	1453
Db	379	SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer	398
QY	1454	CTGAAGTACTTAGACCTTACGCTTCATAGGTGTCACTCGATGAGTGCACACTTATGGGT	1513
Db	399	LeuLysTyLeuAspLeuSerPheAsnAspValIleThrMetGlySerAsnPheLeuLys	418
QY	1514	CTAGAAGAGCTGAATACTGAGACTTTGACAGCTSCACTTTTAAAAAGTGCACAGATTC	1573
Db	419	LeuGluGlnLeuGlnH1sLeuAspPheGlnH1sSerAsnLeuLysGlnMetSerGluPhe	438
QY	1574	TCAGTGTCTTATCTCTTGAAGAAACTTCTTATACCTTGAATCTCTTCATCATTAATCCAA	1633
Db	439	SerValPheLeuSerLeuArgAsnLeuLeuTyLeuAspTrnIleSerH1sThrH1sArg	458
QY	1634	ATTGACTTGAATGGCATATTTCTTGCGCTTATACAGTCTCAACACTTTAAAAATGGCTGCC	1693
Db	459	ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuLysValLeuLysMetAlaGly	478
QY	1694	AATCTTTCAAGAACAACACCTTTCAATGCTTTCAATAACAACAACAACACTTAACTATC	1753
Db	479	AsnSerPheGlnGluAsnPheLeuProAspTrnIlePheTrnGlyLeuArgAsnLeuThrPhe	498
QY	1754	CTGATCTTTCTTAATGCCCACTGGACAGATATCTAGGGGGTATTTTGACACTTAC	1813
Db	499	LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer	518
QY	1814	AGACTCCAGTATTAACATAGTGCACAACAACCTACTGTCTTGAGATCCCATATTT	1873
Db	519	SerLeuGlnValLeuAsnMetSerH1sAsnAsnPhePheSerLeuAspTrnPheProTy	538
QY	1874	AAACAGCTGTACTCCCTCAGAGACTCTTGATTCGACTTTCATTCGGATAGACATCC---	1933
Db	539	LysCysLeuAsnSerLeuGlnValLeuAspTySerLeuAsnH1sIleMetThrSerLys	558
QY	1931	AAAGGAATATCTGCAACATTTTCCAAAGAGCTTAGCGGCTTCAACTGACATTAATCTCT	1990
Db	559	LysGlnGluLeuGlnH1sPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp	578
QY	1991	GTTCCTGTATATGTAATCATCAATTTCTTGACATGGGTCAAGACACAAGAAATGTTCC	2056

QY	Db	Sequence	Accession
QY	Db	579 phealacysrhcyvgslunhseginserphenleuintrp1lelysherpclnarginleu	598
QY	Db	2051 TTGGTGAATGTTGGAACAATGAAATGTCATCACCTTAGACATGAAGGCTCCCTGGTG	2110
QY	Db	599 leuvalgluvalgluargmetglucysalalathrproseraerplysglnglymecproval	618
QY	Db	2111 TTGGATTTTACGAATTCACCTGTATATATATACAAAGTATCATCAGTGTATCGGTGCT	2170
QY	Db	619 leuserleu--Aan1lethrcyvgslmecamsllythrval1leglyvalservalphe	637
QY	Db	2171 AGTGTGCTTGTTGGTGAAGCATGTAGACATTTCTGTATATACCACTTATTTTACCTGATA	2230
QY	Db	638 SerialleuvalvalservalvalvalvalleuvallytryklyspheTryphenislemec	657
QY	Db	2231 CTTATTCGCTGGCTGTAAAAAGTACAGACAGAGAAAGCATCTATGTATGATGATTTGTGATC	2290
QY	Db	658 leuenuhlaiglysy1lelyytryclylarginlylunanthtryzhaerpalphevalille	677
QY	Db	2291 TACTCGAGCCAGATAGAGACTGGGTGTGAARACAGCTGGTAAAGATTTTGAAGAGGA	2356
QY	Db	678 Tyzsergerglnaerpluaptryvalalargsmgluenuvallybasnleuglgluclly	697
QY	Db	2351 GTGCCCGCGCTTTCAGCTTGGCTTCATTTACAGGAGCTTATTCCTGGTGTGCGATTGST	2410
QY	Db	698 ValProthrPheglnleucysylehnietytryatrgasrphelleprogllyvalalalela	717
QY	Db	2411 GCCAACAATCATCCAGAAAGGCTTCCACAAGAGCCGGAAGATTATTTGGTGGTGTCTAGA	2470
QY	Db	718 Alaasnlellelensgluuglyphenislyyserkrnglyval1levalvalvalseroln	737
QY	Db	2471 CACTTATTCAGAGAGCGGTGGTGTATCTTTGAATATATAGATGTTGCTCAGACATGCGATTT	2530
QY	Db	738 Hlpherlelelglnseratrgtrycys1lephelglturyglul1lealaglnthtrtryglinphe	757
QY	Db	2531 CTGAGTGGCCGCTCTGGGCATCATCTTGAATGTCCTTGAGAAAGTGAAGAACTCCCTGGCT	2590
QY	Db	758 leuserserarglaiglylellepherlevalleuclnlysva1glu1ystrhleuenu	777
QY	Db	2591 AGGACAGAGGTGCAATGTATGCGCTTTAGAGAAACACCTACCTCGATGGAGGAGAC	2650
QY	Db	778 Arglnlinalglu1eutytryargleu1euserargysnthtryrlyleuglntprglunap	797
QY	Db	2651 AATGCTCTGGAGAGACATCTTCTGGAGAAAGACTCAAAAAGCCCTGTTGGATGAGAAA	2710
QY	Db	798 SerValleuglyarghis1lelphertryargleuarglysalaleu1eua1spg1lyls	817
QY	Db	2711 GCCTTGAAATCCAGATGAACA 2731	
QY	Db	818 SerTrypanProgluuglythr 824	

RESULT 12

TLR4_BOVIN STANDARD; PRT; 841 AA.

CC Q9GL65; 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUN-2004 (Rel. 44, Last annotation update)

DE Toll-like receptor 4 precursor.

GN Name=TLR4;

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; OC Bovine; Bos.

NC NCBI_TaxID=9913;

LN [1]

SEQUENCE FROM N.A.

RA Guionaud C.T., Dubey C., Jungi T.W.;

RT "Bovine Toll-like receptor 4 (TLR4).";

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Cooperates with MYD and CD14 to mediate the innate immune response to bacterial lipopolysaccharide (LPS). Acts via MYD88, TIRAP and TRAF6, leading to NF-kappa-B activation, cytokine

CC		secretion and the inflammatory response (By similarity).
CC	-1 SUBUNIT:	Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TIR4.
CC	Binds	LY96 via the extracellular domain. Binds WYD88 and TIRAP via their respective TIR domains (By similarity).
CC	-1 SUBCELLULAR LOCATION:	Type I membrane protein (By similarity).
CC	-1 SIMILARITY:	Belongs to the Toll-like receptor family.
CC	-1 SIMILARITY:	Contains 18 leucine-rich (LRR) repeats.
CC	-1 SIMILARITY:	Contains 1 TIR domain.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements/) or send an email to license@ebi.ac.uk .	
CC	EMBL; AF310952;	AAG32061.2; ..
DR	HSSP; O60603;	IPXK.
DR	GO; GO:0004666;	C:lipopolysaccharide receptor complex; ISS.
DR	GO; GO:0001530;	F:lipopolysaccharide binding; ISS.
DR	GO; GO:0004888;	P:transmembrane receptor activity; ISS.
DR	GO; GO:0007250;	P:activation of NF-kappaB-inducing kinase; ISS.
DR	GO; GO:0016046;	P:detection of fungi; ISS.
DR	GO; GO:0009598;	P:detection of pathogenic bacteria; ISS.
DR	GO; GO:0042116;	P:macrophage activation; ISS.
DR	GO; GO:0045576;	P:mast cell activation; ISS.
DR	GO; GO:0045362;	P:negative regulation of osteoclast different.; ISS.
DR	GO; GO:0045304;	P:positive regulation of interleukin-1 biosyn.; ISS.
DR	GO; GO:0045368;	P:positive regulation of interleukin-12 biosy.; ISS.
DR	GO; GO:0045401;	P:positive regulation of interleukin-6 biosyn.; ISS.
DR	GO; GO:0042088;	P:T-helper 1 type immune response; ISS.
DR	InterPro; IPRO004611;	LRR.
DR	InterPro; IPRO004683;	LRR_Cterm.
DR	InterPro; IPRO003591;	LRR_Typ.
DR	InterPro; IPRO00157;	TIR.
DR	Pfam; PF00560;	LRR_13.
DR	Pfam; PF01463;	LRRCT_1.
DR	Pfam; PFO1582;	TIR; 1
DR	PRINTS; PRO0019;	LEUORICRPT.
DR	SMART; SMO0369;	LRR_Type_1.
DR	SMART; SMO0082;	LRRCT_1.
DR	SMART; SMO0255;	TIR; 1.
DR	PROSITE; PS50104;	TIR; 1.
KW	Glycoprotein;	Immune response; Inflammatory response;
KW	Leucine-rich repeat;	Receptor; Signal; Transmembrane Potential.
FT	SIGNAL	1..23
FT	CHAIN	24..841
FT	DOMAIN	24..632 Extracellular (Potential).
FT	TRANSMEM	633..653 Potential.
FT	DOMAIN	654..841 Cytoplasmic (Potential).
FT	REPEAT	53..76 LRR 1.
FT	REPEAT	77..100 LRR 2.
FT	REPEAT	102..124 LRR 3.
FT	REPEAT	149..173 LRR 4.
FT	REPEAT	174..197 LRR 5.
FT	REPEAT	203..225 LRR 6.
FT	REPEAT	277..300 LRR 7.
FT	REPEAT	310..334 LRR 8.
FT	REPEAT	350..372 LRR 9.
FT	REPEAT	373..398 LRR 10.
FT	REPEAT	400..421 LRR 11.
FT	REPEAT	422..445 LRR 12.
FT	REPEAT	446..469 LRR 13.
FT	REPEAT	471..494 LRR 14.
FT	REPEAT	495..518 LRR 15.
FT	REPEAT	520..542 LRR 16.
FT	REPEAT	544..566 LRR 17.
FT	REPEAT	568..592 LRR 18.
FT	DOMAIN	673..819 TIR.
FT	CARBOND	35 N-linked (GlcNAc...) (Potential).

FT	CARBOHYD	73	73	N-linked (G1CNAC . . .)	(Potential)
FT	CARBOHYD	205	205	N-linked (G1CNAC . . .)	(Potential)
FT	CARBOHYD	238	238	N-linked (G1CNAC . . .)	(Potential)
FT	CARBOHYD	282	282	N-linked (G1CNAC . . .)	(Potential)
FT	CARBOHYD	309	309	N-linked (G1CNAC . . .)	(Potential)
FT	CARBOHYD	497	497	N-linked (G1CNAC . . .)	(Potential)
FT	CARBOHYD	526	526	N-linked (G1CNAC . . .)	(Potential)
FT	CARBOHYD	575	575	N-linked (G1CNAC . . .)	(Potential)
FT	CARBOHYD	625	625	N-linked (G1CNAC . . .)	(Potential)
SO	SEQUENCE	841 AA;	96026 MW;	CSE17CB9C798CD16	CRG64;
Alignment Scores:					
Pred. No.:		1.5e-195		Length:	841
Score:		2813.00		Matches:	548
Percent Similarity:		79.19%		Conservative:	118
Best Local Similarity:		65.16%		Mismatch:	169
Query Match:		47.33%		Indels:	6
GB:		1		Gaps:	4

US-09-396-985B-5 (1-3395) x TLR4_BOVIN (1-841)

260 ATGATGCTCTCTTGCATCTGGCTGGACTCTGATCATGCA---TTGTTCCCTTCCCTGC 316

Db 1 MetMetAlaArgAlaArgLeuAlaAlaAlaLeuIleProAlaThrAlaIleLeuSerCys 20

317 CTGAGACCAGGAAGCTTGAATCCCTGCATAGAGGTA

Db 21 LeuArgThrGluSerTrpAspProCysValGlnValProAsnIleSerTyrGlnCys 40

377 ATGGATCAGAAATCTCAGCAAATCCCTCATGACATCCCTTATTCAACCAAGAACCTAGAT 436

Db 41 MetGluLeuAsnLeuTyrLysIleProAspAsnIleProIleSerThrLysMetLeuAsp 60

437 CTGAGCTTCAACCCCTGAAGATCTTAAGAGCTATAGCTTCAACCAATTCTCACAACCTT 496

Db 61 LeuSerPheAsnTyrLeuArgHisLeuGlySerHisAsnPheSerSerPheProGluLeu 80

497 CAGTGGCTGATTTATCCAGGTGTGAATTGAGACAATTGAAGACAAGGCATGGCATGGC 556

Db 81 GlnValLeuAspLeuSerArgCysGluIleLysIleIleGluAspAspThrPheGlnGly 100

557 TTAACCAAGCTCTCAACCTTGCTACTGACAGGAACCTATCAAGAGTTTTCGCCAGGA 616

Db 101 LeuAsnHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaTrpGly 120

617 AGTTTCTGACTAACAAATTAGAGAATCTGGTGCCTGTGGAGACAAATAACCTCT 676

Db 121 AlapheserGlyLeuserSerLeuGlnLysLeuValAlaValGluThrAsnLeuValSer 140

677 CTAGAGGTTTCATATGGACAGCTTATATCCTTAAGAACTAAATGTGGCTCATAAT 736

Db 141 LeuAsnAspPheProIleGlyHisLeuLysAsnLeuLysGluLeuAsnValAlaHisAsn 160

QY 737 CTTATACATTCTTTAAGTTGCCCTGAATATTTTCTAATCTGACAAACCTAGACATGTG 796

Db 161 pheilehissSerPheLysLeuProGluTyrPheSerAsnLeuProAsnLeuGluHisLeu 180

797 GATCTTCTTATACTATATTCAAACTATTCTGTCAAGACTTACAGTTTCTACGTGA 856

Db 181 AspleuSerAsnAsnLysIleGlnAsnIleTyrTrpGluAspValLysValLeuHisGln 200

857 AATCCCAAGTCAATCTCTTTAGACCTGTCTTTAAACCAATTGACTCCATTCAAGCC 916

Db 201 MetProLeuAsnLeuSerLeuAspLeuSerLeuAsnProLeuAspPheIleGluPro 220

917 CAAGCCTTCAGGAATTAGGCTCATGAATTGACTCTAAGAAGTAATTTAATAGCTCA 976

Db 221 GlyThrPheLysGluIleLysLeuAnGlyLeuThrLeuArgSerAsnPheAsnSerSer 240

977 AATGTAAGAAATGTGCCTTCAAAACATGACTGTTACATGTCCATCGGTGATCTTG 103

Db 241 HisValMetLysThrCysIleGlnGlyLeuAlaGlyLeuLysThrAsnArgLeuValLeu 260

OY	1037	GGAGAAATTAAAAAGAAAGGAATCTGGAAAGTTTGAACGGTTCTGATAGGAAGACTA	1098
Db	261	GlycylphenylsanguinaldylvalylleuylinrgPheabapGserPheleuGlulGlyleu	280
OY	1097	TGCATATGCACATTCATGAGTTCAGGTTCAGTTAAACATATTAATATCATTTTTTCA---GATCAT	1153
Db	281	CysaenleuthrlleGlulGlnPheargLlealTryleuabrylPheSerGlyAspasp	300
OY	1154	ATTATTAATCTCAATTCGTTGGCAAAATATTTCTGCAATGTCTTTCACAGGTGTACATATA	1213
Db	301	ThirapleuPheAenCysleuAlaenValSerVallleSerleuLeuSerlleSerleu	320
OY	1214	AAACACATACAGAGATGTTCTTAGAGACTTTTCAAAATGGCAATCTTTATCATATTAAGATGT	1273
Db	321	GlySerleuGlnAlaLeuLysAspPheargTrpGlnlleuGlulIlelleAsnLys	340
OY	1274	CATCTTAAGCCTTTTCCAAAGCTGAGTGTACCTTTTCTTAAAGTGGACCTTAACTAC	1333
Db	341	AspPheabrylPheProAlaLeuLysLeuSerSerleuLysLysPheValPheThrAsp	360
OY	1334	AACAGAGAGATATTCACGTTTGTCATGTGGCTCTGCCAAGTCTCAGATATCTAGATCTT	1393
Db	361	AsnLysAspIleSerThrPheThrGlnPheGlnLeuProSerleuGlnTryleuAspLeu	380
OY	1394	AGTAGAAATGSCATAGACGTTTAGAGGTTCGTCTTTATTTTGATTTTGGAAACAACAC	1453
Db	381	LysArgAsnIlsleuSerPheLysGlyCysSerAsnIlsThrAspPheGlyThrThrAsn	400
OY	1454	CTGAAGTACTTAGACCTTCAGCTTCAATGATGTGCATCTGATAGAGTGCACATTCATGGT	1513
Db	401	LeuLysIlsleuAspLeuSerPheAsnAspVallleThrLeuGlySerAspPheMetGly	420
OY	1514	CTAGAAGCTGAATATACCTGACCTTTCAGACCTTCACACTTTAAAAAGSTACACAAATTC	1573
Db	421	LeuGlnGlnLeuGlnIlsleuAspPheGlnIlsSerThrLeuLysGlnlleAsnAlaPhe	440
OY	1574	TCAGTGTCTTATCTCTTGAAAACCTTTTACCTTGACATCTTTACATTAATACCAAA	1633
Db	441	SerAlaPheleuSerleuArgAsnleuArgLysleuAspIleSerLysThrAsnIlearg	460
OY	1634	ATTGACTTGAATGGATATTTCTTGCGCTGAATACGTCACACATTTAAAAATGGCTGCG	1693
Db	461	IleValllePheIlsGlyllePheThrGlyleuValleSerleuGlnThrleuLysMetAlaGly	480
OY	1694	AATCTTTCAAAGACACACACCTTTCGAATCTTTTCAAAACACACAACTTAAACATTC	1753
Db	481	AsnSerPheGlnAsnAsnleuLeuProAspIleleThrGlnleuThrAsnleuThrVal	500
OY	1754	CTGATCTTTTSTAATGSCAACTGGACACAGATATCTAGGCGGATTTTGACACACTTAC	1813
Db	501	LeuAspLeuSerLysCysGlnleuGlnValleGlnIlsThrAlaPheIlsleuSer	520
OY	1814	AGACTCCAGTATTAACATAGTCACAAACCAACGCTTTCTGGATCCATCCCATAT	1873
Db	521	SerleuGlnValleuAsnMetSerIlsAsnLysleuLeuSerleuAspThrPheleuLys	540
OY	1874	AAACAGCTGTATCCCTCAGACACTTTGATTCAGATTTCATCCGATAGACATCCAAA	1933
Db	541	GlnProleuIlsSerleuArgIlleuAspCysSerPheAsnArgIlleMetAlaSerLys	560
OY	1934	---GGATATCTGCACATTTTCCAAAGAGCTTACGGCTCTCAATCTGACTAATTAATCT	1990
Db	561	GlnGlnGlnleuGlnAsnleuProArgSerleuThrTryleuAsnleuThrGlnAsnAla	580
OY	1991	GTTGGCTGTATATGATATCAGAAATTTCTTGACGTGGGTCACAGACACAAATATGTT	2050
Db	581	PheAlaCysValCysGlnIlsGlnSerPheleuGlnTryValleAspGlnArgGlnleu	600
OY	2051	TTGGTGAATGTTGAACAATATATGTCATCATCCTATAGACATGAAGGCTCCCTGGTG	2110
Db	601	LeuValleGlyAlaGlnGlnMetMetCysAlaGlnProleuAspMetGlnAspMetProVal	620
OY	2111	TTGATTTTACGAATTCACCTGTATATATTAACAAGACTATCATCATGATGTGGTGGTG	2170

[illegible]


```

QY 797 GATCTTTCTTAATACTAATTAATCAACTATTCTGCAAGACTTACAGTTTCTACGTGA 856
DB 181 AspLeuSerAsnAsnLysIleGlnAsnIleTyrrGlnAspValLysValLeuHisGln 200
QY 857 AATCCCAAGTCAATCTCTTTTAGCCTGTCTTTAAACCAATGTGCTCCATCAAGCC 916
DB 201 MetProLeuLeuAsnLeuSerLeuAspSerLeuAsnProLeuAspPheIleGluPro 220
QY 917 CAAGCCTTCAAGGAAATTAGCTCCATGAATTGACTAGAGAATTAATTTAATAGCTCA 976
DB 221 GlyThrPheLysGluIleLysLeuAsnGluLysLeuThrLeuArgSerAsnPheAsnSer 240
QY 977 AATGATGAAATGTGCTTCAAAACATGACTGGTTTACATGTCAATCGGTGATCTTG 1036
DB 241 HisValMetLysThrCysIleGlnGlyLeuValAcLysLysThrAsnArgLeuValLeu 260
QY 1037 GGAGAAATTTTAAATGAAGAAGATCTGGAAGATTGTAACCGTCTGTCAAGAGACTA 1096
DB 261 GlyGluPheLysAsnGlnArgLysLeuGlnArgPheAspArgSerPheLeuGluGlyLeu 280
QY 1097 TGCAGATGAGACATTTGATGATTCAGGTTAACATATTAATCAATTTTCA--GATGAT 1153
DB 281 CysAsnLeuThrIleGluGlnPheArgIleAlaTyrrLeuAspLysPheSerGlyAspAsp 300
QY 1154 ATTTATATCTCAATGTCTGCAAAATATTCTGCAATGTCTTACACAGGTGTACATTA 1213
DB 301 ThrAspLeuPheAsnCysLeuAlaAsnValSerValIleSerLeuLeuSerIleSerLeu 320
QY 1214 AAACACATAGCAGATGTTCTCAGCAGATTCAATGGCAATCTTATCAATCATTAAGAT 1273
DB 321 GlySerLeuGlnAlaLeuLeuLysAspPheArgTrpGlnHisLeuGluIleIleAsnCys 340
QY 1274 CATCTTAAGCCTTTTCCAAAGTGAATGTTTCTTAATAAGTGGACTTTAACTAAC 1333
DB 341 AspPheAspLysPheProAlaLeuLysLeuSerSerLeuLysLysPheValPheThrAsp 360
QY 1334 AACAGAGAGATATCATCTTGTCAGTTGGCTGTCGCAAGTCTCAAGATATCTGATCTT 1393
DB 361 AsnLysAspIleSerThrPheThrGluPheGlnLeuProSerLeuGlnTyrrLeuAspLeu 380
QY 1394 AGTAGAAATGCGATAGCTTTAGAGTGTCTTTTATCTTGAATTTGGAACAACAAC 1453
DB 381 LysArgAsnHisLeuSerPheLysGlyCysSerHisThrAspPheGlyThrThrAsn 400
QY 1454 CTGAAGTACTTAAGACCTCAGCTTCATGTGTCTCATCTGATGAGTCCCACTTACGTG 1513
DB 401 LeuLysHisLysLeuAspLeuSerPheAsnAspValIleThrLeuGlySerAsnPheMetGly 420
QY 1514 CTAGAAGAGTGAATATCTGAGACTTTCAGACCTCCACTTTAAAAAAGGTCACAGAATTC 1573
DB 421 LeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrLeuLysGlnHisAsnAlaPhe 440
QY 1574 TCAGTGTCTTATCTCTTGAATAAATCTTTACCTTGAATCTCTTACATTAATACCAA 1633
DB 441 SerAlaPheLeuSerLeuArgAsnLeuArgTyrrLeuAspIleSerTyrrThrAsnIleArg 460
QY 1634 ATTGACTTTGATGGATTTCTTGAGCTTTCAGTCAAGTCAACATTTAAATAAGTGTGC 1693
DB 461 IleValPheHisGlyLysLeuThrGlyLeuValSerLeuGlnThrLeuLysMetAlaGly 480
QY 1694 AATCTTTCAAGAACAACACCTTTCAATGTCTTTCAAAACAACAACAATTAACATTC 1753
DB 481 AsnSerPheGlnAsnAsnLeuLeuProAspIlePheThrGluLeuThrAsnLeuThrVal 500
QY 1754 CTGATCTTTTAAATGCGCACTGGACAGATATCTAGGGGGGTAATTTGACACACTTAC 1813
DB 501 LeuAspLeuSerLysCysGlnLeuGlnValAlaGlnThrAlaPheHisSerLeuSer 520
QY 1814 AGACTCCAGTTATTTAAATAGTCAACAACATCTGTTCTTGAGATCCCATTTAT 1873
DB 521 SerLeuGlnValLeuAsnMetSerHisAsnLysLeuLeuSerLeuAspThrPheLeuTyrr 540

```

```

QY 1874 AACAGCTGTACTCCCTCAGACACTTGTGATTTGAGATTTCATATGCAATGACATCCAA 1933
DB 541 GluProLeuHisSerLeuAsnArgIleLeuAspCysSerPheAsnArgIleMetAlaSerLys 560
QY 1934 ---GGAATATCTGACAACTTTTCCAAAGAGCTTAGCCGTCTTCAATGTGCTAATAATCT 1990
DB 561 GlnGlnGlnLeuGlnAsnLeuProArgSerLeuThrTrpLeuAsnLeuThrGlnAsnAla 580
QY 1991 GTTGCTGTGATATGTAATATCAATTTCTTGCAATGGGTCAAGACCAAGAAATGTTTC 2050
DB 581 PheAlaCysValLysGlnHisGlnSerPheLeuGlnThrValLysAspGlnArgGlnLeu 600
QY 2051 TTGCTGAATGTGTAACAATAATGAATGTGATCACTATAGACATGAAGCCTCCGTGTC 2110
DB 601 LeuValGlyAlaGlnGlnMetCysAlaGluProLeuAspMetGluAspMetProVal 620
QY 2111 TTGCAATTTACGAATTCACCTGTATATATACAAACTATCATCATGTATTCGGTGTTC 2170
DB 621 LeuSerPheArgAsnAlaThrCysGlnLeuSerLysThrIleIleSerValSerVal 640
QY 2171 AGTGTGCTGTGGTGGCACTGTAGCATTTCTGATATACCACTTCAATTTTCACTGATA 2230
DB 641 ThrValLeuLeuValSerValValGlyValLeuValTyrrLysPheTyrrPheHisLeuMet 660
QY 2231 CTATTGCTGTGCTGTAATAAAGTACAGCAGAGAGAAAGCATCTATGATGATTTGTGATC 2290
DB 661 LeuLeuAlaGlyCysLysLysTyrrGlyArgGlyGlnSerThrTyrrAspAlaPheValIle 680
QY 2291 TACTCGACCGAATGAGACTGGGTGAGAAACGAGCTGTTAAAGAAATTTGAAGAAAGA 2350
DB 681 TyrrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlnGly 700
QY 2351 GTGCGCCGCTGTGAGCTTGTGCTTCAATTAAGGAGACTTTATCTGCTGAGCAATGCT 2410
DB 701 ValProProPheGlnLeuCysLeuHisTyrrArgAspPheIleProGlyAlaAlaIleAla 720
QY 2411 GCCAATCATCTCAGAAAGGCTTCCACAAGACCGGAAAGTTATTTGTGTGTCTAGA 2470
DB 721 AlaAsnIleIleGlnGlnGlyPheHisLysSerArgLysValIleValValIleSerGln 740
QY 2471 CACTTATCCAGAGCGGTGTGTATCTTTGAATATGAGATTGCTCAGACATGGCAGTTT 2530
DB 741 HisPheIleGlnSerArgTrpCysIlePheGlyTyrGlnIleAlaGlnThrTrpGlnPhe 760
QY 2531 CTGAGTACCGCTCTGCGACATCTTCATGTCTTGAAGAAGTGAAGAGTCTTGCTG 2590
DB 761 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeuGlnLysSerLeuLeu 780
QY 2591 AGCAGAGGTCGAATGTATTCGCTTCTTAGCAAGAAACACTACCTCGAGTGGAGAGAC 2650
DB 781 ArgGlnGlnValGlnLeuTyrrArgLeuLeuSerArgAsnThrTyrrLeuGlnIuTrpGluAsp 800
QY 2651 AATGCTTGGGAGAGCAGCATCTTCTGGAAGAACTCAAAAAGCCCTGTGATGAAA 2710
DB 801 SerValLeuGlyArgHisValPheTrpArgArgLeuArgLysAlaLeuAlaGlyLys 820
QY 2711 GCCTGAATCCAGATGAATCAATCAGAGGAGAA-----CAAGAGCAACAACCTTG 2761
DB 821 ProGlnSerProGlnGlyThrAlaAspAlaGlnThrAsnProGlnGlnIuAlaThrThrSer 840
QY 2762 ACC 2764
DB 841 Thr 841

```

RESULT 15
 Q6WCD4
 ID Q6WCD4 PRELIMINARY; PRT; 841 AA.
 AC Q6WCD4;
 DT 05-JUN-2004 (TRMBLrel. 27, Created)
 DT 05-JUN-2004 (TRMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
 DE Toll-like receptor 4.
 GN Name=TLR4;

OS Bos taurus. (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22833971; PubMed=12915733; DOI=10.1073/pnas.1333957100;
 RA White S.N., Taylor K.H., Abbey C.A., Gill C.A., Momack J.E.;
 RT "Haplotype variation in bovine Toll-like receptor 4 and computational
 prediction of a positively selected ligand-binding domain";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10364-10369(2003).
 DR EMBL; AY297043; AAQ62701.1; -
 DR EMBL; AY297041; AAQ62701.1; JOINED.
 DR EMBL; AY297042; AAQ62701.1; JOINED.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR000483; LRR_Cterm.
 DR InterPro; IPR003885; LRR_Cyst.
 DR InterPro; IPR003591; LRR_Cyp.
 DR InterPro; IPR000157; TIR.
 DR Pfam; PF01463; LRRCT; 1.
 DR Pfam; PF00560; LRR_1; 12.
 DR Pfam; PF01582; TIR; 1.
 DR PRINTS; PR00019; LEURICHRPT.
 DR SMART; SM00082; LRCT; 1.
 DR SMART; SM00365; LRR_SD22; 6.
 DR SMART; SM00369; LRR_TYP; 13.
 DR SMART; SM00255; TIR; 1.
 DR PROSITE; PS50104; TIR; 1.
 KM Receptor.
 SQ SEQUENCE 841 AA; 95954 MW; AD6D06ACEF44CC91 CRC64;
 Alignment Scores:
 Pred. No: 1.56e-194 Length: 841
 Score: 2799.00 Matches: 546
 Percent Similarity: 78.95% Conservative: 118
 Best Local Similarity: 64.92% Mismatches: 171
 Query Match: 47.10% Indels: 6
 Gaps: 4
 US-09-396-985b-5 (1-3395) x Q6WCD4 (1-841)
 QY 260 ATGATGCTCTCTTGATCTGCTGGAGACTGTGATCATGGA---TTGTTCTTTCTGCG 316
 Db 1 MetheclalaarglaaagleualalaaleuleuleproalathraalaleuleserCys 20
 QY 317 CTGAGACGAGAACTTGAATCCCTGATAGAGTACTTCTTAATATTAATCTTACCAATGC 376
 Db 21 LeuhgrthrguhsertTprapProCyvalGlnValProahnilleserTyglnCys 40
 QY 377 ATGATCAGAAATCTCAGCAAAATCCCTCATGACATCCCTTAATTCACCAAGAACCTAGAT 436
 Db 41 MetGluuhsenleuTyrlslePProAspAnlleProIleSerThrlyMetLeuAsp 60
 QY 437 CTGAGCTTCAACCCCTGAAGATCTTAAGAGCTATTAACCAATTTCTCAACTT 496
 Db 61 LeuSerPheAnlyrleuAarghlsleuGlySerHisenPheSerPheProGlnleu 80
 QY 497 CAGTGGCTGATTTATTCAGAGTGTGAATGAGCAATTAAGACAAAGCATGGCATGGC 556
 Db 81 GlnValleuhsPleuSerArgCysGlnllelyserlleleGlnhsPaprThrPheGlnGly 100
 QY 557 TTAAACGAGCTTCAACCTTGATGATGACAGAAACCTTCAAGAGTTTTCCTCCAGGA 616
 Db 101 LeuAsnHisleuSerThrleuThrGlyAsnProIleGlnSerleuAlatrgGly 120
 QY 617 AGTTTCTGAGTCAACAAATTAAGAAATGTGGCTGGCTGGAGCAAAATGAACTCT 676
 Db 121 AlapheserGlyleuSerSerleuGlnlyleuValAlaValGlnThrAnleuValSer 140
 QY 677 CTAGAGGTTTCCATATTTGACAGCTTATATCTTAAAGAACTTAATGTGGCTCATAT 736

Db 141 LeuAsnAspPheProIleGlyHisleuLysAsnleuLysGlnleuAsnValAlaHisAsn 160
 QY 737 CTATACATCTCTTAAGTGGCTGAATATTTCTTAATCTGACAACTGACATG 796
 Db 161 PheIleHisSerPheLysleuPro****PheSerAnleuProAsnleuGlnHisleu 180
 QY 797 GATCTTCTTAATATCTTAATCAACATATTTCTCTCAAGACTTACAGTTTCTACGTGA 856
 Db 181 AspLeuSerAnleuLysIleGlnAsnIleTyrlrgLueAspValIysValLeuHisGln 200
 QY 857 AATCCCAAGTCAATCTCTTTAGACCTGTCTTTAAACCAATGACTCCATTCAGACC 916
 Db 201 MetProleuAsnleuSerleuAspLeuSerleuAsnProleuAspPheIleGlnPro 220
 QY 917 CAAGCTTCAAGGAATTAAGCTTCATGAATGACTTAAGATAATTTAATAGCTCA 976
 Db 221 GlyThrPheLysGlnleuLysleuAsnGlyLeuThrleuLysSerAnPheAsnSerSer 240
 QY 977 AATGATCGAAATGTGCTTCAAAAACATGACTGTTTACATGTCATCGGTGATCTG 1036
 Db 241 HisValmetLysThrCysIleGlnGlyLeuAlaGlyleuLysThrAsnArgleuValleu 260
 QY 1037 GAGAAATTTAAATGAAGCAATCTGAAAGTTTGAACCTTCTGCATGAAGAACTA 1096
 Db 261 GlyGlnPheLysAsnGlnArgLysleuGlnArgPheAspTrgSerPheleuGlnGlyleu 280
 QY 1097 TGCATGTGACATGATGATGAGTTCAAGTTAATATTAATCATTTTTC--GATGAT 1153
 Db 281 CysAsnleuThrIleGlnGlnPheArgIleAlaTyrlsleuAspLysPheSerGlyAspAsp 300
 QY 1154 ATTATATATCATATGCTTGGCAAAATATTTCTGCAATGATCTTCAAGAGTGCATATA 1213
 Db 301 ThrAspLeuPheAsnLysleuAlaAsnValSerValIleSerleuLysSerIleSerleu 320
 QY 1214 AAACATACATGACATGTTCTTGAAGCAATTTGAAATGCAATCTTATCATCATTAAGAT 1273
 Db 321 GlySerleuGlnAlaLeuLysAspPheArgTrpGlnHisleuGlnIleIleAsnCys 340
 QY 1274 CATCTTAAGCTTTTCCAAAGCTGACGTACCTTTCTTAAAGTTGAGACTTAACTAC 1333
 Db 341 AspPheAspLysPheProAlaLeuLysleuSerSerleuLysLysPheValPheThrAsp 360
 QY 1334 AACAGAGAGATATACAGCTTGTGACGTTGCTGTCAGATCTGACATATCTGATCTT 1393
 Db 361 AsnLysAspIleSerThrPheThrGlnPheGlnleuProSerleuGlnTyrlsleuAspLeu 380
 QY 1394 AGTAAGATCCATGAGCTTTAGAGTGTGCTGTTCTTATCTGATTTTGAACAACAAC 1453
 Db 381 LysArgAsnHisleuSerPheLysGlyCysCysSerHisThrAspPheGlyThrThrAsn 400
 QY 1454 CTGAAGTACTTAAGCTCAGCTTCAATGTGTCACTCTGATGAGTGAACCTTATGAGGT 1513
 Db 401 LeuLysHisleuAspLeuSerPheAsnAspValIleThrleuGlySerAnPheMetGly 420
 QY 1514 CTGAAGAGCTGAATATCCGAGCTTCAAGACTTCACTTAAAGTCAACAGATTC 1573
 Db 421 LeuGlnGlnleuGlnHisleuAspPheGlnHisSerThrleuLysGlnIleAsnAlaPhe 440
 QY 1574 TCAGTGTCTTATCTCTTGAAGAACTTTTACCTTGAACATCTTCACTTAATACCA 1633
 Db 441 SerAlaPheleuSerleuAsnleuArgLysleuAspIleSerTyrlrThrAnlleArg 460
 QY 1634 ATTGACTTGTATGATATTTCTTGCTGATGATGATCTCAACTTAATAATGAGCTGC 1693
 Db 461 IleValPheHisGlyIlePheThrGlyLeuValSerleuGlnThrleuLysMetAlaGly 480
 QY 1694 AATCTTTCAAGAACCAACCTTCAAAATGTCTTAAACCAACCAACTTAACATTC 1753
 Db 481 AsnSerPheGlnAsnHisleuLysProAspIlePheThrGlyleuThrAnleuThrVal 500
 QY 1754 CTGATCTTCTTAATGCAACTGGAACAGATATCTAGGGGGGATTTTGAACACTCTAC 1813

Db 501 LeuAspLeuSerLysCysGlnLeuGlnValAlaGlnThrAlaPheHisSerLeuSer 520
QY 1814 AGACTCCAGTATTAACATGAGTCACACACACCTACTGTTCTGGATCCATCCATTAT 1873
Db 521 SerLeuGlnValLeuLeuMetSerHisAsnLysLeuSerLeuAspThrPheLeuTyr 540
QY 1874 AACAGCTGACTCCCTCAGAACTCTGATTGCAAGTTTCATCGCATAGACATCCAAA 1933
Db 541 GlnProLeuHisSerLeuArgGlyIleLeuAspCysSerPheAsnArgIleMetAlaSerLys 560
QY 1934 --GAAATCTGCACAACTTTCCAAAGAGTCAGCCGCTTCAATCTGACTAATATCTT 1990
Db 561 GlnGlnGlnLeuGlnAsnLeuProArgSerLeuThrTrpLeuSerLeuThrGlnAsnAla 580
QY 1991 GTTGCTTGATATGTGATATACAGAAATTTCTTGACGTGGGTCAAGACCAAGAAAATGTC 2050
Db 581 PheAlaCysValCysGlnHisGlnSerPheLeuGlnTrpValLysAspGlnArgGlnLeu 600
QY 2051 TTGGTGAATGTTGAACAATGAAATGTGATCACTTATGACATGAAAGCCCTCCCTGGTG 2110
Db 601 LeuValGlyValGlnGlnMetMetCysAlaGlnProLeuAspMetGlnAspMetProVal 620
QY 2111 TTGATTTTACGAATTCACCTGTTATATATACAAAGCTATCATCATGATATCGTGATC 2170
Db 621 LeuSerPheArgPheAlaThrCysGlnLeuSerLysThrIleIleSerValSerValVal 640
QY 2171 AGTGTGCTTGTGTGGCCACTGTAGCATTTCTGATATACCACTTATTTTCACTGATA 2230
Db 641 ThrValLeuLeuValSerValValGlyValLeuValTyrLysPheTyrPheHisLeuMet 660
QY 2231 CTTATTCCTGGCTGTAAATAAGTACAGCAGAGAGAAAGCATCTATGATGCATTTGTGATC 2290
Db 661 LeuLeuAlaGlyCysLysLysTyrGlyArgGlyLysSerIleTyrAspAlaPheValIle 680
QY 2291 TACTGAGCCAGAAATGAGAACTGGTGAAGAAACGAGCTGTAAAGAAATTTAGAAAGAA 2350
Db 681 TyrSerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGly 700
QY 2351 GTGGCCCGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 2410
Db 701 ValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAla 720
QY 2411 GCCAATCATTCAGAAAGCTTCACAAAGACCGGAAAGTTATGTGTGTGTGTAGA 2470
Db 721 AlaAsnIleIleGlnGlnGlyPheHisLysSerArgLysValIleValValSerGln 740
QY 2471 CACTTATCCAGAGCCGCTGTGATCTTTGAATATGAGATTGCTCAGACATGGCAAGTT 2530
Db 741 HisPheIleGlnSerArgTrpCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPhe 760
QY 2531 CTGAGTACCGCTGTGAGATCATCTTCAATTTCTTGAAGAAAGTGGAAGTCTTGTGCTG 2590
Db 761 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysLeuGlnLysSerLeuLeu 780
QY 2591 AGGAGCAGAGTCAATGATGCTTGTGCTTGTGAGAAAACACTACCTCGAGTGGAGGAC 2650
Db 781 ArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTrpGlnAsp 800
QY 2651 AATGCTCTGGGAGGACATCTTGTGAGAAAGCTCAAAAAGCCCTGTGTGATGAAA 2710
Db 801 SerValLeuGlyArgHisValPheTrpArgArgLeuArgLysAlaLeuLeuAlaGlyLys 820
QY 2711 GCCTTGATCCAGATGAACATCAGAGGAAAG-----CAAGAAAGCAACACTTGTG 2761
Db 821 ProGlnSerProGlnGlyThrAlaAspAlaGlnThrAsnProGlnGlnAlaThrThrSer 840
QY 2762 ACC 2764
Db 841 Thr 841

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plu_n2p model

Run on: March 30, 2005, 03:00:48 ; Search time 196.34 Seconds
(without alignments)
16418.453 Million cell updates/sec

Title: US-09-396-985B-1
Perfect score: 8579
Sequence: 1 aaataactccctgcctcaaa.....caaaaaaaaaaaaaaaaa 4668

Scoring table:
BIOSSIM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1407402 segs, 331100923 residues
Total number of hits satisfying chosen parameters: 2814804

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+np_model -DEV=xlh
-Q=/cgnt2_1/USPTO.spool/US09396985/rtunat_28032005_155745_21245/app_query.fasta_1.85098
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonsum62
-TRANS=human40.cdt -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HRAPIZ=500 -MINLEN=0
-MAJLEN=200000000 -USER=US09396985 @CGN_1_1.3955 @rtunat_28032005_155745_21245
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA:*
1: /cgnt2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgnt2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
3: /cgnt2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgnt2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgnt2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgnt2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pep:*
7: /cgnt2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgnt2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgnt2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgnt2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgnt2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgnt2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgnt2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgnt2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgnt2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgnt2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgnt2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*
18: /cgnt2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgnt2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgnt2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result Query

SUMMARIES

No.	Score	Match Length	DB	ID	Description
1	4335.5	50.5	837	10	US-09-950-041-26
2	4141	48.3	799	10	US-09-950-041-8
3	4141	48.3	799	16	US-10-128-166-7
4	4141	48.3	799	16	US-10-732-563-8
5	4141	48.3	799	16	US-10-732-563-8
6	663	7.7	661	15	US-10-038-854-135
7	663	7.7	661	15	US-10-037-417-107
8	629.5	7.3	661	13	US-10-114-893-10
9	629.5	7.3	661	13	US-10-038-854-134
10	603.5	7.0	784	15	US-09-950-041-4
11	603.5	7.0	784	15	US-10-456-947-46
12	602.5	7.0	784	14	US-10-095-627-12
13	602.5	7.0	784	16	US-10-732-563-4
14	602.5	7.0	784	16	US-10-732-796A-4
15	602.5	7.0	784	17	US-10-741-600-1390
16	602.5	7.0	784	17	US-10-741-600-1391
17	599.5	7.0	784	13	US-10-145-014-23
18	580.5	6.8	1032	14	US-09-954-987B-192
19	580.5	6.8	1032	14	US-10-272-502A-31
20	580.5	6.8	1032	15	US-10-407-952-32
21	567	6.6	1050	10	US-09-954-987B-175
22	567	6.6	1050	14	US-10-272-502A-22
23	567	6.6	1050	15	US-10-407-952-26
24	534	6.2	1032	9	US-09-950-041-37
25	534	6.2	1040	9	US-09-864-761-38325
26	534	6.2	1041	10	US-09-954-987B-184
27	534	6.2	1041	10	US-09-954-987B-186
28	534	6.2	1041	14	US-10-272-502A-26
29	534	6.2	1041	15	US-10-407-952-28
30	534	6.2	1041	16	US-10-732-563-16
31	534	6.2	1041	16	US-10-732-796A-16
32	533	6.2	1041	9	US-09-168-978-3
33	533	6.2	1041	9	US-09-978-295A-498
34	533	6.2	1041	9	US-09-978-697-498
35	533	6.2	1041	9	US-09-978-192A-498
36	533	6.2	1041	9	US-09-999-832A-498
37	533	6.2	1041	10	US-09-978-189-498
38	533	6.2	1041	10	US-09-978-608A-498
39	533	6.2	1041	10	US-09-978-585A-498
40	533	6.2	1041	10	US-09-978-191A-498
41	533	6.2	1041	10	US-09-978-403A-498
42	533	6.2	1041	10	US-09-978-564A-498
43	533	6.2	1041	10	US-09-999-833A-498
44	533	6.2	1041	10	US-09-981-915A-498
45	533	6.2	1041	10	US-09-978-824-498

ALIGNMENTS

RESULT 1
US-09-950-041-26
Sequence 26, Application US/09950041
Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Rook, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Ho, Stephen W.K.
TITLE OR INVENTION: RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS
FILE REFERENCE: DK0724XK1
CURRENT APPLICATION NUMBER: US/09/950, 041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293

PRIOR FILING DATE: 1997-05-07
PRIOR APPLICATION NUMBER: 60/072,212
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/076,947
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26
LENGTH: 837
TYPE: PRF
ORGANISM: Homo sapiens
US-09-950-041-26

Alignment Scores:
Pred. No.: 0 Length: 837
Score: 4335.50 Matches: 837
Percent Similarity: 99.88% Conservative: 0
Best Local Similarity: 99.88% Mismatches: 0
Query Match: 50.54% Indels: 1
DB: 10 Gaps: 1

US-09-396-985b-1 (1-4868) x US-09-950-041-26 (1-837)

QY 107 ATGTCGCTCGCCCTGCTGGAACTCTGAATCCAGCATGCGCTTCTCTCGCTG 166
Db 1 MetSer1aSerA1gLeuA1aG1YThrLeu1leProAlaMeCAlaPheLeuSerCyVal1 20
QY 167 AGACAGAAAGCTGGAGCCCTGGCGTGGAGGTGGCTTATATTAATCTATCAATGCA 226
Db 21 ArgProG1uSer1rPgluPrCoCyValG1n--ValProAen1leThrYrGlnCySer 39
QY 227 GAGCTGAATTTCTCAAAATCCCGACAACTCCCTTCTCAACCAAGAACTGCACTG 286
Db 40 GluLeuAenPhe1rYrY1lePrOshpAenLeuProPheSer1rY1aAenLeuAen 59
QY 287 AGCTTTAATCCCTGAGGCAATTTAGGCACTATAGCTTCTTCAATTTCCAGAACTG 346
Db 60 SerPheAenProLeuA1gH1leuG1YSerY1SerPheSerPheProG1uLeuG1n 79
QY 347 GTGCTGATTTATTCAGAGTGGAAATCCAGCAATTTAGATGGGGCATATCAAGCTTA 406
Db 80 ValLeuAenPheSerA1rCySg1u1leG1nThr1leG1uAenP1a1aYrG1nSerLeu 99
QY 407 AGCCACTCTCTACCTTATATTTAGACAGAAACCCATCCAGATTTAGCCTGGAGCC 466
Db 100 Ser1s1eAenSer1rThrLeu1leLeuThrC1YanPro1leG1nSerLeuA1leuG1YAla 119
QY 467 TTTTCTGACTATCAAGTTTACAGAACTGGCTGGAGACAAATCTAGCATCTCTA 526
Db 120 PheSerG1YLeuSerSerLeuG1nYLeuValAlaValG1uThrAenLeuA1aSerLeu 139
QY 527 GAGAACTCCCATTTGGACATCTCAAAACCTTGAAGAACTTATGTCGCTCAAAATTT 586
Db 140 GluAenPhePro1leG1YH1sLeuY1rThrLeuY1sG1uLeuAenValAlaH1sAenLeu 159
QY 587 ATCCAAATCTTCAATTAATCTGAGATTTTCTAATCTGACCAATCTAGACACTGGAC 646
Db 160 I1leG1nSerPheY1leuProG1uYrPheSerAenLeuThrAenLeuG1nH1sLeuAen 179
QY 647 CTTTCCAGCAACAAGATTTAAATTTATTCACAGACTTGGGCTTCTACATCAATG 706
Db 180 LeuSerSerAenY1leG1nSer1leYrCyStrAenPheA1gValLeuH1sG1nMet 199
QY 707 CCCCTACATCTCTCTTTAGACTGTGCTGATCTGATGACTTATGACCAAGCT 766
Db 200 ProLeuAenAenLeuSerLeuAenPheSerLeuAenProMetAenPhe1leG1nProG1Y 219
QY 767 GCATTTAAAGAAATTAGGCTTCATAGCTGACTTTAAGAAATTAATTTGATAGTTAAT 826
Db 220 AlaPheY1sG1u1leH1sG1uAen1sY1sLeuThrLeuA1gAenAenPheAenSerLeuAen 239
QY 827 GTAATGAAGACTTGATTTCAAGGTCGGCTGATTAGAGTCATCGTTTGCTTGGGA 886

Db 240 ValMe1YsThrCyS1leG1nG1YLeuA1aG1YLeuG1uValH1sArgLeuValLeuG1Y 259
QY 887 GAATTTGAATGAAGAACTTGAAGAACTTGAACAAATCTGCTAGAGGGCTGTC 946
Db 260 GluPheArgAenG1uY1aenLeuG1uYpPheAenP1YsSerAlaLeuG1uG1YLeuCyS 279
QY 947 AATTTGACATTTGAGAAATTCGATTTAGCATTAATCTAGACTTCACTGATATTATT 1006
Db 280 AenLeuThr1leG1nG1uPheArgLeuA1aYrLeuAenP1YrYrYrLeuAenAenP1le1le 299
QY 1007 GACTTATTTAATGTTTGAACAAATGTTTCTTCAATTTCCCTGGAGTGGACTTGA 1066
Db 300 AspLeuPheAenCyS1euthrAenValSerSerPheSerLeuValSerVal1Thr1leG1u 319
QY 1067 AGGGTAAACACTTTTCTTAATTTCCGATGGCAACTTGAATTAATGATTAATCTG 1126
Db 320 ArgValY1sAenPheSerYrAenPheG1YrPglHn1sleuG1uLeuValA1sCyS1Ys 339
QY 1127 TTTGACAGTTTCCACATTTGAAATCTCAATCTCCAAAGGCTTACTTCACTTCCAC 1186
Db 340 PheG1YG1nPheProThrLeuY1sLeuY1sSerLeuY1sArgLeuThrPheThrSerAen 359
QY 1187 AAAGTGGGAATGCTTTTTCAGAAATTTGATCTACCAAGCTTGAAGTTCTAGACT 1246
Db 360 LysG1YG1Y1aenA1aPheSerG1uValA1sPheProSerLeuG1uPheLeuAenPheSer 379
QY 1247 AGAAATGGCTTGAAGTTTCAAGGTGCTTCCAAAGGATTTTGGACAAACGAGCTA 1306
Db 380 ArgAenG1YLeuSerPheY1sG1YCyS1eSerG1nSerAenPheG1YThrThrSerLeu 399
QY 1307 AAGTATTTAGATCTGACCTTCAATGCTGTTATTTACCAATGAGTTCAAACTTGGAGCTTA 1366
Db 400 LysrYrLeuAenPheSerPheAenG1YVal1leThrMetSerSerAenPheLeuG1YLeu 419
QY 1367 GAACAACTTAAGAACTCTGATTTCCAGACTTCCAAATTTGAACAAATGAGTGA 1426
Db 420 GluG1nLeuG1uH1sLeuAenPheG1nH1sSerAenLeuY1sG1nMetSerG1uPheSer 439
QY 1427 GTATCTCATCACTCAGAAACCTTATTAACCTTGAACATTTCTCACTACACAGAGTT 1486
Db 440 ValPheLeuSerLeuA1gAenLeu1leYrLeuAenP1leSerH1sThrH1sThrA1YVal 459
QY 1487 GCTTTCAATGGCACTTCAATGGCTTGTCCAGTCTCCAGACTTGAAGATGGCTGAGCAAT 1546
Db 460 AlaPheAenG1Y1lePheAenG1YLeuSerSerLeuG1uValLeuY1sMetA1aG1YAen 479
QY 1547 TCTTTCCAGAAACCTTCTTCCAGATATCTTACAGAGCTGAGAACTTGACCTTCTG 1606
Db 480 SerPheG1nG1uAenPheLeuProAenP1lePheThrG1uLeuA1rG1aenLeuThrPheLeu 499
QY 1607 GACCTCTCAGTGTCAACTGGAGCACTGTCCTCCAAAGCACTTAACTCACTCCAGT 1666
Db 500 AspLeuSerG1nCyS1nLeuG1nG1uLeuSerProThrAlaPheAenSerLeuSerSer 519
QY 1667 CTTGAGTACTTAATATGACCAACAACACTTCTTTCAATGATAGCTTCTTATPAG 1726
Db 520 LeuG1nVal1leuAenMetSerH1sAenAenPhePheSerLeuAenP1rPheProY1Y1s 539
QY 1727 TGTGTGAACCTCCCTCCAGGTTCTTGAATTAACAGTCTCAATCAATATGACTTCCAAAAA 1786
Db 540 CyS1eAenAenSerLeuG1nVal1leuAenP1YrSerLeuAenH1s1leMetThrSerY1s 559
QY 1787 CAGGAATCAAGCACTTTCCAGAGTCTAGCTTCTTAATCTTACTCGAATGAGCTTT 1846
Db 560 G1nG1uLeuG1nH1sPheProSerSerLeuA1aPheLeuAenLeuThrG1nAenAenPhe 579
QY 1847 GCTTGACTTGTGAACAACAAGTTTCTGCAATGATCAAGACAGAGCAAGCTCTTG 1906
Db 580 AlaCyS1rYrCySg1uH1sG1nSerPheLeuG1nThr1leY1sAenG1nA1gG1nLeuLeu 599
QY 1907 GTGGAAGTTGAACGATGAAATGTGCAACACTTCAGATTAAGAGGCAATGCTGTGCTG 1966
Db 600 ValG1uValG1uArgMetG1uCyS1a1aThrProSerAenP1YsG1nG1nMetProValLeu 619

```

QY 1967 AGTTGATATACACCTGTACATGAATGAACATCATTTGGTGTGCTGCTGAGTGTG 2026
Db 620 SerLeuSenIleThrCysGlnMetAsnIleThrIleIleGlyValSerValLeuSerVal 639
QY 2027 CTTTGTATATTTGTTGTGACAGCTTCTGTCTATTAAGTTCTTATTTTCCACTGATCTTCTT 2086
Db 640 LeuValValSerValValAlaValLeuValIleThrIlePheIleIleMetLeuLeu 659
QY 2087 GCTGCGCATTAAGTTATGTTAGAGGTGAAGAACATCATGATGCTTTGTTATCTACTCA 2146
Db 660 AlaIleCysIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 679
QY 2147 AGCCAGATGAGACCTGGGTGAAGAAATGAGCTAGTAAAGATTAGAAGAGGGGTGCT 2206
Db 680 SerClnIlePheIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 699
QY 2207 CCATTTGAGCTCTGCTTCTACTACAGAGACTTTATTCCTGGGTGTGCTGCTGCTGCAAC 2266
Db 700 ProPheGlnLeuIleCysIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 719
QY 2267 ATCATTCATGAAGGTTTCCATTAAGCGGAAGGTGATGTTGTGTGTGCTGCTGCTGCTGCT 2336
Db 720 IleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 739
QY 2327 ATCCAGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2386
Db 740 IleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 759
QY 2387 AGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2446
Db 760 SerArgIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 779
QY 2447 CAGGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2506
Db 780 GlnAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 799
QY 2507 CTGGGGCGGACACTCTTCTGAGAGACACTGAGAAAGCCCTGCTGCTGCTGCTGCTGCTGCTGCT 2566
Db 800 LeuGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 819
QY 2567 AATCAGAGAGAGACAGTGGGTACAGATGCAATTTGGAGAGAGACACTGCTATC 2620
Db 820 AsnProIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 837

```

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-950-041-8

Alignment Scores:
Score: No.: 0 Length: 799
Percent Similarity: 100.00% Matches: 799
Best Local Similarity: 100.00% Conservative: 0
Query Match: 48.27% Mismatches: 0
DB: 10 Indels: 0 Gaps: 0

US-09-396-985b-1 (1-4868) x US-09-950-041-8 (1-799)

QY 224 ATGAGAGCTGAATTTCTACAAATCCCGACAACTCCCTTCTGACCAAGAACCTGAGC 283
Db 1 MetGlnLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 20
QY 284 CTGAGCTTTAATCCCTGAGAGCAATTGAGCACTATAGCTTTCTTCACTTCCCGAAGCTG 343
Db 21 LeuSerPheAsnProLeuArgHisLeuGlySerIleIleIleIleIleIleIleIleIleIleIle 40
QY 344 CAGGTGCTGATTTATCCAGGTGGAATCCAGCAATTAAGATGAGGAGCTATCCAGAGC 403
Db 41 GlnValLeuAsnProLeuSerArgCysGlnIleIleIleIleIleIleIleIleIleIleIleIle 60
QY 404 CTAGACCACTCTTACCTTATATATGACAGAAACCCATCCAGACTTAGCCCTGGGA 463
Db 61 LeuSerHisLeuSerThrIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 80
QY 464 GCCTTTCTGAGCTATATCAAGTTTACAGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 523
Db 81 AlaPheSerGlyLeuSerSerIleGlnIleValAlaValGlnIleIleIleIleIleIleIleIle 100
QY 524 CTGAGAGAACTCCCGCATTTGACATCTCAAAACTTTGAAGAACTTAATGCTGCTGCTGCTGCT 583
Db 101 LeuGlnAsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 120
QY 584 CTATCCAACTCTTCAATTAATCTGAGTATTTTCTATGCTGACCAATCTAGAGCACTTG 643
Db 121 LeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 140
QY 644 GACCTTTCCAGCAACAAATTAAGTATTTATGACAGACTTGGGGTTCTTACATCA 703
Db 141 AspLeuSerSerAsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 160
QY 704 ATGCCCTACTCAATCTCTTATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 763
Db 161 MetProLeuLeuAsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 180
QY 764 GGTGCAATTTAAGAAATTAAGCTTCAATGACCTTAAAGAAATATTTGATAGTTTA 823
Db 181 GlyAlaPheIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200
QY 824 AATGTAATGAAACTTGTATTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 883
Db 201 AsnValMetIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 220
QY 884 GAGAAATTTAAGAAATGAGGAACTTGAAGAACTTTGAAGAACTTGAAGGAGGCTG 943
Db 221 GlyGlnPheArgAsnGlnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 240
QY 944 TGCATTTGACATTTGAGAAATTCGATTTAGACTTACTTACTTACTTACTTACTTACTTACTT 1003
Db 241 CysAsnLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 260
QY 1004 ATGACTTATTTATTTGTTGACAAATGTTTCTTCAATTTTCCCTGCTGAGTGTGACTTAT 1063
Db 261 IleAspLeuPheAsnCysIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 280

```

[illegible]

Db	661	SerserGlnaapGlnaapTTrpValaArganGlnuLeuValaAsnLeuGlnuGlnuVala	660
Qy	2204	CCTCCATTTCAGCTCTGCGCTTCACATACAGAGACTTTATTCCTCCGCTGGCCATTGCTGCTC	226
Db	661	ProPhePheGlnLeuCyLeuHisIleThrValaArgaPheIleProGlyValaIleIleAla	680
Qy	2264	AACATCATCCATGAAGGTTTCATATAAAGCCGAAAGGATGATTGTGTGTGCCAGAC	232
Db	661	AsnIleIleHisGlnGlyPheHisIleLysSerArgLysValaIleValaValaSerGlnHis	700
Qy	2384	TTTCATCCAGAGCCCGCTGGTGTGTATCTTTGAATATATGATTTGCTCAACCTCGACATTTCTG	238
Db	701	PheIleGlnSerArgTrpCysIlePheGluTrpGlnIleAlaGlnThrTrpGlnPheLeu	720
Qy	2384	AGCAGCTCGTCTGTATCATCTTCATATTCCTTCAGAAAGTGAGAGAAAGCCTGCTCAG	244
Db	721	SerserArgAlaGlyIleIleIlePheIleValleuGlnLysValaGlnuThrLeuLeuArg	740
Qy	2444	CAGCAGGTGGAGCTGTATCCGCTTTCACGACAGAAACATTACTGAGTGGAGAGACAT	250
Db	741	GlnGlnValaGlnLeuTrpArgLeuLeuSerArgaantTrpLysGlnuTrpGlnuSpSer	760
Qy	2504	GTCCCTGGGGCGGCACATCTTCCTCGAGAGACCTCAGAAAAGCCTGCTGATGTAAATCA	256
Db	761	ValleuGlyArgHisIlePheTrpArgLeuArgLysAlaLeuLeuAspGlyLysSer	780
Qy	2564	TGGAATCCAGAAAGAACAGTGGGTTCAGAGATGCATTTGGACGAGAACACATCTATC	2620
Db	761	TrpAsnProGlnuGlnuGlyThrValaGlyThrGlyCysAsnTrpGlnuIleHisSerIle	799
RESULT 3			
US-10-128-166-7			
; Sequence 7, Application US/10128166			
; Publication No. US2003007279A1			
GENERAL INFORMATION:			
; APPLICANT: ARDITI, MOSHE			
; APPLICANT: RAUVAHISHTH, TRIPATHI			
; APPLICANT: SHAH, PREDIMAN K.			
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING			
; TITLE OF INVENTION: TOLL-LIKE RECEPTOR-4			
; FILE REFERENCE: 81476-0255398			
; CURRENT APPLICATION NUMBER: US/10/128,166			
; CURRENT FILING DATE: 2002-04-23			
; NUMBER OF SEQ ID NOS: 7			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 7			
; LENGTH: 799			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-128-166-7			
Alignment Scores:			
Pred. No.:			
Score:			
Percent Similarity:			
Best Local Similarity:			
Query Match:			
Db:	14	Gaps:	0
US-09-396-985B-1 (1-4868) x US-10-128-166-7 (1-799)			
Qy	224	ATGAGCTGAATTTTCTACAAAATCCCGCAACCTTCCTTCACACAAAGACTTGAGC	283
Db	1	MetGlnLeuAsnPheTrpIleProAlaPheLeuProPheSerThrLysAsnLeuAsp	20
Qy	284	CTGAGCTTAATCCCTGAGGACATTTAGGACGATATAGCTTCTTCAGTTTCCAGAACTG	343
Db	21	LeuSerPheAsnProLeuArgHisLeuGlySerTrpSerPhePheSerPheProGlnLeu	40
Qy	344	CAGGCTCTGATTTATCCAGGTGTAAATCCAGACAAATTGAAGATGGGGCATTCAGAGC	403
Db	41	GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnuAspGlyAlaTrpGlnSer	60

404 CTAAGCCACCTCTTACCTTAATATTTGACAGAAACCCCATCCAGATTAGCCCTGGGA 463
Db LeuSerHisLeuSerThrLeuLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
464 GCCTTTTGGACATACAGATTACAGAAAGCTGGCTGGCTGGAGACAAATCTACATCT 523
Db AlaPheSerGlyLeuSerSerLeuGlnLeuValAlaValGluThrAsnLeuAlaSer 100
524 CTAGAGACTTCCCATTTGACATCTCAAAATTTGAAAGAACTTAATGGCTCCACAT 583
Db LeuGluAsnPheProIleGlyHisLeuLeuSerThrLeuGlyLeuAsnValAlaHisAsn 120
584 CTATTCACATCTTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAATCTGAGACCTTG 643
Db LeuIleGlnSerPheLeuLeuProGluThrPheSerAsnLeuThrAsnLeuGlnHisLeu 140
644 GACCTTTCAGACAAAGATTCAAAAGTATTATTTGACAGACCTTGCGGGTCTACATCAA 703
Db AspleuSerSerAsnLeuIleGlnSerIleGlyCysThrAspLeuArgValLeuHisGln 160
704 ATGCCCTTCAATCTCTTTTACACCTGTCCCTGATCCCTAATCACTTATTCACACA 763
Db MetProleuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
764 GGTGCAATTAAGAAATTTAGGCTTCATAGAGCTGATTAAGAAATTTGATAGTTTA 823
Db GlyAlaPheLeuGlyLeuIleArgLeuHisGlyLeuThrLeuArgAsnAspPheSerLeu 200
824 AATGTAATGAATACTTGTATTCAGAGTCTGGCTGGCTTTAGAAATCCATCGTTGGTCTG 883
Db AsnValMetCysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 220
884 GGAATTTTAAAGAAAGAAAGAACTTTGAAAGTTTGACAAATCTGCTCTAGAGGCTTG 943
Db GlyLeuPheArgAsnGlyLeuAsnLeuGlyLeuPheAspLeuSerAlaLeuGlnGlyLeu 240
944 TGCAATTTGACCATTTGAGAAATTCGATTAAGACTTACACTTACCTGATGATAT 1003
Db CysAsnLeuThrIleGluGluPheArgLeuAlaIleThrLeuAspIle 260
1004 ATTTGATTTAATTTGTTTGAACAATGTTTCTTCAATTTCCCTGGAGTGTGATAT 1063
Db IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
1064 GAAAGGTTAAAGAAAGCTTTCTTATTAATTCGATGACCAATTTGATTTAGTTACTGT 1123
Db GluArgValLeuAspPheSerTyrosPheGlyTyrGlnHisLeuGluLeuValAsnCys 300
1124 AAATTTGAGAGTTTCCACATTTGAAACTCAAAATCTCAAAAGGCTTACTTTCACCTCC 1183
Db LysPheGlyGlnPheProThrLeuLeuLeuSerLeuGlyArgLeuThrPheThrSer 320
1184 AACAAAGGTGGAAATGCTTTTTCAGAGTTGATCTTACCAAGGCTTGAATTTCTAGATCTC 1243
Db AsnLysGlyLeuAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340
1244 AGTGAAGATGGCTTGAATTTCAAGGTTGCTGTTCTCAAGGATTTTGGGCAACCGC 1303
Db AGTGAAGATGGCTTGAATTTCAAGGTTGCTGTTCTCAAGGATTTTGGGCAACCGC 1303
341 SerArgAsnGlyLeuSerPheLeuGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
1304 CTAAGATTTTAAAGTCTGAGCTTCAATGGTGTATTAACATGAGTTCAACTCTTGAGC 1363
Db LeuLysTyThrLeuAspLeuSerPheAsnGlyValIleHisMetSerSerAsnPheLeuGly 380
1364 TTAGAACAACTAGAACATCTGGATTTCCAGATTTCCAAATTTGAAACAATAGAGTGT 1423
Db LeuGluGlnLeuGluHisLeuAspPheGlnHisSerSerAsnLeuGlyGlnMetSerGluPhe 400
1424 TCAGATTTCTTATCTCTGAGAAACCTCAATTTACCTTGAACATTTCTCAATCTCACCGCA 1483
Db SerValPheLeuSerLeuArgAsnLeuIleTyThrLeuAspIleSerHisIleThrHisArg 420

1484 GTTGCTTTCAATGGCAATCTTCAATGGCTTTCCAGTCTGAAAGTCTTGAATAAGCTGGC 1543
Db ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 440
1544 AATTTCTTCCAGAAATCTTCTTCCAGATTTCTTCAAGAGCTTGAAATCTTGACCTTC 1603
Db AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 460
1604 CTGGACCTCTCCAGTGTCACTGGAGAGTGTCTCCAAAGCACTTAATCACTCTCC 1663
Db LeuAspLeuSerGlnCysGlnLeuGluLeuLeuSerProHisAlaPheAsnSerLeuSer 480
1664 AGTCTTCAAGTATTAATATGAGCCACAACAATCTTTTTCATTTGATGATACGTTCTTAT 1723
Db SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 500
1724 AAGTGTGAACTCCCTCCAGGTTCTTGATTAACGTCTCAATCAATCAATATGACTTCCAA 1783
Db LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 520
1784 AAACAGAGACTACAGCAATTTTCCAAAGTGTAGCTTTCTTAATCTTACTCAGAAATGAC 1843
Db LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrIleLysAspGlnArgGlnLeu 560
1904 TTGGTGAAGTTGAACGAAATGGAATGTGCAACACCTTCAATTAAGCAGGAGCTGTG 1963
Db LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 580
1964 CTGAGTTGATATCACCTGTCAATGAAATGAATGAACCAATCTTGGTGTGGCTCGTCA 2023
Db LeuSerLeuAsnIleThrCysGlnMetCysAsnThrIleIleGlyValSerValLeuSer 600
2024 GTGCTGTAGATCTGTGTGAGAGTTCTGTGCTATTAAGTTCTATTTTCACTGATGCTT 2083
Db ValLeuValAlaSerValAlaValLeuValLysLysPheTyrPheHisLeuMetLeu 620
2084 CTTCGTGGCTGCAATTAAGTATGTGAGGTGAAACATCTATGATGCTTTGTTATCTAC 2143
Db LeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnIleTyrosAlaPheValIleTyr 640
2144 TCAAGCCAGATGAGAGCTGGGTAAAGATGAGCTAGTAAGATTTGAAGAAGGGGTG 2203
Db SerSerGlnAspGluAspTyrValArgAsnGluLeuValLysAsnLeuGlnGlyVal 660
2204 CCTCCATTTCAAGCTGTGGCTTCACTACAGAGACTTTATTCGGGTGGCCATTTGCTGC 2263
Db ProProPheGlnLeuCysLeuHisIleTyrosArgAspPheIleProGlyValAlaIleAla 680
2264 AACATCATCATGAAGTTTCCATTAAGCCGAAAGGTGATTTGTTGGTGTCCAGAC 2323
Db AsnIleIleHisGluGlyPheHisLysSerArgValIleValAlaValSerGlnHis 700
2324 TTTCATCAGAGCCCTGGTGTATCTTTGAATATGAGATGTCTGACCTGGCAGTTTCTG 2383
Db PheIleGlnSerArgTyrCysIlePheGluTyrGluIleAlaGlnThrTyrGlnPheLeu 720
2384 AGCAGTGTGTATCATCTTCAATTTGCTTGGAGAAAGTGGAGAAAGCCCTGCTCAG 2443
Db SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLeuArg 740
2444 CAGCAGGTGAGCTGACCGCTTCTCAGAGAAACATTAACCTGAGTGGAGAGACGT 2503
Db GlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGluTyrGluAspSer 760
2504 GTCTGGGGGGGCAATCTTCTGAGACGACTCAAGAAAGCCCTGGAGTGAATATCA 2563
Db ValLeuGlyArgHisIlePheTyrArgLeuArgLysValAlaLeuLeuAspGlyLysSer 780
2564 TGAATCCAGAAAGAAAGTGGGTACAGATGCAATTTGGCAGAAAGCAATCTATC 2620

```
Db      781  TTPAsnProGluGlyThrValGlyThrGlyCysAsnTrpGlnGlnAlaThrSerIle 799
RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 58183MO003
; CURRENT APPLICATION NUMBER: US/10/732,563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-732-563-8

Alignment Scores:
Pred. No.:      0      Length:      799
Score:          4141.00    Matches:      799
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%    Mismatches: 0
Query Match:      48.27%      Indels:      0
Db:              16          Gaps:      0

US-09-396-985b-1 (1-4868) x US-10-732-563-8 (1-799)
QY      224  ATGAGAGTGAATTTCTACAAATCCCGACAACTCCCTTCTCAACCAAGAACTTGAC 283
Db      1    MetGluLeuAsnPheTyrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 20
QY      284  CTGAGCTTTTATCCCGAGGCACTTTGAGGCACTTATGAGTCTTCACTTCCCGAACTG 343
Db      21  LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 40
QY      344  CAGGTGCTGATTTATCCAGGTGTGAATCCAGACAATTGAAGATGGGGCATATCAGAGC 403
Db      41  GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaTyrGlnSer 60
QY      404  CTAAAGCACTCTCTACCTTAATATTTGACAGAAACCCCATCCAGAGTTTACCCCTGGGA 463
Db      61  LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
QY      464  GCGTTTCTGACATCAAGTTTACAGAAAGCTGGGTGCTGGAGAGCAAACTTAGCATCT 523
Db      81  AlaPheSerGlyLeuSerSerLeuGlnIlyAsnValAlaValGlnThrAsnLeuAlaSer 100
QY      524  CTAGAGAACTTCCCATTTGACATCTCAAACTTTGAAGAATTATATGGCTCACAAAT 583
Db      101  LeuGlnAsnPheProIleGlyHisIleuLysThrLeuLysGlnLeuAsnValAlaHisAsn 120
QY      584  CTATATCCATCTTTTCAATTTACCTGAGATTTTCTAATCTGACCAATCTTACAGACTTG 643
Db      121  LeuIleGlnSerPheLysLeuProGlnTyrPheSerAsnLeuThrAsnLeuGlnHisIleu 140
QY      644  GACCTTTCAGACAAAGATTCAAAAGTATTTATTTGACAGACTTGCGGGGTTCTACATGA 703
Db      141  AsnLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGln 160
QY      704  ATGCCCTACTCAATCTCTTTTAGACCTGTCCCTGAACTCTATGAACTTTATCCAAACA 763
Db      161  MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
QY      764  GGTGCATTTAAAGAAATTTAGGCTTCATAGAGTGACTTTAAGAAATATTTTGATGTTTA 823
Db      181  GlyAlaPheLysGlnIleArgLeuHisIleLysLeuThrLeuArgAsnAsnPheAspSerLeu 200
```

```
QY      824  AATGTAATGAAAACCTTGATTCAGAGCTGCTGCTGTTTAGAAGTCCATCGTTTGCTTG 883
Db      201  AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeu 220
QY      884  GAGAAATTTAGAAATGAGAAACTTGAAAAGTTTGACAAATCTGCTCTAGAGGCTTG 943
Db      221  GlyIlePheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 240
QY      944  TGCATTTTGCCTTCAAGAAATCCGATTTAGCATCTTACTGACTACCTCGATGATATT 1003
Db      241  CysAsnLeuThrIleGlnGlnPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 260
QY      1004  ATTGACTTATTTATTTGTTGACAAATGTTTCTTCAATTTCCCTGGTGAAGTGTGACTAT 1063
Db      261  IleAspLeuPheAsnLysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
QY      1064  GAAAGGTTAAAGACTTTTCTTAAATTTGGATGGCAACATTTAGAAATTTAGTTAACTGT 1123
Db      281  GlnArgValLysAspPheSerTyrAsnPheGlyTyrGlnHisIleuGlnLeuValAsnCys 300
QY      1124  AAATTTGACAGTTTCCCATGAAATCGAAATCTCTCAAAAGGCTTACTTCACTTCC 1183
Db      301  LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 320
QY      1184  AACAAAGTGGAGATGCTTTTTCAGAAATTGATCTCAAGCCCTTGAGTTTCTAGATCTC 1243
Db      321  AsnLysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeu 340
QY      1244  AGTGAAGATGGCTTGAGTTTCAAGGTTGCTGTTCTCAAGTGAATTTGGGACAACTGAC 1303
Db      341  SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
QY      1304  CTAAAGATTTAATCTGAGCTTCAATGAGTGTATTTACATGAGTTGAAACTTCTGGGC 1363
Db      361  LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrIleSerSerAsnPheLeuGly 380
QY      1364  TTAGAACATCTAGAACATCTGATTTTCCAGATTTCCAAATTTGAACAAATGAGTGAATT 1423
Db      381  LeuGlnGlnLeuGlnHisLeuAspPheGlnHisSerThrAsnLysGlnMetSerGlnPhe 400
QY      1424  TCAATATTTCTATCACTCAAGAACTTCATTTACTTGAACATTTCTACATCTCACACAGA 1483
Db      401  SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisArg 420
QY      1484  GTTGCTTTCAATGSCACTTCAATGGCTGTGTCAGAGTCCGAAGCTTGAAGAAATGGCTGGC 1543
Db      421  ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly 440
QY      1544  AATCTTTCCAGGAAAACCTTCTCCAGATATCTTCAAGAGCTGAGAAACTTGACCTTC 1603
Db      441  AsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPhe 460
QY      1604  CTGAGACTCTCTCAGTGTCAACTGAGAGAGTGTCTCCAAACAGCATTTTAATCACTCTCC 1663
Db      461  LeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSer 480
QY      1664  AGCTTGAGGATCTAAATATGAGGCAACAACCTTTTTCATTTGATGAGTTTCTTAT 1723
Db      481  SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrProTyr 500
QY      1724  AAGTGTCAAGCTCCCTCCAGGTTCTTGATTAAGTCAATCAATCAATATGACTTCCAA 1783
Db      501  LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 520
QY      1784  AAACAGAACTACAGCAATTTTCCAAAGTGTAGCTTTTAAATCTTTACTCAGAAATGAC 1843
Db      521  LysGlnGlnLeuGlnHisIlePheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
QY      1844  TTTGCTTGATCTTTTGAACACCAAGTTCCTGAAAGATTCAGACCAAGAGGACAGCTC 1903
Db      541  PheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleTyrLysArgGlnAspGlnLeu 560
QY      1904  TTGCTGAAGTTGAACGAATGGAATGTGCAACACTTCAGATTAAGCAGGACATCCTGTG 1963
```


|||||
Db 341 SerArgasnGlyLeuSerPheLyGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
QY 1304 CTAAAGATTTAGATCTGAGCTTCAATGCGCTTTATTCACATGAGTTCAAACTTTGGGC 1363
Db 361 LeuLySerIleuAspLeuSerPheAsnGlyValIleThrMetSerSerAspPheLeuGly 380
QY 1364 TTGAACAACATAGACATCTGATTTTCAGACATTCATTAATTGAACAAATAGAGATT 1423
Db 381 LeuGlnIleuGlnIleuAspPheGlnIleSerAsnLeuLySerGlnMetSerGlnPhe 400
QY 1424 TCAGATATTCCTGACCTCAGAACTCATTTACCTTGACATTTCTCATCTACACAGA 1483
Db 401 SerValPheLeuSerLeuArgAsnLeuIleTyThrLeuAspIleSerIleThrArg 420
QY 1484 GTTGCTTCAATGACATCTTCAATGCGCTTGCGAGCTCCAGAGCTTGAAAATGGCTGGC 1543
Db 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLyMetAlaGly 440
QY 1544 AATCTTTCCAGAAACTTCCTCCAGATATCTTCACAGAGCTGAGAACTTGACCTTC 1603
Db 441 AsnSerPheGlnGlnIleuAspPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPhe 460
QY 1604 CTGACCTCTCTCAGTGTCAACTGAGCAGATTGTCTCCAAACAGCATTTAACACTCTCC 1663
Db 461 LeuAspLeuSerGlnCysGlnLeuGlnIleuSerProThrAlaPheAsnSerLeuSer 480
QY 1664 AGCTTTACAGGATCAATAATATAGCCACAACAACCTTTTATTTGATGATGCTTCTTAT 1723
Db 481 SerLeuGlnValLeuAsnMetSerIleAsnAspPheSerLeuAspThrPheProTyr 500
QY 1724 AAGGTCTGAACCTCCCTCAGAGTCTTGATTAAGTCAAGTCAATCAATATGACTTCCAA 1783
Db 501 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnIleMetThrSerIle 520
QY 1784 AAACAGAACTACAGCAATTTTCAAGTATGCTTAAATCTTAAATCTTCAAGATGAC 1843
Db 521 LysGlnIleuGlnIleAspPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
QY 1844 TTTCCTGTACTTTGTAACAACACAGATTTCTGCAATGATGACACAGACAGCAGCTC 1903
Db 541 PheIleCysThrCysGlnIleGlnSerPheLeuGlnIleTyrIleLysAspGlnArgGlnLeu 560
QY 1904 TTGGTGAAGATTGAACGAATGGAATGTGCAACCTTCAGATTAAGCAGGAGCAGCTGTG 1963
Db 561 LeuValGlnValGlnIleGlnMetGlnCysAlaIleThrProSerAspLysGlnGlyMetProVal 580
QY 1964 CTGAGTTGAATATCACCTGTCAAGATGAATAAGACCATCATGTGTGTGCTCTCAGT 2023
Db 581 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 600
QY 2024 GTGCTTGTAGATCTGTGTGAGCAGTTTGGTCTATTAAGTTCTATTTTCACTGATGCTT 2083
Db 601 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheIleLeuMetLeu 620
QY 2084 CTTCGTGGCTGATTAAGATGATGATGAGGTAAGAAACATCTATGATGCTTGTATATCATC 2143
Db 621 LeuAlaGlyCysIleLysTyrGlyArgGlyIleuAsnIleTyraAspAlaPheValIleTyr 640
QY 2144 TCAAGCCAGATAGAGACTGGGTAAGATGAGATGATGAAGATTTGAAGAAAGGGGTG 2203
Db 641 SerSerGlnAspGlnLysAspTyrValArgAsnGlnLeuValLysAsnLeuGlnGlnGlyVal 660
QY 2204 CCTCATTTGAGCTCTGCTTCACTACAGACATTTATTCCTGGGTGGCCATTTGCTGCC 2263
Db 661 ProProPheGlnIleuCysLeuIleTyraAspPheIleProGlyValAlaIleAlaIle 680
QY 2264 AACATCATTCATGAAGTTTCATTAAGCCGAAAGGATGTTGTTGGTGGCCAGAC 2323
Db 681 AsnIleIleIleGlnGlyPheIleIleLysSerArgLysValIleValValValSerGlnIle 700
QY 2324 TTATCCAGACCGGTGTATCTTTGAATATGATGTGCTCAGACCTGCGAGTTTCTG 2383
|||||

Db 701 PheIleGlnSerArgTyrCysIlePheGlnTyrGlnIleAlaGlnThrTyrGlnPheLeu 720
QY 2384 AGCAGTGTGCTGATATCATCTTCAATGCTCTCCAGAAAGGTGAGAAAGCCTGCTCAGG 2443
Db 721 SerSerArgAlaGlyIleIleIlePheIleValLeuGlnIleValGlnIleTyrThrLeuArg 740
QY 2444 CACAGGTGAGAGCTGTATCCGCTCTTCAGCAGAAACATTAACCTGAGTGGAGAGCAGT 2503
Db 741 GlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrPglLysPser 760
QY 2504 GTCTGGGGCGGCACATCTTCTGAGACGACCTCAGAAAACCTGCTGATGTGAATCA 2563
Db 761 ValLeuGlyArgIlePheThrPArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 780
QY 2564 TGGATCCAGAAAGAACAGTGGGTACAGATGCAATTGGCAGGAAAGCAATCATCATC 2620
Db 781 TrpAsnProGlnIleuTyrThrValGlyIleThrGlyCysAsnThrPglIleAlaThrSerIle 799
RESULT 6
US-10-038-854-135
; Sequence 135, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Verne, Corine
; APPLICANT: Eissen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shinkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patlurajan, Meera
; APPLICANT: Gusev, Vladimyr
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Sureh G
; APPLICANT: Raetelli, Luca
; APPLICANT: Caeman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038, 854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683

PRIOR FILING DATE: 2001-04-25
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 411
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 135
 LENGTH: 661
 TYPE: PRT
 ORGANISM: Mus musculus
 US-10-038-854-135

Alignment Scores:
 Pred. No.: 1,11e-54 Length: 661
 Score: 663.00 Matches: 196
 Percent Similarity: 45.68% Conservative: 116
 Best Local Similarity: 28.70% Mismatches: 289
 Query Match: 7.73% Indels: 82
 DB: 15 Gaps: 16

US-09-396-985B-1 (1-4868) x US-10-038-854-135 (1-661)

```

QY 143 GCCATGGCCCTCTCTCTGCG---GTGAGACAGAAAGCTGGAGCCCTGGTGAGGTG 199
DB |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12 AlaleuPheleuAlaSerCyArgAlaThrThreSerSerArgGlnCySileGlnCyS
QY 200 GTTCCTAATATTACTTATCAATGCAATGAGCTGAATTTCTACAAATCCCGACAACTC 259
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 32 GluValAsnIysThrTyAsnCySgluAsnIeuGlyLeuAsnGlnIleProGlyThreIeu 51
QY 260 CCCTTCTCAACCAAGAACTGAGCTGAGCTTAAATCCCTGAGGACATTTAGGACGTAT 319
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 52 ProAsnSerThrGluCySleuGluPheSerPheAsnValIeuProThrIleGlnAsnThr 71
QY 320 AGCTTCTTCACTTCCAGAACTGAGCTGAGCTGATTTATCCAGGTGAGAAATCCAGACA 379
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 72 ThrPheSerArgIleAsnIeuThrPheIeuAsnIeuThrArgGlnIleTyTrp 91
QY 380 ATTGAAGTGGGAGATATCAAGCTTAAGCCACTCTACCTTATATTTGACAGAAAC 439
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 92 IleIleGluAsnThrPheGlnSerGlnHisArgIleAsnThrIleValIeuThrAlaAsn 111
QY 440 CCCATCCAGAGTTAGCCCTGGAGCCCTTTTCTGACATATCAAGTTTACAGAGCTGTG 499
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 112 ProIleuPheMetAlaGluThrAlaIeuSerGlyProIysAlaIeuIysIleuPhe 131
QY 500 GCTGTGAGAGCAATCTAGACTCTCTAGAGAACTTCCCATTTGACATCTGAAAACCTTG 559
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 PheIleGlnThrGlyIleSerSerIleAsnPheIleProIeuHisAsnGlnIysThrIeu 151
QY 560 AAAAGACTTAATGAGGCTCAATCTTATCCATCTTCAATCTTCAATACCTGATTTTCT 619
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 152 GluSerIeuIysIleGlySerAsnHisIleSerSerIleIysIleuProIysGlyPhePro 171
QY 620 AATTCGACCAATCTAGAGCACTTGACCTTCCAGACACAGATTCAAAGTATTTATTCG 679
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 172 Thr---GluIysIeuIysValIeuAsnPheGlnAsnAsnAlaIleHisTyIeuSerIys 190
QY 680 ACAGACTTCGGGGTCTTACATCAAAATGCCCTACTCAATCTCTCTTTAGACCTGTCCCTG 739
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 191 GluAsnSerSerIeuGlnGln-----AlaThrIeuSerIeuAsnIeuAsnIeuAsnIy 208
QY 740 AATCTTATGAATTTATTCACCAAGCTGATTTAAAGAAATTAAGGCTTCATAGCTGACT 799
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 209 AsnAsnIleAlaGlyIleGlnProGlyAlaPheAsnSerAlaValPheGlnSerIeu--- 227
QY 800 TTAAAGATAATATTTGATAGTTTAAATGTAATGAAGAACTTGATTCAGAGCTGTGCTGT 859
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 228 -----AsnPheGlyIyThrGlnAsnIeuIeuValIlePheIysGlyIeuIysAsn 244
QY 860 TTAAAGATTCATCGTTGGTCTTCTGGAGAGATTTTGAAGAAAGAACTTGAAAAGTTT 919
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 245 SerThrIleGlnSerIeuIyPheGlyIyThrPheGlnIysMetAsnAsp---GluAsnIle 263
QY 920 GACAAATGCTGTAGAGGCGCTGTGCAATTTGACATTTGAAGAAATTCGATTTGCAATAC 979
  
```

```

DB 264 SerProAlaValPheGlnIyIyIeuCySgluMetSerValGluSerIleAsnIeu---Gln 282
QY 980 TTAGACTTACTACCTCCAGATGATATATTGACTTATTTATTTGATTCAGAAATGTTCTTCA 1039
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 LysHisTyPhePheAsnIleSerSerAsnThrPheHisCyPheSer----- 298
QY 1040 TTTTCCCTGGAGTGTGACATGATTTGAAGGGTAAAGACTTTCTTATTAATTTGCGATGG 1099
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 299 -----GlyIeu 300
QY 1100 CAACATTAGAAATTAATGTAATCTGTAATTTGACAGCTTTCCACA-----TTGAAATCTC 1153
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 301 GlnIleuIeuAsnIeuIleThrAlaThrHisIeuSerGluIeuProSerGlyIeuValGlyIeu 320
QY 1154 AATCTCTCAAGAGCTTACTTCTTCACTTCCACAAGAGTGGGAAAT-----GCTTTTCA 1207
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 321 SerThrIeuIysIyIeuValIleuSerAlaAsnIysPheGlnIeuIeuCySgluIleSer 340
QY 1208 GAATGTGATCTACCAAGCTTGAAGTT----- 1234
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 341 AlaSerAsnPheProSerIeuThrHisIeuSerIleIySgluAsnThrIysArgIeuGlu 360
QY 1235 -----CTAGATCTCAGTAGAAT 1252
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 361 IeuGlyThrGlyCySleuGluAsnIeuGluAsnIeuIySgluIeuAsnIeuAsnIeuSerHisAsp 380
QY 1253 GCGTTGAGTTTCAAGAGTGTGCTGTCTCAAGATGATTTGGGACACAGGCTTAAAGTAT 1312
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 381 AspIleGluThrSerAspCySAsnIeuGlnIeuIyArgAsnIeuSerHisIleuGlnIser 400
QY 1313 TTATCTGAGCTTCATAGGCTTATTAACATGATTCAGAACTTTCTGAGGCTTGA 1369
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 401 IeuAsnIeuSerTyAsnGluIeuProIeuSerIeuIyThrGluAlaPheIysGlyCyPhePro 420
QY 1370 CAATGAGACATCTGAGATTTCCAGCATTTCCAAATTTGAAACAAATGAGTGAATTTTCTGATA 1429
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 421 GlnIeuIleuIeuAsnIeuAsnIeuAlaPheThrArgIeuIySValIysAsnAlaGlnSerPro 440
QY 1430 TTCTATCACTCAGAAACCTCATTTACTTGTGACATTTTCTCATCTACACAGAGTGTCT 1489
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 441 PheGlnAsnIeuHisIleuIySValIeuAsnIeuSerHisSerIeuIeuAspIleSer 460
QY 1490 TTCAATGGAATCTTCATAGGCTGTGCTGAGCTGTGCAAGCTTGAAGAGCTGGGAGATTTCT 1549
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 461 SerGlnIeuPheAspGlyIeuProIalaIeuGlnHisIeuAsnIeuGlnIyAsnHis 480
QY 1550 TTCAGAGAAACCTTCTT-----CCAGATATCTTCCACAGAGCTGAGAACTTGACCTTC 1603
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 481 PheProIySgluAsnIleGlnIySThrAsnSerIeuGlnThrIeuGlyArgIeuGluIle 500
QY 1604 CTGACCTCTCTCAGTGTCACTGAGCAAGTGTCTCCAAACAGATTTAACTCACTCTCC 1663
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 501 IeuValIeuSerPheCyAsnIeuSerSerIleAspGlnHisAlaPheThrSerIeuIys 520
QY 1664 AGTCTTACGATCAATATGAGGACACAACTTCTTTTCATTTGATGATGACTTTCCTTAT 1723
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 521 MetIeuAsnHisValaIlePheSerHisAsnArg-----LeuThrSerSerIle 537
QY 1724 AAGGTCTGAACCTCCCTCAG-----GTTCTTGATTAACAGTCAATCAATATGACT 1777
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 538 GluAlaIeuSerHisIeuIySgluIyIleTyIeuAsnIeuAlaSerAsnHisIleSerIle 557
QY 1778 TCCAAAAACAGAACTACAGCATTTTCCAAAGTACTGACTTCTTAT----- 1825
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 558 Ile-----LeuProSerIeuIeuProIleIeuSerGlnIyArg 570
QY 1826 -----AATCTTACTCAGAAATGACTTGTGCTTGTGATCTTGAACACAGATTTCTCGAA 1879
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 571 ThrIleAsnIeuArgGlnAsnProIeuAspCySThrIySerAsnIleTyPheIeuGlu 590
QY 1880 TGGATCAAGACACAGAGAGCTCTTGTGGAAGTTGAAGAAATGGAATGTGCAACACT 1939
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
  
```

Db 591 TrpTyrIleGluAsnMetGlnLysLeuGluAspThrGluAspThrLeuCysGluAsnPro 610
Qy 1940 TCAGATAGCAGGCGATCCCTGCTGAGTTTGAATATTCACCTTCAGATGAATAGACC 1999
Db 611 ProLeuLeuArgIleValArgLeuSerAspValThrLeuSerCysSerMetAlaAlaVal 630
Qy 2000 ATCATGTGTGTGTCGCTCAGAGTGTCTGAGTCTGATCTGTTGTCAGGAGTTCTGCTCAT 2059
Db 631 GlyIlePhePheLeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePheAlaVal 650
Qy 2060 AAGTTCAT 2068
Db 651 LysTyrPhe 653
RESULT 7
US-10-037-417-107
Sequence 107, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchenev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Verneil, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 107
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus

US-10-037-417-107
Alignment Scores:
Pred. No.: 1,11e-54 Length: 661
Score: 663.00 Matches: 196
Percent Similarity: 45.68% Conserves: 116
Best Local Similarity: 28.70% Mismatches: 289
Query Match: 7.73% Indels: 82
DB: 15 Gaps: 16
US-09-396-985b-1 (1-4868) x US-10-037-417-107 (1-661)
Qy 143 GCCATGGCCTTCCCTCTCTGCTGCTGAGCAGCAAGCTGGAGCCCTGAGAGTGG 199
Db 12 AlaLeuPheLeuAlaSerCysArgAlaThrThrSerSerArgGlnLysCysIleGluLys 31
Qy 200 GTTCCATATATTAATTATTCATGATGATGAGAGCTGAATTTTCAAAATCCCGACACATC 259
Db 32 GluValAsnLysThrTyrLeuSerCysGluValLeuGlyLeuAsnGluIleProGlyThrLeu 51
Qy 260 CCGTTCGACAGCAAGCAAGCTGAGCTGATTAATCCCTGAGGACATTTAGGAGCTAT 319
Db 52 ProAsnSerThrGluCysLeuGluPheSerPheAsnValLeuProThrIleGlnAsnThr 71
Qy 320 AGCTTCTTCAGTTTCCAGAACTGCAAGTCTGATTTATTCAGAGTGAATTCAGACA 379
Db 72 ThrPheSerArgLeuIleAsnLeuThrPheLeuAspLeuThrArgCysGlnIleTyr 91
Qy 380 ATTGAAGATGGGAGATATCAAGAGCTTAAGCAAGCTTCACTTATATTTGACAGAAAC 439
Db 92 IleIleGluAspThrPheGlnSerGlnIleArgLeuAspThrLeuValIleThrAlaAsn 111
Qy 440 CCGATCCAGAGTTTAAAGCCCGGAGAGCTTTTGGATATCAATGATTTAGCAAGCTG 499
Db 112 ProLeuIlePheMetAlaGluThrAlaLeuSerIleTyrGluValLeuLysIlePhe 131
Qy 500 GCTGTGAGACAAATCTAGATCTGATGAGAACTCCCAATGGACATCCAAACTTTG 559
Db 132 PheIleGlnThrGlyIleSerSerIleAspPheIleProLeuIleAsnGlnLysThrLeu 151
Qy 560 AAGAACTTAATGTGGTCAATCAATTTTCAATTTTCAATTTTCAATTTTCT 619
Db 152 GluSerLeuTyrLeuGlySerAsnIleIleSerSerIleLysLeuProLysGlyPhePro 171
Qy 620 AATGTACAAATCTGAGCAAGTCTTCCAGCAAGAACTTCAAAAGATTTATGTC 679
Db 172 Thr--GluLysLeuLysValLeuAspPheGlnAsnAlaIleIleTyrLeuSerLys 190
Qy 680 ACAGACTTGGGGTTTCAATCAATCAATCCCTTCAATCTCTTTAGACCTGCTG 739
Db 191 GluAspMetSerSerLeuGlnGln-----AlaThrAsnLeuSerLeuAsnLeuAsnGly 208
Qy 740 AATCTTAATGAATTTATTCACCAAGTGCATTTTAAAGAAATTAGGCTTCATAGCTACT 799
Db 209 AsnAspIleAlaGlyIleGluProGlyAlaPheAspSerAlaValPheGlnSerLeu--- 227
Qy 800 TTAAGAAATATTTTGAATGTTTAAATGTAAGAAACTGTATCAAGGCTGCTGCT 859
Db 228 -----AsnPheGlyGlyThrGlnAsnLeuLeuValIlePheLysGlyLeuLysAsn 244
Qy 860 TTAGAGTCCATCTTTGTTGTTCTGGAGAAATTTAGAAATGAGAACTTGGAAAAGTTT 919
Db 245 SerThrIleGlnSerLeuThrPheGlyThrPheGluAspMetAspAsp---GluAspIle 263
Qy 920 GACAAATCTGCTTAGAGGGGCTGTGCAATTTGACATTTGACAAATTTCCGATTCATAC 979
Db 264 SerProAlaValPheGluGlyLeuCysGluMetSerValGlnSerIleAsnLeu---Gln 282
Qy 980 TTAGACTATCACTCCAGATGATATATGACTTATTTATTTGACAAAGTTTCTTCA 1039
Db 283 LysHisTyrPhePheAsnIleSerSerAsnThrPheHisCysPheSer----- 298
Qy 1040 TTTTCCCTGGAGTGAAGTAAATGAAAGGTAAGAACTTTTCTTATTTTGGATGG 1099

```

Db      299 -----GlyLeu 300
QY      1100 CAACATTGAAATTAAGTAAATTTGACAGTTTCCACA-----TTGAAATC 1153
Db      301 GlnGluLeuAspLeuThrAlaThrHisLeuSerGluLeuProSerGlyLeuValGlyLeu 320
QY      1154 AAATCTCAAAAGGCTTACTTTCCTCCAAACAAGGTGGAAAT-----GCTTTTCA 1207
Db      321 SerThrLeuLysLeuValLeuSerAlaSerHisLeuGlnLeuValLeuSer 340
QY      1208 GAAGTCATCTACCAAGCTTGAATT----- 1234
Db      341 AlaSerAsnProSerLeuThrHisLeuSerIleLysGlyAsnThrLysArgLeuGlu 360
QY      1235 -----CTAGATTCAGAGAAT 1252
Db      361 LeuGlyThrGlyCysLeuGluAsnLeuGlnAsnLeuArgLeuAspLeuSerHisAsp 380
QY      1253 GGCTTGAGTTTCAAGGCTGCTTCTCAAAAGTATTTGGACACACAGCTTAAGTAT 1312
Db      381 AspIleGluThrSerAspCysAsnLeuGlnLeuArgAsnLeuSerHisLeuGlnSer 400
QY      1313 TTGAGATTGAGCTTCAATGGTGTATTATCAATGATCAAC--TTCTGGGCTTAGAA 1369
Db      401 LeuAsnLeuSerLysArgGlnProLeuSerLeuThrGluAlaPheLysGluCysPro 420
QY      1370 CAATGAGACATCTGATTTCCAGCATTCCAATTGAAACAATGAGTGAAGTTTCAGTA 1429
Db      421 GlnLeuGlnLeuLeuAspLeuAlaPheThrArgLeuLysValLysAspAlaGlnSerPro 440
QY      1430 TTCTCATCACTCAAGAACTCATTTACTTATTCATGACTGACACAGAGTGTCT 1489
Db      441 PheGlnAsnLeuHisLeuLeuLysValLeuAsnLeuSerHisSerLeuLeuAspIleSer 460
QY      1490 TTCATGAGCATCTTCAATGGCTGTTCGATCTCGAAGCTTGAATAGCTGGCAATCT 1549
Db      461 SerGlnGlnLeuPheAspGlyLeuProAlaLeuGlnHisLeuAsnLeuGlnGlyAsnHis 480
QY      1550 TTCAGAGAAACTTCCT-----CCAGATATCTTCACAGAGCTGAGAACTTGACCTTC 1603
Db      481 PheProLysGlnLysAsnIleGlnLysThrAsnSerLeuGlnThrLeuGlyArgLeuGlnIle 500
QY      1604 CTGAGACTCTCTAGTGTCAACTGAGACAGTGTCTCCAAACAGACTTTAACTCACTGCC 1663
Db      501 LeuValLeuSerThrCysAspLeuSerSerIleAspGlnHisAlaPheThrSerLeuLys 520
QY      1664 AGTCTTCAGGTACTAAATATATGAGCCACACAACTTCTTTCAATTGATGAGTTCTTAT 1723
Db      521 MetMetAsnHisValAspLeuSerHisAsnArg-----LeuThrSerSerSerIle 537
QY      1724 AATGTCTGAACTCCCTCCAG-----GTTCTTGATTAACAGTGCATCACTCATATGACT 1777
Db      538 GlnAlaLeuSerHisLeuLysGlyIleLysLeuAsnLeuAlaSerAsnHisIleSerIle 557
QY      1778 TCCAAAAAACAAGAACTACAGACTTTTCCAAGTAGTCTAGCTTCTTA----- 1825
Db      558 Ile-----LeuProSerLeuLeuProIleLeuSerGlnGlnArg 570
QY      1826 -----AATCTTACTGAAATGACTTTGCTTACTTGTGACACACAGAGTTTCTTCAA 1879
Db      571 ThrIleAsnLeuArgGlnAsnProLeuAspCysThrCysSerAsnIleLysPheLeuGlu 590
QY      1880 TGAGTCAAGACACAGACGAGCTCTTGAGTGAAGTGAAGTGAATGGAATGCAACCT 1939
Db      591 TrpLysLysGlnAsnMetGlnLysLeuGlnAspThrGlnAspThrLeuCysGlnAsnPro 610
QY      1940 TCAGATTAAGACGAGGACATGCTGTGCTGAGTTTGAATATCACTGTGACAGATTAAGACC 1999
Db      611 ProLeuLeuArgGlyValArgLeuSerAspValThrLeuSerCysSerMetAlaAlaVal 630
QY      2000 ATCATTTGGTGTGGCTCTCAAGTGTGCTTGTAGTATCTGTGACAGTTCTGGTCTAT 2059

```

```

Db      631 GlyIlePhePheLeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePheAlaVal 650
QY      2060 AAGTTCTAT 2068
Db      651 LysThrPhe 653

RESULT 8
US-10-114-893-10
; Sequence 10, Application US/10114893
; Publication No. US20020193567A1
GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Spaulding, Vikki
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT APPLICATION NUMBER: US/10/114,893
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; EARLIER FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-893-10

Alignment Scores:
Pred. No.: 2,036-51 Length: 661
Score: 629.50 Matches: 199
Percent Similarity: 45.90% Conservative: 109
Best Local Similarity: 29.66% Mismatches: 274
Query Match: 7.34% Indels: 89
DB: 13 Gaps: 24

US-09-396-985b-1 (1-4868) x US-10-114-893-10 (1-661)
QY      176 AGCTGGAGGCC--TGCGTGAGGTGGTCTTAATTAATTAATCAATGATGAGACTG 232
Db      23 SerThrAspGlnMetCysIleGlnLysGlnAlaAsnLysThrTyraAsnLysGlnAsnLeu 42
QY      233 AATTTTCAAAATCCCGGCAACCTCCCTTCAACCAAGAACTGAGACTGATTT 292
Db      43 GlyLeuSerIleLeuProAspThrLeuProAsnThrThrGlnPheLeuGlnPheSerPhe 62
QY      293 AATCCCTGAGGATTAAGCAGATTAAGCTTCTTCAAGTTTCCAGAACTGCAAGTGTG 352
Db      63 AsnPheLeuProThrIleHisAsnArgThrPheSerArgLeuMetAsnLeuThrPheLeu 82
QY      353 GATTTTCCAGGTGTGAATCCAGACAACTGAAGATGAGGACGAGCTTAAGCCAC 412
Db      83 AspLeuThrArgCysGlnIleAsnThrIleHisGlnAspThrArgHisGlnSerHisGln 102
QY      413 CTCTTCACTTAATATTAAGACGAAACCCATCCAGATTCAGATTAAGCTTGGAGCTTTTCT 472
Db      103 LeuSerThrLeuValLeuThrGlnAsnProLeuIlePheMetAlaGluThrLeuAsn 122
QY      473 GAGCTATCAAGTTTCAAGAACTGAGGCTGTGAGGACCAATATGACATCTTAAGAAC 532
Db      123 GlyProLysSerLeuLysHisLeuPheLeuIleGlnThrGlyIleSerAsnLeuGluPhe 142
QY      533 TTCCCATTTGACATCTCAAAACTTTGAAGAACTTAATGTGCTCAAACTTATTCAA 592

```



```

Db      143  ILeProValHisLeuLeuGluLeuSerLeuTyLeuGlySerAsnHisIleSer 162
Qy      593  TCCTTCAAAATTAAGTATTTTCTTAATCAATCAATTAAGCACTTGACCTTCC 652
Db      163  SerCileysheProlyAspPhePro--AlaArgAsnLeuValIleAspPheGln 181
Qy      653  AGCAACAAGATTAAGATTAATGTCACAGCACTTGCGGGTCTTACATCAATAGCCCTTA 712
Db      182  AsnAsnAlaIleHisTyIleSerArgGluAspMetArgSerLeuGluGln-----Ala 199
Qy      713  CTCGAATCTCTTTAGACCTGCTCCCTGAATCTTAAGCACTTATCCAAACAGGTGCAATT 772
Db      200  IleAsnLeuSerLeuAsnPheAsnGlyAsnAsnValIleGlyIleGluLeuGlyAlaPhe 219
Qy      773  AAGAAATTAGGCTCATAGCTGACTTAAAGAAATATTGATAGTAAATGTAATG 832
Db      220  AspSerThrValPheGlnSerLeu-----AsnPheGlyGlyThrProAsnLeu 235
Qy      833  AAAAAGTGTATCAAGGCTGCTGGCTGTTAGAAAGTCAATGTTGGTCTGGAGAAATT 892
Db      236  SerValIlePheAsnGlyLeuGlnAsnSerThrThrGlnSerLeuThrPhe 255
Qy      893  AGAAATGAAGAACTTGAAAGATTGACAAATCTGCTTAAGAGGCTGTGCATTTG 952
Db      256  GluAspIleAspAsp--GluAspIleSerSerAlaMetLeuGlyLeuGlyLeuMet 274
Qy      953  ACCATTCAGAAATTCGATTAAGCACTTAAGCACTTAAGTATTAATTTAGAC-- 1009
Db      275  SerValGlnSerLeuAsnLeuGln-----GluHisArgPheSerAspIleSerSerThr 292
Qy      1010  TTATTTATTTATTTGACCAATGTTTCTTCAATTTCCCTGGAGTGCATTAAGAAAG 1069
Db      293  ThrPheGlnGlySerPheThrGlnLeuGlnGlyLeuAspLeuThrAlaThrIleLeuGly 312
Qy      1070  GTAAAGACTTTTCTTAATTTCCGATGCGAACATTTAAGATTAAGTTAAC-- 1120
Db      313  LeuProSer-----GlyMetIleGlyLeuAsnLeuGlySlyLeuVal 327
Qy      1121  -----TGTAATTT-----GGACAGTTTCCCAACTTG 1147
Db      328  LeuSerValAsnHisPheAspGlnLeuGlySerAlaAlaAsnPheProSerLeu 347
Qy      1148  -----AACTCAAACTCTGCAAAAGGCTTACTTTCATCTTCCAAAC 1186
Db      348  ThrHisLeuTyIleArgGlyAsnValIlyIleLeuHisIleGlyValGlyCysLeuGln 367
Qy      1187  AAGAGTGGAAATGCTTTTTCAGAAATGATCTACAAAGCTTGAGTTTCTAGATCTAGT 1246
Db      368  LysLeuGlyAsn-----LeuGlnThrIleAspLeuSer 378
Qy      1247  AGAAATGGCTTGAGTTTCAAAAGTGTCTGTTCTCAAAAGTATTTGGGACAAACAGCTTA 1306
Db      379  HisAsnAspIleGluAlaSerAspCysCysSerLeuGlnLeuTyAsnLeuSerHisLeu 398
Qy      1307  AAGTATTTAGTCACTGAGCTTCAATAGTGTATTAACATGATCAAACTTTCTTGAGGC 1363
Db      399  GlnThrLeuAsnLeuSerHisAsnGlnProLeuGlyLeuGlnSerGlnAlaPheGly 418
Qy      1364  TTAGAAACAATAAGCAATCTGGAATTTCCAG-----CAATCCAAATTTGAAACAA 1411
Db      419  CysProGlnLeuGlnLeuLeuAspLeuAlaPheThrArgLeuHisIleAsnAlaProGln 438
Qy      1412  ATGAGTCAAGTTTCA-----GTATTCCTATCACTCAAGAAACCTCATTTAC-----CTT 1459
Db      439  ---SerProPheGlnAsnLeuHisPheLeuGlnValIleuAsnLeuThrTyCysPheLeu 457
Qy      1460  GACATTTCTCACTACTACACACAGAGTTGCTTTCATAGGCACTTCAATGCTGTCCAGT 1519
Db      458  AspHisSerArgAsnGlnHis-----LeuLeuAlaGlyLeuProVal 470
Qy      1520  CTCGAAGCTTTGAAATGGCTGGCAATTTCTTTCAGAGAAATTCCTT-----CCAGAT 1573
Db      471  LeuArgHisLeuAsnLeuGlyAsnHisPheGlnAspGlyThrIleThrIleThrAsn 490

```

```

Qy      1574  ATCTTCACAGAGCTGAGAACTTACCTTCTGACCTCTGACCTCTCACTGATGACAGCAG 1633
Db      491  LeuLeuGlnThrValGlySerLeuGluValIleuIleLeuSerSerCysGlyLeuLeuSer 510
Qy      1634  TTGTCTCCAAACAGCATTTAATCACTCTCCAGTCTTCAAGTACTAATATAGCCACAC 1693
Db      511  IleAspGlnGlnAlaPheHisSerLeuGlyLysMetSerHisValAspLeuSerHisAsn 530
Qy      1694  AACTTCTTT-----TCATTGATTAAGTTTCCTTAT-----AAG 1726
Db      531  SerLeuThrCysAspSerIleAspSerLeuSerHisLeuGlyIleTyIleAsnLeu 550
Qy      1727  TGTCTGACATCCCTCCAGGCTTGTGATTAACAGTCTCAATCAATTAAGCACTTCCAAA 1786
Db      551  AlaIleAsnSerIleAsnIleIleSerProArgLeuLeuProIleLeu----- 566
Qy      1787  CAGAACTACAGCATTTTCCAAAGTACTAGCTTTCTTAATATCTTCAATCAATGACTTT 1846
Db      567  -----SerGlnGlnSerThrIleAsnLeuSerHisAsnProLeu 579
Qy      1847  GCTTGATCTTGTGAACACAGAGTTTCTGCAATGATCAAGACCAAGAGCAAGCTTTG 1906
Db      580  AspCysThrCysSerAsnIleHisPheLeuThrTyIleGlyAsnLeuHisSlyLeu 599
Qy      1907  GTGGAGTTGACGAATGGAATGGAATGCAACCTTCAGATTAAGCAGGCGATGCTGCTG 1966
Db      600  GlnGlySerGlnGluThrThrCysAlaAsnProProSerLeuArgGlyValIlyIleSer 619
Qy      1967  AGTTGAAATATCACTGTCCAGATGAATTAAGACCAATGTTGTGTGCTGCTTCAAGTGTG 2026
Db      620  AspValIysLeuSerCysGlyIle-----ThrAlaIleGlyIlePhePheLeuIleVal 637
Qy      2027  CTGTGATCACTGTGTGAGCAATTCGTGTCTAT 2059
Db      638  PheLeuLeu-----LeuLeuAlaIleLeuLeuPhe 647

RESULT 9
US-10-038-854-134
: Sequence 134, Application US/10038854
: Publication No. US20040022781A1
: GENERAL INFORMATION:
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Li, Li
: APPLICANT: Molenc, Adam R
: APPLICANT: Vermet, Corine
: APPLICANT: Eisen, Andrew J
: APPLICANT: Liu, Xiaohong
: APPLICANT: Malyankar, Uriel M
: APPLICANT: Shmukets, Richard A
: APPLICANT: Tchernen, Velizar
: APPLICANT: Spaderna, Steven K
: APPLICANT: Gorman, Linda
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Paturajan, Meera
: APPLICANT: Gusev, Vladimir Y
: APPLICANT: Gangoli, Raha A
: APPLICANT: Guo, Xiaojia S
: APPLICANT: Shenoy, Suresh G
: APPLICANT: Rastelli, Luca
: APPLICANT: Caeman, Stacie J
: APPLICANT: Boldog, Ferenc
: APPLICANT: Burgess, Catherine E
: APPLICANT: Edinger, Shlomit R
: APPLICANT: Ellerman, Karen
: APPLICANT: Gunther, Erik
: APPLICANT: Smithson, Glenda
: APPLICANT: Millet, Isabelle
: APPLICANT: MacDougall, John R
: TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
: FILE REFERENCE: 21402-230
: CURRENT APPLICATION NUMBER: US/10/038, 854
: CURRENT FILING DATE: 2003-01-22

```



```

Qy 1175 TTCACTTCCAAAGAGTGGAAATGCTTTTCAGAAAGTGAATCTACCAAGCCTTGAGTTT 1234
Db 358 -----HisLeuLysSerLeuGluTyr 364
Qy 1235 CTGAATCTCAGTGAAGAT-----GGCTTGAGTTTCAAGGTTGCTGTTCT 1279
Db 365 LeuAspLeuSerGluAsnLeuMetValGluGluTyrLeuLysAsnSerAlaCys----- 382
Qy 1280 CAAGTGAATTTGGGACACACAGCCTTAAGTATTTAGATCTGAGCTTCAATGAGTGTATT 1339
Db 383 -----GluAspAlaTyrProSerLeuGlnThrLeuIleLeuValGlnAsn----- 397
Qy 1340 ACCATGAGTTCAAACTTCTGGGCTTAGAACACTAGACATCTGAGATTTCAGCATTC 1399
Db 398 -----HisLeu-----Ala 400
Qy 1400 AATTGAAACAAGAGTGAAGTTTTCAGTATTTCTATCACTGACAGAACTTCATTTACCTT 1459
Db 401 SerLeuGluLysThrGlu-----ThrLeuLeuThrLeuLysAsnLeuThrAsnIle 418
Qy 1460 GACATTTCTCATCTACACACAGAGTTGCTTCAATGAGCATCTTCAATGGCTTGCCAGT 1519
Db 419 AspIleSerLys----- 422
Qy 1520 CTCGAAGCTTGAAAGATGGCTGGCAATCTTTCCAGAAACTTCCTCAGATATCTTC 1579
Db 423 -----AsnSerPheHisSer-----MetProGluThrCys 432
Qy 1580 ACAGAGCTGAGAACTTGACCTTCCTGGACCTCTCTCAGTGTCAACTGAGACAGTTGCT 1639
Db 433 GlnTrpProGluLysMetLysTyrLeuAsnLeuSerSerThrArgGlnIleHisSerValThr 452
Qy 1640 -----CCAAACAGCATTTAACTCACTCTCCAGTCTTCAGAGTAAATAATGAGCAC 1690
Db 453 GlyCysIlePro-----LysThrLeuGluIleLeuAspValSerAsn 466
Qy 1691 AAC-----AACTTCTTTCATGTGAT----- 1711
Db 467 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGluLeuTyrIleSerArg 486
Qy 1712 -----ACGTTTCCT-----TATAAGTGTGAACTCCCTCCAGGTTCTTGATTAC 1756
Db 487 AsnLysLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValLeuLysIle 506
Qy 1757 AGCTCAATCACTATATGACTTCCAAAAACAGAACTACAGCACTTTTCCAAAGTGTATA 1816
Db 507 SerArgAsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe-----HisThrLeu 525
Qy 1817 GCTTCTTAATCTTACTCAGATGACTTGTGCTGTTGTTGTTGAAACACAGAGTTTCCTG 1876
Db 526 LysThrLeuGluAlaGlyGlyAsnAsnPheIleCysSerCysGluPheLeuSerPheThr 545
Qy 1877 CAATGATCAAGACAGACAGGACGCTTGTGTGAAGTT-----GAAACA 1921
Db 546 Gln-----GluGlnGlnAlaLeuAlaLysValLeuIleAspTyrProAlaAsn 561
Qy 1922 ATGGAATGTGCAACACTTTCAGATAGCAGGCGATGCTGTGAGATTGAATATCAC 1981
Db 562 TyrLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgSer 581
Qy 1982 -----TGTCAAGATGAATTAAGACATCTTGTTGGTGTGGGTCTCAGTGTGTTGTA 2032
Db 582 ValSerGluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeuPheLeuLeu 601
Qy 2033 GTATCTGTTTGAAGACTCTGCTATATAGTTTAT-----TTTCACCTGATGCTTCTT 2086
Db 602 IleLeuLeuThrGlnValLeuLeuCysHisArgPheHisGlyLeuTyrTyrMetLysMetCet 621
Qy 2087 GCTGCTGCATTAAGTATGTTAAG-----GGTGAACAATC---TAT 2135
Db 622 TrpAlaTrpLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTyr 641
Qy 2126 GATGCTTTGTTATCTACTCAAGCAGATGAGAGCTGGTGAAGGAATGACTGTGTAAG 2185

```

```

Db 642 AspAlaPheValSerTyrSerGluArgAspAlaTyrTrpValGluAsnLeuMetValGln 661
Qy 2186 AATTAGAAAGAGGGGCGCTCCATTTTCAGTCTGCTCTCACTACAGACATTTATCCC 2245
Db 662 GluLeuGlnAsnPheAsnProProPheLysLeuCysLeuHisLysArgAspPheIlePro 681
Qy 2246 GGTGTGGCATTTGCTGCGCAACATCATCATGAAGTTTCCATAAAGCCGAAAGTAT 2305
Db 682 GlyLysTrpIleIleAspAsnIleIle-----AspSerIleGluLysSerHisLysThrVal 700
Qy 2306 GTTGTGTGTCCCAAGCACTTCATCCAGAGCGCGTGTATCTTTGAATATGATGATGCT 2365
Db 701 PheValLeuSerGluAsnPheValLysSerGluTyrProCysLysTyrGluLeuAspPheSer 720
Qy 2366 CAGACTGGCAGATTCTTGAGCAGTCGTGCTGGTATCATCTTCATTTGCTCCGAAAGTGT 2425
Db 721 HisPheArgLeuPheGluGluAsnAsnAspAlaAlaIleLeuIleLeuGluProIle 740
Qy 2426 GAGAAAGCCGTGCTCAGACAGCAG-----GTGAGCTGTACCGCTTCTCAGAGGAACT 2482
Db 741 GluLysLysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThr 760
Qy 2483 TACCTGAGTGGGAGGAGCAGATGTCTCGGGGCGGACATCTTCTGAGACGACTGAGAAA 2542
Db 761 TyrLeuGluTrpProMetAspAlaGlnArgGluGluPheTrpValAsnLeuArgAla 780
Qy 2543 GCCCTG 2548
Db 781 AlaIle 782

RESULT 11
US-10-456-947-46
; Sequence 46, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456,947
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 784
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-10-456-947-46

Alignment Scores:
Pred. No.: 7.54e-49 Length: 784
Score: 603.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 7.03% Indels: 219
DB: 15 Gaps: 38

US-09-396-985B-1 (1-486b) x US-10-456-947-46 (1-784)
Qy 245 ATCCCGCAACAACGCTTCTTCAACAAGACCTGAGCTTTAATCCCTGAGG 304
Db 46 IleProSerGlyLeuThrGlnAlaValLysSerLeuAspSerAsnAsnArgIleThr 65
Qy 305 CATTTAGACAGCTTATGACTTCTTCACTTCCAGAACTGAGAGGCTGTGATTTACAGG 364
Db 66 TyrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValIleThrSer 85

```

```

QY 365 TGTGAATCCAGACATTGAAGATGGGACATATCAGACCTTAAGCCACTTCTACCTTA 424
Db 86 AsnGly11LeuasnThr11GluGluAspSerPheSerLeuGlySerLeuGluHisLeu 105
QY 425 ATATTGACAGGAAACCCCATCCAGATTAGCCCTGGAGCCTTTCTGACATACAGT 484
Db 106 AspLeuSerYrAnnyrLeuSerAsnLeuSerSerSerThrPheLysProLeuSerSer 125
QY 485 TTACAGAACTG----- 508
Db 126 LeuThrPheLeuAsnLeuLeuGlyAsnProYrLysThrLeuGlyLutThrSerLeuPhe 145
QY 509 ACAAAATCAGATCTCAGAGAACTCCCATGGACATCTCAAAACT----- 556
Db 146 SerHisLeuThrLysLeuGlnHisLeuAspArgValGlyAsnMetAspThrPheThrLysIle 165
QY 557 -----TTGAAGAACTTAATGTGGCTCAACATCTT 586
Db 166 GlnArgLysAspPheAlaGlyLeuThrPheLeuGluGluLeuGluHisLeuAlaSerAsp 185
QY 587 ATCCAAATCTTTCAAAATTAAGTATTTCTATCTGACCAATCTAGACACTTGGAC 646
Db 186 LeuGlnSerYrGlu-----ProLysSerLeuSerSerLeuGlnAsnValSerHisLeuIle 204
QY 647 CTTTCCAGCAACAAG-----ATTCAAGATAT 673
Db 205 LeuHisMetLysGlnHisIleLeuLeuLeuGluHisLeuValAspValThrSerSerVal 224
QY 674 TATTGACAGACCTTGGGTTCTACATCAAAATGCCCTACTCAATCTCTTTAGACCTG 733
Db 225 GluCysLeuGluLeuLeuArg-----AspThr 232
QY 734 TCCCTGAATCCTTAAGACTTT-----ATCCACAGAGTGCATTTAAGAAATTAAGCTT 787
Db 233 AspLeuAspThrPheHisPheSerGluLeuSerThrGlyLutThrAsnSerLeu---Ile 251
QY 788 CATAGACGATCTTAAGAAAT-----AATTTGATAGTTTA---AATGATAGAAA 835
Db 252 LysLysPheThrPheHisPheAsnValLysIleThrAspGluSerLeuPheGlnValMetLys 271
QY 836 ACTGT-----ATTCAAGGTCTGGCTGGTTAGAAAGTCATCGTTGGTTCTG----- 883
Db 272 LeuLeuAsnGlnHisLeuSerGlyLeuLeuGluLeuGluPheAspAspCysThrLeuAsnGly 291
QY 884 ---GGAGAAATTAAGAAAGAACTTGGAAAAGTTTGCAAAATCGCTCTAGAGGAC 940
Db 292 ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyLysValGlu--- 310
QY 941 CTGACATTTTGAACATTAAGAAATTCGATTTAGCA-----TACTTAGCTACTACTC 994
Db 311 -----ThrLeuThrHisArgArgLeuHisIleProAspPheThrLeuPheThr----- 326
QY 995 GATGATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1054
Db 327 ---AspLeuSerThrLeuThrSerLeuThrGluArgValLys-----Arg 340
QY 1055 GTGACTATTAAGAAAGGATAAGACTTTTCTTAATTAATTCGATGAGCAACATTAGAAATTA 1114
Db 341 IleThrValGluAsnSerLysValPhe-----Leu 350
QY 1115 GTTAACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1174
Db 351 ValProCysLeuLeuSerGln----- 357
QY 1175 TTCACTTCCAAACAAAGGTGGAAATGCTTTTTCAGAAATGATCTACAAAGCTTGAGTTT 1234
Db 358 -----HisLeuLysSerLeuGluLutYr 364
QY 1235 CTAGATCTCAGTGAAT-----GGCTTGAGTTTCAAAAGTTGCTGTTCT 1279
Db 365 LeuAspLeuSerGluAsnLeuMetValGluGluLutYrLeuLysAsnSerAlaCys----- 382

```

```

QY 1280 CAAAGTATTTTGGGCAACACAGCTTAAGATTAATTAATTAATTAATTAATTAATTA 1339
Db 383 -----GluAspAlaThrProSerLeuGlnThrLeuHisLeuAspArgLysAsn----- 397
QY 1340 ACCATAGATTCAAACTTTCTGGGCTTAAGAAACATGAACATTTGGATTTCCAGCATTC 1399
Db 398 -----HisLeu-----Ala 400
QY 1400 AATTTGAACAAATGAGTGAAGTTTCAGTATTCCTATTCACGTGAACACCTTACTTACCTT 1459
Db 401 SerLeuGluLutThrGlyLut-----ThrLeuThrThrLeuLysAsnLeuThrAsnIle 418
QY 1460 GACATTTCTCATCTGACACACAGAGTTGCTTTCAATGGCATTTCAATGGCTTGTCCAGT 1519
Db 419 AspIleSerLys----- 422
QY 1520 CTGAAAGTCTTGAATAATGCTGCGCAATTTCTTTCCAGGAAAATCTTCCCTGCAATCTTC 1579
Db 423 -----AsnSerPheHisSer-----MetProGluThrCys 432
QY 1580 ACAGAGCTGAGAAACTTGAACCTTCTGGAACCTTCTCAGTGTCAAGTGCAGAGAGTTGCT 1639
Db 433 GlnThrProGluLutMetLysYrLeuAsnLeuSerSerThrArgIleHisSerValThr 452
QY 1640 -----CCACAGCATTTAATCACTCTCCAGTCTTTCAGGTACTTAATATGAGCCAC 1690
Db 453 GlyCysIlePro-----LysThrLeuGluHisLeuAspValSerAsn 466
QY 1691 AAC-----AAGTTCTTTTCAATGAT----- 1711
Db 467 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGluLeuYrHisLeuSerArg 486
QY 1712 -----ACGTTTCT-----TATTAAGTGTGAACCTTCCGAGTTTCTTATTAAC 1756
Db 487 AsnLysLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValLeuLysIle 506
QY 1757 AGTCTCAATCAACAATTAATGATCTTCCAAAACACAGAACTACAGCATTTTCCAAAGTACTA 1816
Db 507 SerArgAsnAlaIleThrThrPheSerLysGluGlnLeuAspPhePhe---HisThrLeu 525
QY 1817 GCTTTCTTAATCTTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1876
Db 526 LysThrLeuGluLutAlaGlyLysAsnAsnPheHisCysSerCysGluPheLeuSerPheThr 545
QY 1877 CAATGATCAAGACCCAGAGAGCTCTGTGTGAAGTT-----GAACGA 1921
Db 546 Gln-----GluGlnGlnAlaLeuAlaLysValLeuHisLeuThrProAlaAsn 561
QY 1922 ATGGAATGTCACACCTTCAAGATTAAGACAGGACATGCTGTGATGATTTGAATATCAC 1981
Db 562 TyrLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581
QY 1982 -----TGTCAGATGAATTAAGACCATTTGCTGTGTGCTGTGCTGTGCTGTGCTGTA 2032
Db 582 ValSerGluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeuPheLeuLeu 601
QY 2033 GTATCTGTGTGAGAGTCTGCTATTAAGTTCTAT-----TTTCACTGATGATCTTCT 2086
Db 602 IleLeuLeuThrGlyValLeuCysHisArgPheHisIleGlyLeuThrPyrMetLysMetMet 621
QY 2087 GCTGCTGATTAAGATATGATGATGAT-----GGTGAACAAATC---TAT 2125
Db 622 ThrAlaThrPheGluGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysEyr 641
QY 2126 GATGCTTTTGTATCTACTGACAGCAGATGAGGACTGGGTGAAGATAGCTGTGAAG 2185
Db 642 AspAlaPheValSerYrSerGluArgAspAlaYrThrValGluAsnLeuMetValGln 661
QY 2186 AATTTAAGAAAGGGGCTCCATTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2245
Db 662 GluLeuGluAsnPheAsnProPheLysLeuLysLeuHisIleLysArgAspPheThrIlePro 681
QY 2246 GGTGTGCCCATTTGCTGCCAACATCATCATGAAGATTTCATTAAGCCGAAAGGTGATT 2305

```

```

Db      682 GlyLysTrpIleIleAspAsnIleLe--AspSerIleGluLysSerHisLeuThrVal 700
Qy      2306 GTTGCGGTGTCCTCCAGCACTTATCCAGCGCGGTGATCTTTGATATGAGATTGCT 2365
Db      701 PheValLeuSerGluAsnPhenValIysSerGluTrpCysLysTyrGluLeuAspPheSer 720
Qy      2366 CAGACTGGCAGATTCTTGAGCAGTCGTGTCGTATCATCTTCATCTGTCCTCAGAGAGTG 2425
Db      721 HisPheArgLeuPheGluGluAsnAsnAspAlaIleLeuIleLeuLeuGluProIle 740
Qy      2426 GAGAAGACCTTGCTCAGCAGCAG--GTGAGCTGTACCGCTTCTCAGACGAGAACT 2482
Db      741 GluLysValAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrIleThr 760
Qy      2483 TACTGAGGTGGAGGAGCAGTGTCTGTGGGGGCGGACATCTTCTGAGACGACTCAGAAA 2542
Db      761 TyrLeuGluTrpPrometAspGluAlaGlnArgGluGlyPheTrpValAsnLeuArgAla 780
Qy      2543 GCCCTG 2548
Db      781 AlaIle 782

```

```

RESULT 12
US-10-095-627-12
; Sequence 12, Application US/10095627
; Publication No. US20030027260A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
            Godowski, Paul J.
            Gurney, Austin
            Mark, Melanie
            Yang, Ruey-Bing
TITLE OF INVENTION: Human Toll Homologues
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,627
FILING DATE: 11-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/105,413A
FILING DATE: 26-Jun-1998
APPLICATION NUMBER: 60/083322
FILING DATE: 28-Apr-1998
APPLICATION NUMBER: 60/065311
FILING DATE: 13-Nov-1997
APPLICATION NUMBER: 60/062250
FILING DATE: 17-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marechang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1154-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

```

US-10-095-627-12
Alignment Scores:
Pred. No.: 9,44e-49 Length: 784
Score: 602.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 7.02% Indels: 219
DB: 14 Gaps: 38
US-09-396-985B-1 (1-4868) x US-10-095-627-12 (1-784)
Qy      245 ATCCCGCAGACCTCCCTTCACCAAGAACTGACCTGACCTTAATCCCTGAGG 304
Db      46 IleProSerGlyLeuThrGluAlaValLysSerLeuAsnLeuSerAsnAsnArgIleThr 65
Qy      305 CATTAGCAGCTATAGCTTCTTCAAGTTTCCAGAACTGCAAGTGTCTGATTTACAGG 364
Db      66 TyrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValLeuThrSer 85
Qy      365 TGTGAATCCAGCAATTGAAGATGGGCATATGACGCTTACGCCACCTCTACCTTA 424
Db      86 AsnGlyIleAsnThrIleGluGluAspSerPheSerSerLeuGlySerLeuGlnHisIle 105
Qy      425 ATATTGACAGAGAAACCCCATCCAGAGTTTAGCCCTGGAGCCTTTCTGAGTATCAAGT 484
Db      106 AspLeuSerTyrAsnTyrLeuSerAsnLeuSerSerSerTrpPheLysProLeuSerSer 125
Qy      485 TTACAGAGCTG-----GTGGCTGTGAG 508
Db      126 LeuThrPheLeuAsnLeuLeuGlyAsnProTyrLysThrLeuGluGluThrSerLeuPhe 145
Qy      509 ACAATATGACATCTCTAGAGAACTTCCCATATGCAATCTCAAACT----- 556
Db      146 SerHisLeuThrLysLeuGlnIleLeuArgValGlyAsnMetCysPheThrPheThrLysIle 165
Qy      557 -----TTGAAGAAGTTAATGTGGCTCACAATCTT 586
Db      166 GlnArgLysAspPheAlaGlyLeuThrPheLeuGluGluLeuGluIleAspAlaSerAsp 185
Qy      587 ATCCATCTTTCAATTAATCTGAGTATTTTCTAATCTGACCAATCTAGAGCACTGAGC 646
Db      186 LeuGlnSerTyrGlu---ProLysSerLeuLysSerIleGlnAsnValSerHisLeuIle 204
Qy      647 CTTTCCAGCAACAAG-----ATTCAAAGATTT 673
Db      205 LeuHisMetLysGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerVal 224
Qy      674 TATTGACAGACTTGGCGGTTTCAATCAATGCCCCCTACTCAATCTCTTAGACCTG 733
Db      225 GluCysLeuGluLeuArg-----AspThr 232
Qy      734 TCCCTGAATCTTAGACCTT-----ATCCAACAGGTGCATTTAAGAATTAGGCTT 787
Db      233 AspLeuAspThrPheHisPheSerGluLeuSerThrGlyIleThrAsnSerLeu---Ile 251
Qy      788 CATAGCTGACTTAAGAAAT-----AATTTGATAGTTTA---AATGTAATGAAA 835
Db      252 LysLeuPheThrPheArgAsnValLysIleThrAspLysLeuSerPheGlnValMetLys 271
Qy      836 ACTTGT-----ATCAAGGTCTGGCTGGTTTGAAGTCCATGCTGTTGGTTCTG----- 883
Db      272 LeuLeuAsnGlnIleSerGlyLeuLeuGluLeuGluIlePheAspSerCysThrLeuAsnGly 291
Qy      884 ---GGAGATTTTGAAGAAATGAGAACTTGGAAGAAAGTTTGAACAATCTGCTTAGAGGCG 940
Db      292 ValGlyAsnPheArgLysSerAspAsnAspArgValIleAspProGlyLysValGlu--- 310
Qy      941 CTGTCGAATTTGACCAATGAGAAATCCGATTTGCA-----TACTAGACTTACTACTC 994
Db      311 -----ThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyr----- 326
Qy      995 GATGATATTATTGACTTATTATTATTGTTTGAACAATGTTTCTTCAATTTCCCTGGTAGT 1054

```

```

Db      327  ---AspLeuSerThrLeuTyrSerLeuThrGluArgValLys-----Arg 340
Qy      1055 GTGACTATGAAAGGATTAAGACTTTTCTTAATTAATTCGATGCAACATTGAAATTA 1114
Db      341  ILeuThrValGluAsnSerLysValPhe-----Leu 350
Qy      1115 GTTAAGCTGTAATTAATTGGACGATTGCCACATTGAAACTCAAAATCTTCAAAAGGCTTACT 1174
Db      351  ValProCysLeuLeuSerGln----- 357
Qy      1175 TTCACTTCACAAAGGTTGGAAATGCTTTTTCAGAAAGTTGATCTACCAAGCCTTGAGTTT 1234
Db      358  -----HisLeuLysSerLeuGluTyr 364
Qy      1235 CTAGATCTCAGTAGAAT-----GGCTTGAGTTTCAAAAGTTGCTGTCTTCT 1279
Db      365  LeuAspLeuSerGluAsnLeuMetValGluGluTyrLeuLysAsnSerAlaCys----- 382
Qy      1280 CAAGGTGATTTGGGACACACGAGCTTAAGTAATTAAGTCTGAGCTTCGAATGATGTTATT 1339
Db      383  ---GluAspAlaATPrProSerLeuGlnThrLeuLysLeuArgGlnAsn----- 397
Qy      1340 ACCATGAGTTCAAACTTCTGGGCTTAGAACACACTGACATTCGATTTCCACAGATTCC 1399
Db      398  -----HisLeu-----Ala 400
Qy      1400 AATTGAAACAATGAGTGAATTTTCAGTATTCCTATACCTACAGAAACTTCATTACCTT 1459
Db      401  SerLeuGluLysThrGlu-----ThrLeuLeuThrLeuLysAsnLeuThrAsnLe 418
Qy      1460 GACATTTCTCACTACACACAGAGTTGCTTTCAATGGCATCTTCATATGGCTTGCCAGT 1519
Db      419  AspLeuSerLys----- 422
Qy      1520 CTCGAAAGCTTGAAATGCTGGCAATTCCTTCCAGAGAAACTTCCTCCAGATATCTTC 1579
Db      423  -----AsnSerPheHisSer-----MetProGluThrCys 432
Qy      1580 ACAAGCTGAGAAACTTGACCTTCCTGACCTCTCTGACAGTTCACACTGAGACAGTTCCT 1639
Db      433  GlnTrpProGluLysMetLysTyrLeuAsnLeuSerSerThrArgGluLeuSerValThr 452
Qy      1640 -----CCAACGACATTTAACTCACTCTCCAGTCTTCAGTACGTAATATATAGCCAC 1690
Db      453  GlyCysLeuPro-----LysThrLeuGluIleLeuAspValSerAsn 466
Qy      1691 AAC-----AACTCTTTTCATTGGAT----- 1711
Db      467  AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGluLeuTyrIleSerArg 486
Qy      1712 -----ACGTTTCCT---TATAAGTCTGGAACCTCCCTCCAGGTTCTTGATTAC 1756
Db      487  AsnLysLeuMetTrpLeuProAspAlaSerLeuLeuProMetLeuValLeuLysIle 506
Qy      1757 AGTCTCAATCATATGATGACTCTCAAAAACAGAACTACAGCAATTTTCCAAGTATGCTA 1816
Db      507  SerArgAsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe---HisThrLeu 525
Qy      1817 GCTTTCTTAATCTTACTCAGAAATGACTTTCCTGTTACTTGTGACACACAGAGTTTCTCG 1876
Db      526  LysThrLeuGluAlaGlyLysAsnAsnPheIleCysSerCysGluPheLeuSerPheThr 545
Qy      1877 CAATGATCAAGACGACGACGCTCTTGAGAAAGT-----GAACGA 1921
Db      546  Gln-----GluGlnGlnAlaLeuAlaLysValLeuLysLeuLeuLeuLeuLeuLeu 561
Qy      1922 ATGGAATGTCACACCTTCAGATTAAGACGAGGCAATGCTGTGCGAGTTGAATATACAC 1981
Db      562  TyrLeuCysAspSerProSerHisValArgGluGlnGlnValGlnAspValArgLeuSer 581
Qy      1982 -----TGTCAAGATGAATTAAGACATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGT 2032

```

```

Db      582  ValSerGluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeuPheLeu 601
Qy      2033 GTATCTGTTTACACAGTTCTGCTGTCTAATAGTCTAT-----TTTCAACCTGATGCTTCT 2086
Db      602  IleuLeuLeuThrGluValLeuCysHisArgPheIleGluLeuTyrLysMetLysMetMet 621
Qy      2087 GCTGAGCTGCAATAAAGTATGTTAGT-----GGTCAAAACATC---TAT 2125
Db      622  TrpAlaTrpLeuGlnAlaLysArgLysProArgLysValaProSerArgAsnIleCysTyr 641
Qy      2126 GATGCTTTGTATCTTACTCAAGCCAGAGATGAGAGCTGGGTAAAGAACTGATGAAG 2185
Db      642  AspAlaPheValSerTyrSerGluArgAspAlaTyrTrpValGluAsnLeuMetValGln 661
Qy      2186 AATTGAAAGAAGGGGCTGCATTCAGCTTCGCTTCCTCACTACAGAGACTTATATCCC 2245
Db      662  GluLeuGluAsnPheAsnProProPheLysLeuCysLeuHisLysAspAspPheIlePro 681
Qy      2246 GGTTGGCCATGCTGCTGCACATCATTCATGAAAGTTTCCATAAAGCCGAAAGTGATT 2305
Db      682  GlyLysTrpIleIleAspAsnIleIle---AspSerIleGluLysSerHisLysThrVal 700
Qy      2306 GTTGTGTTGCCAGACATTCATCCAGAGCCGCTGTTATCTTTGAATATGAGATTCT 2365
Db      701  PheValLeuSerGluAsnPheValLysSerGluTyrCysLysTyrGluLeuAspPheSer 720
Qy      2366 CAGACCTGGCAGTTTCTGACACAGTCGTCGTGATCATCTTCATTTGCTTCGAGAAAGTG 2425
Db      721  HisPheArgLeuPheAspGluAsnAsnAspAlaIleLeuLeuLeuLeuGluProIle 740
Qy      2426 GAGAAACCTGCTGCTCAGGACAGCAG--GTGAGCTGTACCGCTTCACACAGAACT 2482
Db      741  GluLysLysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThr 760
Qy      2483 TACTGAGTGGAGAGACAGTGTCTGGGGCGGACATCTTCTGGAGACACTCAGAAAA 2542
Db      761  TyrLeuGluTyrProMetAspGluAlaGlnArgGluGluTyrPheTrpValaAsnLeuArgAla 780
Qy      2543 GCCCTG 2548
Db      781  AlaIle 782

RESULT 13
US-10-732-563-4
: Sequence 4, Application US/10732563
: Publication No. US20040132079A1
: GENERAL INFORMATION:
: APPLICANT: Gupta, Shalley K.
: APPLICANT: Ghosh, Tarun K.
: TITLE OR INVENTION: Assays Relating to Toll-Like Receptor Activity
: FILE REFERENCE: 58183W003
: CURRENT APPLICATION NUMBER: US/10/732,563
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: Patent version 3.2
: SEQ ID NO 4
: LENGTH: 784
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-732-563-4

Alignment Scores:
Pred. No.: 9,44e-49 Length: 784
Score: 602.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 219
Query Match: 7.02% Indels: 219
DB: 16 Gaps: 38

US-09-396-985b-1 (1-4868) x US-10-732-563-4 (1-784)
Qy      245  ATCCCGACAACCTCCCTTCTCAACCAAGACCTGAGCTTGAATCCCTGAGG 304

```

```

Db      46  ILeProSerGlyLeuThrGluAlaValIysSerLeuAspLeuSerAsnAsnArgIleThr 65
Qy      305  CATTAGGACGACTAGCTTCTTCAGTTCCCAAGACTGCAAGCTGCTGGATTTATCCAG 364
Db      66  TyrIleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValLeuThrSer 85
Qy      365  TGTAAATCCAGCAATGGAAGATGGGATATGAGCATGAGCCACTGCTCTCACTTA 424
Db      86  AsnGlyIleAsnThrIleGluGlnAspSerPheSerSerLeuGlySerLeuGlnIleu 105
Qy      425  ATATTGACAGGAAACCCCATCCAGAGTTTACCCCTGGAGCCCTTTCTGACATCAAGT 484
Db      106  AspLeuSerTyrAsnTyrLeuSerAsnLeuSerSerSerTyrPheTyrProLeuSerSer 125
Qy      485  TTACAGAACTG-----GTGGCTGTGAG 508
Db      126  LeuThrPheLeuAsnLeuLeuGlyAsnProTyrIleThrLeuGlyGluThrSerLeuPhe 145
Qy      509  ACAATCTAGCATCTCTAGAGAACTTCCCATGAGACTCAAACT----- 556
Db      146  SerIleLeuThrTyrSleuGlnIleLeuArgValGlyAsnMetAspThrPheThrIle 165
Qy      557  -----TTGAAAGACTTAATGTGGCTCACAACTTT 586
Db      166  GlnArgIysAspPheAlaGlyLeuThrPheLeuGlnIleuGluIleAspAlaSerAsp 185
Qy      587  ATCCAAATCTTCAATTAACCTGAGATTTTCTAATCTGACCAATCTAGACACTTGGAC 646
Db      186  LeuIleuSerTyrGln-----ProIysSerLeuIysSerIleGlnAsnValSerIleuIle 204
Qy      647  CTTTCCAGCAACAAG-----ATCCAAAGTATT 673
Db      205  LeuIleuSerTyrGlnIleIleLeuLeuGlnIlePheValAspValThrSerSerVal 224
Qy      674  TATTGACACAGCTTGGGGTTCTACATCAAAATGCCCTTACCAATCTCTTGTAGACCTG 733
Db      225  GluCysLeuGlnLeuArg-----AspThr 232
Qy      734  TCCCTGGAATCCTAAGACTTT-----ATCCACACAGCTGATTTAAAGAAATAGCTT 787
Db      233  AspLeuAspThrPheIleAspSerGlnLeuSerThrArgIleuThrAsnSerLeu---Ile 251
Qy      788  CATAGAGCTGACTTTAAGAAAT-----AATTTGATAGTTTA---AATGTAATGAAA 835
Db      252  LysIysPheThrPheArgAsnValIysIleThrAspGlnSerLeuPheGlnValMetCys 271
Qy      836  ACTTGT-----ATTCAAGTCTGCTGCTGTTAGAGTCATCGTTGGTCTG----- 883
Db      272  LeuLeuAsnGlnIleSerGlyLeuLeuGlnIleuGlnPheAspArgCysThrLeuAsnGly 291
Qy      884  ---GGAGATTTAAGAAATGAAAGAACTTGAAAGAACTTGCAAAATCTGCTAGAGGCG 940
Db      292  ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyIleValGln--- 310
Qy      941  CTGTCGCAATTTGACCATTTGAAGAATTCGATTAGA-----TACTTAGACTACTGCTC 994
Db      311  ---ThrLeuThrIleArgArgLeuHisIleProArgPheTyrLeuPheTyr----- 326
Qy      995  GATATATATTGACTTATTATTAATTTGTTTGAACAATGTTCTTCATTTTCCCTGGTAGT 1054
Db      327  ---AspLeuSerThrLeuTyrSerLeuThrGlnArgValIys-----Arg 340
Qy      1055  GTGACTATTGAAAGGTTAAAGACTTTCTTATATATTTCCGATGGCAACATTAGAATTA 1114
Db      341  IleThrValGlnAsnSerIleValPhe-----Leu 350
Qy      1115  GTAACGTGAATATTGACAGATTTCACCATTTGAACATCAATCTCAAAAAGGTTACT 1174
Db      351  ValProCysLeuLeuSerGln----- 357
Qy      1175  TTCACCTCCAACAAAAGGTGGAAATGCTTTTTCAGAAAGTTGATCTACCAAGCCTTGAGTTT 1234

```

```

Db      358  -----HisLeuIysSerLeuGlnIleTyr 364
Qy      1235  CTAGATCTCAGTAAGAT-----GGCTTGAGTTTCAAAAGTTGCTGTTCT 1279
Db      365  LeuAspLeuSerGlnAsnLeuMetValGluGluTyrLeuIysAsnSerAlaCys----- 382
Qy      1280  CAAAGATTTTGGAGAACACCAAGCTTAAGATTAGATCTGAGCTTCAATGCTGTATT 1339
Db      383  ---GlnAspAlaTyrProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 397
Qy      1340  ACAATGAGTTCAAACTTCTGGGCTTAGAACACTAGAACATCTGGATTTCCAGACTTCC 1399
Db      398  -----HisLeu-----Ala 400
Qy      1400  AATTGAAACAATAGAGAGTTTTCAGTATTCCTATCACTCAGAAACCTGATTAAGCTT 1459
Db      401  SerLeuGluIysThrGlyGlu-----ThrLeuLeuThrLeuIysAsnLeuThrAsnIle 418
Qy      1460  GACATTTCTCATTACTCAACACAGAGTTGCTTCAATGAGCATCTTCAATGAGCTGTCCAGT 1519
Db      419  AspIleSerIys----- 422
Qy      1520  CTGCAAGCTTGAATAATGGCTGGCAATTTCTTCCAGAGAAACCTTCTCCAGATATCTTC 1579
Db      423  -----AsnSerPheIleSer-----MetProGluThrCys 432
Qy      1580  ACAGAGCTGAGAAACTTGACCTTCTGAGCCTCTCTCAGTGTCAAGTGCAGACATGTCT 1639
Db      433  GlnThrProGluIysMetIysTyrLeuAsnLeuSerSerThrArgIleHisSerValThr 452
Qy      1640  ---CCAAAGCATTTAACTCACTCCAGCTTTCAGTACGTTAATATAGAGCCAC 1690
Db      453  GlyCysIlePro-----LysThrLeuGlnIleLeuAspValSerAsn 466
Qy      1691  AAC-----AAGTTTCTTTCATTTGATGAT----- 1711
Db      467  AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuIysGluLeuTyrIleSerArg 486
Qy      1712  -----AGTTTCCCT---TATTAAGTGTGAACTCCCTCCAGTTCTTGATTAC 1756
Db      487  AsnIysLeuMetThrIleuProAspAlaSerLeuLeuProMetLeuValLeuIysIle 506
Qy      1757  AGTCTCAATGACATTAATGACTTCCAAAAAACAGAACTACAGACTTTTCCAAAGTAGCTA 1816
Db      507  SerArgAsnAlaIleThrThrPheSerIysGlnIleuAspSerPhe---HisThrLeu 525
Qy      1817  GCTTCTTAAATCTTACTCAGAAATGACTTGTGTTGACTTGTGAACACAGAGTTTCTG 1876
Db      526  LysThrLeuGlnIleGlyGlyAsnAsnPheIleCysSerCysGlnPheLeuSerPheThr 545
Qy      1877  CAATGATCAAGAACAGAGGACGACTTGTGTGAAGTT-----GAACGA 1921
Db      546  Gln-----GlnGlnGlnAlaLeuAlaIysValIleuIleAspTyrProAlaAsn 561
Qy      1922  ATGGAATGTGCAACACCTTCAATGAAGAGGAGGAGCTGCTGAGCTTGAATATACAC 1981
Db      562  TyrLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581
Qy      1982  ---TGTCAATGAATTAAGACCATCATTTGGTGTGCTGCTCCAGTGTCTTGTATA 2032
Db      582  ValSerGlnCysHisArgThrAlaLeuValSerGlyMetCysCysValaLeuPheLeu 601
Qy      2033  GTATCTGTGTGAGAGTTCTGGTGTATTAAGTTCTAT-----TTTCACTGATGCTTCTT 2086
Db      602  IleuLeuThrGlnValIleuCysHisArgPheHisGlyLeuTyrTyrMetIysMetMet 621
Qy      2087  GCTGCTGCAATAAGTAGTAGTA-----GGTGAACATC---TAT 2125
Db      622  ThrAlaThrLeuGlnAlaIlyHisGlyIysProArgIlyAlaProSerArgAsnIleCysTyr 641
Qy      2126  GATGCTTTGTATTATCTACAGCCAGAGATGAGAGCTGGGTGAAGAAATGAGCTTAGAAG 2185
Db      642  AspIleAlaPheValSerTyrSerGlnArgAspAlaTyrThrValGlnAsnLeuMetValGln 661

```

```

Qy 2186 AATTAGAGAGGGGTCCTCATTTAGCTGCTCTGACAGACTTATATCCC 2245
    |||||
Db 662 GtuleugluasnPhreanProPhoPhelyeucylslysaAgapPheillePro 681
Qy 2246 GGTCGTGACATTGCTGCAACATCATCATGAGGTTTCCATMAAGCCGAAAGTATT 2305
    |||||
Db 682 GlyLysEtrilleleAspamillele---AsperilleglulysSerHislyThrVal 700
Qy 2306 GTTGTGTGTCCTCCAGACTTCATCCAGACCGCTGGTGATCTTTGAATATGATGCT 2365
    |||||
Db 701 PhealileuSerGluasnPheValLysSerGluTrpCysLysTrpGluLeuAspPheSer 720
Qy 2366 CAGACTGCGAGTTTCTGAGACGCTGCTGATCATTTCTTCAATTCCTGCAAGAGT 2425
    |||||
Db 721 HisPheargLeuPheaspGluasnAsnAspAlaAlaIleleuIleLeuLeuGluProIle 740
Qy 2426 GAGAGAGCCCTGCTCAGGACAGAG--GTGAGCTGTACCGCTTCTCAGAGAGACAT 2482
    |||||
Db 741 GlulysLysAlaIleProGlnargPheCysLysLeuargLysIleMetAsnThrLysThr 760
Qy 2483 TACCTGAGTGGAGAGACAGTCTCGGGGACACATCTTCTGAGACACATCAGAAA 2542
    |||||
Db 761 TyrluenglutPrpMetAspGluAlaGlnargLugluPheTrpValAsnLeuargAla 780
Qy 2543 GCCCTG 2548
    |||||
Db 781 AlaIle 782

RESULT 14
US-10-732-796A-4
; Sequence 4, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732,796A
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-732-796A-4

Alignment Scores:
Pred. No.: 9,44e-49 Length: 784
Score: 602.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 7.02% Indels: 219
DB: 16 Gaps: 38

US-09-396-985B-1 (1-4868) x US-10-732-796A-4 (1-784)
Qy 245 ATCCCGACAACTCCCTTCTCAACCAAGAACTGAGCTTAAATCCCTTAAAG 304
    |||||
Db 46 IlleProserGlyLeuThrGluAlaValLysSerLeuSerLeuSerAsnAsnArgIleThr 65
Qy 305 CATTTAGGACGCTATAGCTTCTTCAAGTTTCCCAAGATCGAGGCTGCTGATTTATCCAGG 364
    |||||
Db 66 TyrlleSerAsnSerAspLeuGlnargCysValAsnLeuGlnAlaLeuValLeuThrSer 85
Qy 365 TGTAATTCAGCAATTTGAAGATGGGACATATCAGAGCCCTTAAGCACTTCTTACCTTA 424
    |||||
Db 86 AsnGlyLysLeuThrIleGluGluAspSerPheSerSerLeuGluHisLeu 105
Qy 425 ATATTGACAGAAACCCCATTCAGATTATGACCTGTGGAGCCTTTTCTGACATCAAGT 484
    |||||

```

```

Db 106 AspleuSerTyraNtyrLeuSerAsnLeuSerSerSerTrpPheLysProLeuSerSer 125
Qy 485 TTAACAGAGCTG----- 508
Db 126 LeuThrPheLeuAsnLeuLeuGluGlyAsnProTyrlThrLeuGluGluThrSerLeuPhe 145
Qy 509 ACAATCTAGACATCTTAGAGAACTTCCCATTTGACATCTCAAACT----- 556
    |||||
Db 146 SerHisLeuThrLysLeuGluGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIle 165
Qy 557 -----TTGAAAGAACTTATGTGGCTCAATCTT 586
    |||||
Db 166 GlnArgLysAspPheAlaGlyLeuThrPheLeuGluGluLeuGluIleAspAlaSerAsp 185
Qy 587 ATCCAACTTTCAAAATTACCTGAGTATTTTCTAATCTGCAATCTAGACACTTGAC 646
    |||||
Db 186 LeuGlnSerTyrlu---ProLysSerLeuLysSerIleGlnAsnValSerHisLeuIle 204
Qy 647 CTTCGACCAACAG-----ATTCAAAGTATT 673
    |||||
Db 205 LeuHisMetLysGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerVal 224
Qy 674 TATTGACAGACTTGGCGGCTTACATCAATGCCCCCTACTCAATCTCTTTAGACCTG 733
    |||||
Db 225 GlucLysLeuGluLeuArg-----AspThr 232
Qy 734 TTCCTGAATCCTATGAACTT-----ATCCAAACAGTGCATTTAAGAAATTAGCTT 787
    |||||
Db 233 AspleuAspThrPheHisPheSerGluLeuSerThrGlyGluThrAsnSerLeu---Ile 251
Qy 788 CATAGCTGACTTTAAGAAAT-----AATTGTATGATTTA---AATGTATAGAAA 835
    |||||
Db 252 LysLysPheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMetLys 271
Qy 836 ACTTGT-----ATTCAGGCTCGCGCTTGAAGTCCATGCTTGGTTCG----- 883
    |||||
Db 272 LeuLeuAsnGlnIleSerGlyLeuLeuGluLeuGluPheAspAspCysThrIleAsnGly 291
Qy 884 ---GGAATTTTGAATGAAGAACTTGAAAGTTTGAACAATCTGCTTAGAGGCG 940
    |||||
Db 292 ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyLysValGlu--- 310
Qy 941 CTGTGCAATTTGACCATTTGAAGAAATCCGATTAACA-----TACTTGAATCTACTC 994
    |||||
Db 311 -----ThrlleuThrIleArgArgLeuHisIleProArgPheThrLeuPheTyx----- 326
Qy 995 GATGATATTATTTGACTTATTTAATTTGTCACAAATGTTTCTTCATTTTCCCTGGTAGT 1054
    |||||
Db 327 ---AspleuSerThrLysTyrlSerLeuThrGluArgValLys-----Arg 340
Qy 1055 GTGACTATTGAAAGGTTAAAGAACTTTTCTTATTAATTTGGATGGCAACATTAGAAATTA 1114
    |||||
Db 341 IlleThrValGluAsnSerLysValPhe-----Leu 350
Qy 1115 GTTAACTGTAATTTTGGACATTTCCCACTGTAACAAATCTCAAAAGGCTTACT 1174
    |||||
Db 351 ValProCysLeuLeuSerGln----- 357
Qy 1175 TTCACTTCCAAACAAAGGTGGGAATGCTTTTTCAGAAAGTTATCTTACCAAGCTTGAAGTT 1234
    |||||
Db 358 -----HisLeuLysSerLeuGluTyx 364
Qy 1235 CTAGATCTCAGTAGAAT-----GGCTTAGTTCAAAGGTGCTGTCTT 1279
    |||||
Db 365 LeuAspleuSerGluAsnLeuMetValGluGluTyrlLeuLysAsnSerAlaCys----- 382
Qy 1280 CAAAGTATTTTGGGCAACACAGCTTAAATATTTAGATCTGAGCTTCAATGTGTTATT 1339
    |||||
Db 383 -----GluAspAlaTrpProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 397
Qy 1340 ACATAGATTCAAACTTCTTGAGCTTAAGAAACAATGACATGTCGATTTCCAGCATTC 1399
    |||||
Db 398 -----HisLeu-----Ala 400

```


Oy		1400	AATTGAAACAAAGAGCGATTTTCACTAGTATCCCATGACACGAAAACCTATTACTTC	1499
Db		401	Seriesglnylstinglylu-----ThileuLeuthrleuyshenleThasnille	418
Oy		1460	GACATTTCCTCACTACACACAGAGTGCTTTCAATGGCATTCTTAATGAGCTTGCCAGT	1519
Db		419	AspIleSerLyS-----	422
Oy		1520	CTCGAAGCTTGAAATAATGGCTGCAGCAATCTTTCACGAAAACTTCCTCCAGATATCTTC	1579
Db		423	-----AsnserPheHisSer-----MetProGlnThrCyS	432
Oy		1580	ACAGAGCTGAGAACTTGACCTTCCTGGACACCTCTCCAGTGCTCAACTGACAGACTGTCT	1639
Db		433	GlnlTrProGlnUlysmetylerTytleuasnleueserThrArgLlenIsSerValThr	452
Oy		1640	-----CCAAcGAcATTTAActCACTCACTCCAGTCTTCAGAGTCTAATAATAGAACCAC	1690
Db		453	GlyCySllePro-----LysThrleuglnlleleuaspvalSerAsn	466
Oy		1691	AAC-----AACTCTTTCAATTGGAT-----	1711
Db		467	AsnAsnleuAsnleuPheSerleuAsnleuProGlnleuLySglnleuTyrlleSerArg	486
Oy		1712	-----ACGTTTTCT---TATAAGTGCTGAACCTCCCTCCAGGTTCTTGATTAC	1756
Db		487	AsnUlysmetThrleuProaspIleSerleuLeuPrometleuLeuValleuLySle	506
Oy		1757	AGTCTCAATCACTATATAGCTTCCAAAACAAGAACATCAKGCATTTTCCAAGTAGTGA	1816
Db		507	SerArgAsnAlallethrPheserLySglnleuAsnSerPhe--HisThrleu	525
Oy		1817	GCTTCTTAAATCTTACACAGATAGCTTGTCTGACTTGTGAACACCAAGTTCCTGTG	1876
Db		526	LysThrleuGlnAlaglyGlyAsnAsnHelleCySerSerGlnPheleuSerPheThr	545
Oy		1877	CAATGGATCAAGACACAGAGGAGCTCTTGSTGCAATT-----GACAGA	1921
Db		546	Gln-----GlnGlnGlnAlaleuAlaleuAlaySvalleuIleAspTrpAlaAsn	561
Oy		1922	ATGGAATGTGAAACCTTCAGATAGAAGGGAGCGCTGTGCTGAGTTGAATATACAC	1981
Db		562	TyrleucYsaPseProSerHileValArgelGlnGlnAlvalGlnAspValArgleuSer	581
Oy		1982	-----TGTCAAGATAAATAAGCACATCACTTGCTGTGTGTGGCTTCCAGTGTGCTGTA	2032
Db		582	ValSerGlnCyShArgThrAlaleuValSerGlnMetCySvalAleuPheleuLeu	601
Oy		2033	GTATCTGTGTGAACAGTTCTGTGTATAGAATTCTAT-----TTTCACTGATGCTTCTT	2086
Db		602	IleleuLeuThrGlyValleuCysHArgPheHisGlyleuTrpUmetUlyMetMet	621
Oy		2087	GCTGGCTCAATAAGTATGTAGA-----GGTAAACATC---TAT	2125
Db		622	ThrAlatrpLeuGlnAlalyArgUlysrProArgUlyslalArPseRghAsnilleCySerUx	641
Oy		2126	GATGCTTGTGTATCTACTCAAGSCCAGATAGAGACTGGGTAGAGATGASTAGTAAG	2185
Db		642	AspAlarPheValSerUlySerGlnUArgspAlatUtyTrValGlnleuLeuMetValGln	661
Oy		2186	AATTTAGAAGAGGGGTGCTCAATTTCAGCTGTGCTTCACTACAGAGATTATATCCC	2245
Db		662	GlnleuGlnUasnPheAsnProPheUlySerUlyCysleuHilySArgAspPheIleTo	681
Oy		2246	GGTGTGCCATTTGCTGCCACATCATCTCCATGAAGAGGTTCSCATTAAGSCGGAAGGTGAT	2305
Db		682	GlyUlystrIlelleleaspAnillele---AspserlleGlnUlySerHileUlyThrVal	700
Oy		2306	GTGTGGTGTCCCSAGACTTCACTCAKAGCCSGGTGTGTATCTTGAATATGACATTGCT	2365
Db		701	PheValleuSerGlnUasnPheVallySerGlnUlyTrpCySlyGlyUlyleuAspPheSer	720

```

OY 2366 AGACCTGGCAGTCTTGAGCAGCTGCTGGTATCATCTTATGTCCTGAGAGAGG 2425
Db 721 Hispeargleupheaspgluabnshnabpalaiaalleuileuileuulguproile 740
OY 2426 GAGAGAACCTGCTCAGGACAG--GTGAGCTGTACCGCTTCTGACAGAACT 2482
Db 741 GlutylsyalatleProgluhargheCysylsleuAglYsileMetcanthrlYsThr 760
OY 2483 TACCTGTAGTGAGAGACAGTGTCTGGGGGGGCACATCTTGAGAGACTGAGAAA 2542
Db 761 TyrlleuglurPpromeaspglualaglnhrglulgYpethrvalasnleuArgala 780
OY 2543 GCCCTG 2548
Db 781 Alatile 782

RESULT 15
US-10-741-600-1390
; Sequence 1390, Application US//10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENOMIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1390
; LENGTH: 784
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-741-600-1390

Alignment Scores:
Pred. No.: 9,44e-49 Length: 784
Score: 602.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 7.02% Indels: 219
DB: 17 Gaps: 38

US-09-396-985B-1 (1-4868) x US-10-741-600-1390 (1-784)
OY 245 ATCCCGCAGCACTGCCCTTCTCAACCAAGAACTGAGCTGAGCTTATCCCTGAGG 304
Db 46 IleProserglYleuthrgluAlavallysserleuAAspleuserAshnarnargilethr 65
OY 305 CATTAGGACACTAGCTTCTTTCAGTGTCCCAAGAACTGCAGGCTGAGCTGATTATTCACAG 364
Db 66 TyrlleSerasnserAAspleuglnhrgCysvalasnleuGlnAlaleuvalleuthrser 85
OY 365 TGTAAATCCAGCAAGATTGAAGATGGGGCATATCAGACCTTAAAGCACCTCTCACTTA 424
Db 86 AsnnglylleanthrlleuglnuAsperheseSerleuGlySerleuGlnuhsleu 105
OY 425 ATATTGACAGAAACCCCATCCAGAGTTTAGCCCTGGAGACCTTTTTCGACTATCAACT 484
Db 106 AspleuserTyrlasnTyrlleuserAasnleuserSerTirPheIysProleuserSer 125
OY 485 TTACAGAACTG-----GTGCTGTGAG 508
Db 126 LeuthrPheleuAenleuenglyAsnProTyrlYsThrleuGlyGlnThrserleuPhe 145
OY 509 ACAATCTAGCATCTTGAAGAACTTCCCATGAGCACTTCAAACT-----556
Db 146 SerhlsleuthrlYsleuGlnlleuAryvalGlyAsnMetAspThrPheThrYsile 165
OY 557 -----TTGAAAGAACTTAAGTGCGCTACAAATCT 586
Db 166 GlnhrglyAspPheAlaglyleuthrPheleuGlnuglnleuGlnIleAspAlaserAAsp 185

```


Db 781 Alarie 782

Search completed: March 30, 2005, 04:39:32
Job time : 311.34 secs

116

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 30, 2005, 03:00:48 ; Search time 153.708 Seconds
(without alignments)
16418.453 Million cell updates/sec

Title: US-09-396-985B-3

Perfect score: 6724

Sequence: 1 acagggcactgctgcac.....tctcactgacaggaacta 3811

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 2814804

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh
-O=/cgn2_1/USPRO.spool/US09396985/runat_28032005_155745_21245/app_query.fasta_1.85098
-DB=Published Applications AA -QPM=faastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09396985@cgn_1_1_3955 @runat_28032005_155745_21245
-NCPU=6 -ICPU=3 -NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSELOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result *
Query

No.	Score	Match Length	DB	ID	Description
1	4315.5	64.2	837	10	US-09-950-041-26
2	4141	61.6	799	10	US-09-950-041-8
3	4141	61.6	799	16	US-10-128-166-7
4	4141	61.6	799	16	US-10-732-563-8
5	4141	61.6	799	16	US-10-732-796A-8
6	656.5	9.8	661	15	US-10-038-854-135
7	656.5	9.8	661	15	US-10-037-417-107
8	619.5	9.2	661	13	US-10-114-893-10
9	619.5	9.2	661	13	US-10-038-854-134
10	603.5	9.0	784	10	US-09-950-041-4
11	603.5	9.0	784	15	US-10-456-947-46
12	602.5	9.0	784	14	US-10-095-627-112
13	602.5	9.0	784	16	US-10-732-563-4
14	602.5	9.0	784	16	US-10-732-796A-4
15	602.5	9.0	784	17	US-10-741-600-1390
16	602.5	9.0	784	17	US-10-741-600-1391
17	599.5	8.9	784	13	US-10-145-014-23
18	580.5	8.6	1032	10	US-09-954-987B-192
19	580.5	8.6	1032	14	US-10-272-502A-31
20	580.5	8.6	1032	15	US-10-407-952-32
21	567	8.4	1050	10	US-09-954-987B-175
22	567	8.4	1050	14	US-10-272-502A-22
23	567	8.4	1050	15	US-10-407-952-26
24	533	7.9	1032	10	US-09-950-041-37
25	533	7.9	1040	9	US-09-864-761-38325
26	533	7.9	1041	9	US-09-168-978-3
27	533	7.9	1041	9	US-09-978-295A-498
28	533	7.9	1041	9	US-09-978-697-498
29	533	7.9	1041	9	US-09-978-192A-498
30	533	7.9	1041	9	US-09-999-832A-498
31	533	7.9	1041	10	US-09-978-189-498
32	533	7.9	1041	10	US-09-978-608A-498
33	533	7.9	1041	10	US-09-978-585A-498
34	533	7.9	1041	10	US-09-978-191A-498
35	533	7.9	1041	10	US-09-978-403A-498
36	533	7.9	1041	10	US-09-978-564A-498
37	533	7.9	1041	10	US-09-999-833A-498
38	533	7.9	1041	10	US-09-981-915A-498
39	533	7.9	1041	10	US-09-978-82A-498
40	533	7.9	1041	10	US-09-918-82A-498
41	533	7.9	1041	10	US-09-999-834A-498
42	533	7.9	1041	10	US-09-978-423A-498
43	533	7.9	1041	10	US-09-978-193A-498
44	533	7.9	1041	10	US-09-999-830A-498
45	533	7.9	1041	10	US-09-978-757A-498

ALIGNMENTS

RESULT 1
US-09-950-041-26
Sequence 26, Application US/09950041
Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kaetelehn, Robert A.
APPLICANT: Ho, Stephen W.K.
TITLE OR INVENTION: RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS
FILE REFERENCE: DK0724XX1
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US/09/950,041
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293

```

; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-26

Alignment Scores:
Score: 0 Length: 837
Percent Similarity: 4315.50 Matches: 837
Best Local Similarity: 95.33% Conservative: 0
Query Match: 64.18% Indels: 41
DB: 10 Gaps: 1

US-09-396-985b-3 (1-3811) x US-09-950-041-26 (1-837)
QY 48 ATGTCGCTGCGCGCTGGCTGGACTCTGATCCAGCCATGAGCCTTCCTCGTGGCTG 107
Db 1 MetserAlaserArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCysVal 20
QY 108 AGACCAAAAGCTGGAGACCCCTGGCTGGAGACTTGGCCCTTAACCAACAGAAAGCTGG 167
Db 21 ArgProGluSerThrPgluProCysValGlu----- 30
QY 168 CATGAACCCAGAGCTTCAGACGCCGAGCCTCAGCCCTTACCCCGATTCCATTGCTT 227
Db 30 ----- 30
QY 228 CTGCTAAATGCTGCGCTTTTATACAGGAGGTGTTCTTAATATTACTTATCAATGCAATG 287
Db 31 -----ValProAlaIleThrTyrGlnCysMet 39
QY 288 GAGCTGAATTTCTCAAAATCCCGACAACCTCCCTTCTCAACCAAGAACCTGGACCTG 347
Db 40 GluLeuAlaSerPheTyrIleProAspAlaLeuProPheSerThrTyrAsnLeuAspLeu 59
QY 348 AGCTTAAATCCCGTAGGACATTTAGGAGCTATAGCTTTCAGATTGCCAGAACTGGAG 407
Db 60 SerPheAsnProLeuAlaGlnIleuSerIleuSerPhePheSerPheProGluLeuGln 79
QY 408 GTGCTGATTTATCCAGGTGTGAATCCAGACAATTGAAGATGGGCAATATCAGACCTTA 467
Db 80 ValLeuAlaPheLeuSerArgCysGluIleGlnThrIleGluAlaPylAlaTyrGlnSerLeu 99
QY 468 AGCCACCTCTCTACTTAAATATTTGACAGAAACCCATCCAGATTTTGGCCCTGGAGACC 527
Db 100 SerHisIleuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaIleuGlyAla 119
QY 528 TTTTCTGACATATCAAGTTTACAGAAAGCTGGGTGGTGGAGACAAATCTGACATCTGTA 587
Db 120 PheSerGlyLeuSerSerLeuGlnIleuValAlaValGluThrAsnLeuAlaSerLeu 139
QY 588 GAGAACTTCCCATTTGACATCTCAAACTTTGAAAGAACTTAATGTGGCTCACAATCTT 647
Db 140 GluAlaSerPheProIleGlyHisIleuSerThrLeuIleuValAlaIleHisAlaSerLeu 159
QY 648 ATCCAAATCTTTCAATTTACCTGAGATTTTCTAATCTGACCAATCTGAGACATTTGGAC 707
Db 160 IleGlnSerPheTyrIleuProGluTyrPheSerAlaLeuThrAsnLeuGlnHisIleuAsp 179
QY 708 CTTTCAGACAAATTCAAAGTATTTATTGACACAGACTTGGCGGTTCTCATCAATAATG 767
Db 180 LeuSerSerAsnTyrIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGlnMet 199
QY 768 CCCCTACTCAATCTCTCTTAGACCTGTCCCTGAACCCATGAACCTTTATCCAAACAGAT 827
```

```

Db 200 ProLeuLeuAlaSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnProGly 219
QY 828 GCATTTAAAGAAATTTAGGCTTCTAAGCTGACTTATAGAAATTAATTTGATGTTAAAT 887
Db 220 AlaPheLeuGluIleArgLeuHisTyrLeuThrLeuArgAsnAsnPheAspSerLeuAsn 239
QY 888 GTAATGAAACCTGTATTTCAAGGTCTGGCTGTTTGAAGTCCATGCTTTGTTCTGGGA 947
Db 240 ValMetTyrThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeuGly 259
QY 948 GAATTTGAATGAAGGAAACTTGAAGAACTTTGACAAATCTGCTCTAGAGGCGCTGTGC 1007
Db 260 GluPheArgAsnGluGlyAsnLeuGluTyrPheAspLysSerAlaLeuGluGlyLeuCys 279
QY 1008 AATTGACCATTTGAAGAAATTCGATTTAGCATCTTATGACATCACTCCATGATATTAAT 1067
Db 280 AsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAlaIle 299
QY 1068 GACTTATTTAATGTTTGAACAAATGTTTCTTCAATTTCCCTGGTGAAGTGACTATTGAA 1127
Db 300 AspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIleGlu 319
QY 1128 AGGATAAAGACTTTTCTTATAATTTGAGTGCACAACTTATGAAATTTAGTAACTGTAAA 1187
Db 320 ArgValLysAspPheSerTyrAsnPheGlyTyrPgluHisIleuGluValAlaCysTyr 339
QY 1188 TTTGACAGTTTCCCATATGAACCTCAAAATCTCTCAAAAGGCTTACTTCACTTCCAAC 1247
Db 340 PheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSerAsn 359
QY 1248 AAAGTGGGAATGCTTTTTCAGAAAGTTGATCTACCAAGCCTTGAAGTTTCTGATCTCAGT 1307
Db 360 LysGlyGlyAsnAlaPheSerGluValAspLeuProSerIleuGluPheLeuAspLeuSer 379
QY 1308 AGAAATGCTTGAAGTTTCAAAAGTTGCTGTTCTCAAAAGTATTTGGGACACACAGCTTA 1367
Db 380 ArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSerLeu 399
QY 1368 AAGTATTTAATGCTGAGCTTCANAGGTGATTAATCAATGATGTTCAAACTCTGGGGCTTA 1427
Db 400 LysTyrLeuAspLeuSerPheAsnGlyValIleThrCysSerAsnPheLeuGlyLeu 419
QY 1428 GAACCAATGACATCTGAGATTTCCAGACATTTCCAAATTTGAAACAAATGATGAGTTTCA 1487
Db 420 GluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPheSer 439
QY 1488 GTATTCCTATCACTCAGAAATCTCATTTACCTTGAACATTTTCTCAACACAGATT 1547
Db 440 ValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThrArgVal 459
QY 1548 GCTTTCAATGGCACTTCANAGGCTTGCAGAGCTCGAAGTCTTGAAGAAATGGCTGCAAT 1607
Db 460 AlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGlyAsn 479
QY 1608 TCTTTCCAGAAAACTTCTTCCAGATATCTTCAAGAGCTGAGAAACTTGACCTTCTG 1667
Db 480 SerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPheLeu 499
QY 1668 GACCTCTCTCACTGCTCACTGAGACAGTTGTCTCCAAACAGCATTTTAACTCACTCTCAGT 1727
Db 500 AspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSerSer 519
QY 1728 CTTGAGTACTTAATATAGAGCAACAACATCTTTCATTTGATGATAGTTTCTTATTAAG 1787
Db 520 LeuGlnValLeuAsnMetSerHisAsnAspPhePheSerLeuAspThrPheProTyrLys 539
QY 1788 TGTCTGAATCCCTCCAGAGTCTTGATTAAGTCTCAATCAATCAATAGACTTCCAAAAA 1847
Db 540 CysLeuAsnSerLeuGlnValIleAspTyrSerLeuAsnHisIleMetThrSerLys 559
QY 1848 CAGGAATCAACAGATTTTCCAGTAGTCTAGCTTCTTAAATCTTACTCAGATGACTTT 1907
Db 560 GlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
```

QY 1908 GCTTGATCTGTGAACACAGAGTTTCTGCAATGATCAAGACAGAGCAGCTCTTG 1967
 Db 580 AlacysrhrcysglwhisginserPheleuglntripleysabpqlnarginleu 599
 QY 1968 GTGGAATTGAACGAATGAATGTGCAACACCTTCAGATTAAGAGGCGATCCTGCTG 2027
 Db 600 ValGluValGluArgmetGluCysAlaThrProserapysglnGlymetProValleu 619
 QY 2028 AGTTGAATATCCCTTCAGATGAATGAACCACTCATTTGCTGTGCTGCTTCAAGTGTG 2087
 Db 620 SerleuasnilletrCysGlnmeCasnlyshrrilleleglyalSerValleuSerVal 639
 QY 2088 CTGTGATATCTGTGTAGACAGTCTGATCTAATGATTTATTTACCTGATCTCTT 2147
 Db 640 LeuValValSerValValAlaValLeuValTyrIshetheryPhehlsleuMeleuLeu 659
 QY 2148 GCTGGCTGCAATTAAGTATGAGAGTGAACCACTGATGATGCTTTGTTATCTACTCA 2207
 Db 660 AlaglyCysilleuetyrglyArgglyGluasnilletyrshpalapheValilletyrSer 679
 QY 2208 AGCCAGATGAGACCTGGGTGAAGATGAGCTAGTAAAGATTGAAGAAAGGGGTGCTT 2267
 Db 680 SerGlnaspGluaspTrpValArgAsnGluLeuValIysAsnLeuGluGluValPro 699
 QY 2268 CCAATTCAGCTCTGCTTCACTACAGAGACTTTATCCCGGTGAGCATTGCTGCGCAAC 2327
 Db 700 ProPheGlnleuCysleuhsrlyrArgaspheilleProglYalAlaAlaAsn 719
 QY 2328 ATCATTCATGAAGTTTCAATTAAGCCGAAGGTGATTTGTTGATGCTGCCAGACTTC 2387
 Db 720 IlellehsigluGlyPhehlslyserArglyValilleValValSerGlnHisPhe 739
 QY 2388 ATCCAGAGCCGCTGTGTATCTTGAATATGAGATTGCTCAGACCTGGCAGTTTCTGAC 2447
 Db 740 IleGlnserArgTrpCysIlePheGluTyrGluIlelaGlnThrTrpGlnPheLeuSer 759
 QY 2448 AGTCGCTCTGTATCATCTTCATTTGCTCTGAGAGAGGTGAGAGACCCGCTGAGGAG 2507
 Db 760 SerArgAlaGlyIlellePheilleValleuGlnlyValGluTyrlnrleuLeuAsnGln 779
 QY 2508 CAGGTGAGGTGATACCGCTTCTCAGACAGAAACCTTACCTGAGTGGAGACAGTGC 2567
 Db 780 GluValGluLeuTyrArgleuLeuSerArgAsnThrTyrleuGluTyrGluAspSerVal 799
 QY 2568 CTGGGGGGGACATCTTCTGAGACGACTCAAAAACCCCTGCTGATGTTAAATCAATGG 2627
 Db 800 LeuGlyArgHisIlePheTrpArgleuArglysalaleuLeuaspGlylyserTrp 819
 QY 2628 AATCCAGAGAAACAGTGGGTACAGATGCAATTGGAGAGAGCAATCATCTATC 2681
 Db 820 AspProGluGlyThrValGlyIleGlyCysAsnTrpGlnIleAlaThrSerIle 837
 RESULT 2
 US-09-950-041-8
 ; Sequence 8, Application US/09950041
 ; Publication No. US20030032090A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hardiman, Gerard T.
 ; APPLICANT: Rock, Fernando L.
 ; APPLICANT: Bazan, J. Fernando
 ; APPLICANT: Kastelehn, Robert A.
 ; APPLICANT: Ho, Stephen W.K.
 ; APPLICANT: Liu, Yong-Jun
 ; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
 ; FILE REFERENCE: DX0724X1
 ; CURRENT APPLICATION NUMBER: US/09/950, 041
 ; PRIOR FILING DATE: 2002-05-06
 ; PRIOR APPLICATION NUMBER: 09/728,540
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 60/207,558
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 09/073,363

; PRIOR FILING DATE: 1999-06-05
 ; PRIOR APPLICATION NUMBER: 60/044,293
 ; PRIOR FILING DATE: 1997-05-07
 ; PRIOR APPLICATION NUMBER: 60/072,212
 ; PRIOR FILING DATE: 1998-01-22
 ; PRIOR APPLICATION NUMBER: 60/076,947
 ; PRIOR FILING DATE: 1998-03-05
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 799
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-950-041-8

Alignment Scores:
 Pred. No.: 0 Length: 799
 Score: 4141.00 Matches: 799
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 61.59% Indels: 0
 DB: 10 Gaps: 0

US-09-396-985b-3 (1-3811) x US-09-950-041-8 (1-799)

QY 285 ATGAGCTGAATTTCTACAAAATCCCGACACCTCCCTTCAACCAAGAACTTGAC 344
 Db 1 MetGluLeuasnThrlyrlyslleProaspAsnleuProPheSerThrlyshleuAsp 20
 QY 345 CTAGCTTTAATCCCTGAGGCAATTAAGCAGCTATAGCTTCTTCACTTCCGAACTG 404
 Db 21 LeuSerPheasnProleuArgHisleuGlySerlyserPhePheSerPheProGluLeu 40
 QY 405 CAGGTGCTGATTTATCCAGGTGTGAATATCAACAAATTGAAGTGGGCATATCAGAC 464
 Db 41 GluValleuaspLeuSerArgCysGluIleGlnThrIleGluaspGlyAlaTyrGlnSer 60
 QY 465 CTAGGCACCTCTCTACCTTAATATTGACAGAAACCCCATCCAGAGTTTACGCTGGA 524
 Db 61 LeuSerHisleuSerThrleuIleleuThrGlyAsnProIleGlnSerleuAlaIleuGly 80
 QY 525 GCCTTTCTGCACTATCAAGTTTACAGAAAGCTGTGCTGTGAGACAAATCTAGCATCT 584
 Db 81 AlaPheSerGlyleuSerSerleuGlnlyleuValAlaValGluThrAsnleuAlaSer 100
 QY 585 CTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAAGAATTATGTGCTCACAAT 644
 Db 101 LeuGluAsnPheProIleGlyHisleuIysThrleuIysGluLeuAsnValAlaHisAsn 120
 QY 645 CTATATCAATCTTTCAAAATTACCTGAGTATTTTCTAATCTGACCAATCTAGGCACTTG 704
 Db 121 LeuIleGlnSerPheIysleuProGluTyrPheSerAsnleuThrAsnleuGluHisleu 140
 QY 705 GACCTTTCCAGCAACAAGATTCAAGTATTTATGACAGACTTGCGGGTTCTACATCAA 764
 Db 141 AspLeuSerSerAsnlyslleGlnSerIleTyrCysThrAspLeuArgValleuHisGln 160
 QY 765 ATGCCCTTACTCAATCTCTTTTGAACCTGTCCCTGAACCTTATGAACTTTATCCAA 824
 Db 161 MetProleuLeuasnleuSerleuAspLeuSerleuAsnProMetAsnPheIleGlnPro 180
 QY 825 GGTCGATTTAAAGAAATTGAGCTTCAATAGCTGACCTTAAAGAAATATTGATAGTTA 884
 Db 181 GlyAlaPheIysGluIleArgleuHislyslleuThrleuArgAsnAsnPheaspSerleu 200
 QY 885 AATGTATGAAGAACTTGATTTCAAGGCTGCGCTGTTTGAAGTCCATCGTTGGTTCTG 944
 Db 201 AsnValMetIysThrCysIleGlnGlyleuAlaGlyleuGluValHisArgleuValleu 220
 QY 945 GGAAGATTTGAAGAAAGAACTTGAAAGAACTTGAACAATCTGCTTGAAGGGCTTG 1004
 Db 221 GlyGluPheArgAsnGluGlyAsnleuGluIysPheAspIysSerAlaIleuGluGlyLeu 240

QY 1005 TGCAATTGACATGTAAGAATCCGATGATGACATTAAGTACTGATGATATT 1064
 DB 241 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrLeuAspTyrTyrLeuAspAspIle 260
 QY 1065 ATTGACTTAATTAATGTTGACAAATGTTTCTTCATTTTCCGTGAGTGTGACTATT 1124
 DB 261 IleAspLeuPheAsnGlySerLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
 QY 1125 GAAAGGTAAAGACTTTCTTAATTAATTTGGAGGACATTTAGAAATTAAGTTAACTGT 1184
 DB 281 GluArgValIlysAspPheSerTyrAsnPheGlyTyrGlnIleSLeuGluLeuValAsnGly 300
 QY 1185 AAATTTGACAGTTTCCACATGTAAGAACTCAATCTGCAAAAGGCTTACTTTCATCTCC 1244
 DB 301 LysPheIleGlnPheProThrLeuLysLeuLysSerLeuLysAspGluThrPheThrSer 320
 QY 1245 AACAAAGGTGGAAATGCTTTTTCAGAAAGTTGATTCACAAAGCTTGAGTTTTCATGATCTC 1304
 DB 321 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340
 QY 1305 AGTAGAATGCTGAGTTTCAAAAGGTGCTGTTCTGAAGTGAATTTTGGAGCAACAGC 1364
 DB 341 SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
 QY 1365 CTAAAGATTTAGATCTGAGCTCAATGAGTGTGTTATTCATGAGTTCAAACTTCTGGGC 1424
 DB 361 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
 QY 1425 TTGAACAACATGAAACATCTGAGATTTCAGACATTCCAATTTGAAACAAATGAGTGAATT 1484
 DB 381 LeuGluGlnLeuGluIleLeuAspPheGlnIleSerAsnLeuLysGlnMetSerGluPhe 400
 QY 1485 TCGATTATTCATACCTCAAGAACTCAATTAACCTTGAACATTTTCTTACTCAACACAGA 1544
 DB 401 SerValIleLeuSerLeuLeuAsnLeuIleTyrLeuAspIleSerIleThrIleSerIle 420
 QY 1545 GTTGCTTTCAATGAGCATCTTCATAGGCTGTGTCAGATCTCGAAGCTTGAATAATGGCTGAC 1604
 DB 421 ValAlaIleAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 440
 QY 1605 AATTCTTTCCAGAAAACCTTCTTCAGATATCTTTCACAGAGCTGAGAAACTTGACCTTTC 1664
 DB 441 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuAspLeuThrPhe 460
 QY 1665 CTGACCTCTCTGAGTCAACCTGAGCAAGTGTCTCAACAGACTTAATTCATCTCTCC 1724
 DB 461 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 480
 QY 1725 AGTCTCAGGTAATAATATGAGCCACAACAATCTTTTCATTTGATGATACGTTTCTTTAT 1784
 DB 481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 500
 QY 1785 AAGTGTGAATCTCCCTCCAGGTTCTTGATTAACGTTCAATCAATCAATATGACTTCCAA 1844
 DB 501 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 520
 QY 1845 AAAAGAGAACTACAGCAATTTTCCAGAGTACTACTTTCTTAATCTTAACTCAAGAAATGAC 1904
 DB 521 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
 QY 1905 TTGCTGTGATCTTGAACACCAAGTTTCTGCAATGATCAAGACCAAGGACAGCTC 1964
 DB 541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTyrIleLysAspGlnArgGlnLeu 560
 QY 1965 TTGCTGAAGTTGAACGAATGATGCAACCTTCAGATTAAGACAGGAGGACTGCTGTG 2024
 DB 561 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 580
 QY 2025 CTGAGTTGATATCACTGTCAGATGAATGAACATCATTTGGTGTGCTGCTCAGT 2084
 DB 581 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 600
 QY 2085 GTGCTGTGATGATCTGTTGAGCAAGTTCTGCTATAAGTTCTAATTTCCACCTGATGCTT 2144

DB 601 ValLeuValIleSerValIleValIleValLeuValTyrLysPheTyrPheHisLeuMetLeu 620
 QY 2145 CTGCTGCTGCTGCAATAAGATGTGTAGAGGTGAAAACATCATATGATCCCTTTTATCTAC 2204
 DB 621 LeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnIleTyrAspAlaPheValIleTyr 640
 QY 2205 TCAGGACAGATGAGACTGTGGTAAGAAATGAGCTGTGAAGATTTAGAAAGAGGGGTG 2264
 DB 641 SerSerGlnAspGluAspTyrValAlaArgAsnGluLeuValLysAsnLeuGluGlyVal 660
 QY 2265 CCTGCATTTCAAGCTGTGCTTCACTACACAGACTTATTTCCGCTGTGCCATTTGCTGCC 2324
 DB 661 ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyAlaIleAlaIle 680
 QY 2325 AACATATCCATGAAGTTTCCATAAAGCCGAAAGGTATGTTGGTGTGCCAGCAC 2384
 DB 681 AsnIleIleHisGluIlePheHisLysSerArgLysValIleValValIleSerGlnHis 700
 QY 2385 TTGATCCAGAGCCGCTGTGTATCTTGAATATGATGATGCTGACCTGACCTGAGTTTCTG 2444
 DB 701 PheIleGlnSerArgTyrCysIlePheGluTyrGluIleAlaGlnThrTyrGlnPheLeu 720
 QY 2445 AGCAGTGTGCTGTGATTCATCTTCAATGTCTGACAGAGGTGAGAGACCTGCTCAGG 2504
 DB 721 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLysArg 740
 QY 2505 CACGAGGTGAGCTGTACCGCTTCTCAGCAGAAACATTAACCTGAGAGTGGAGACACT 2564
 DB 741 GlnGlnValGluLeuTyrGlnLeuLeuSerArgAsnThrTyrLeuGluTyrGluAspSer 760
 QY 2565 GTCTGTGGGCGGACACTCTCTGAGACGACTCAGAAAAGCCTGCTGATGTGTAATCA 2624
 DB 761 ValLeuGlyArgHisIlePheThrPargLysLeuArgLysAlaLeuLeuAspGlyLysSer 780
 QY 2625 TGGAAATCCAGAAAGAACAGTGGGTACAGATGCAATTTGGCAGGACCAACTTATTC 2681
 DB 781 TrpAsnProGluGlyThrValGlyThrGlyCysAsnTrpGlnGluAlaThrSerIle 799

RESULT 3
 US-10-128-166-7
 ; Sequence 7, Application US/10128166
 ; Publication No. US2003007279A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ARDITI, MOSHE
 ; APPLICANT: RAJAVASHISTH, TRIPATHI
 ; APPLICANT: SHAH, FREDIMAN K.
 ; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
 ; FILE REFERENCE: 81476-0255398
 ; CURRENT APPLICATION NUMBER: US/10/128,166
 ; CURRENT FILING DATE: 2002-04-23
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 799
 ; TYPE: PRN
 ; ORGANISM: Homo sapiens
 ; US-10-128-166-7

Alignment Scores:
 Pred. No.: 0 Length: 799
 Score: 4141.00 Matches: 799
 Percent Similarity: 100.008
 Best Local Similarity: 100.008 Mismatches: 0
 Query Match: 61.59% Indels: 0
 DB: 14 Gaps: 0

US-09-396-985b-3 (1-3811) x US-10-128-166-7 (1-799)
 QY 285 ATGAGCTGAATTTTCAAAAATCCCGACACCTCCCTTTCACAAAGAACTGGAC 344
 DB 1 MetGluLeuAsnPheTyrLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 20

Db 741 GlnGlnValGluLeuYrFrgLeuLeuSerFrgsnhrYrLeuGluTrpGluAspSer 760
 QY 2565 GTCTGGGGGGGCGACATCTTTGGAGACGACTCAAAAAGCCCTGCTGATGTGTAATCA 2624
 Db 761 ValLeuGlyTrgHisIlePheTrpArgRgLeuArgYsaIaleuLeuAspGlyLysSer 780
 QY 2625 TGGAAATCCAGAAAGACAGTGGGTACAGATGCAATTTGGCAGAGCAACATCTATC 2681
 Db 781 TrpAsnProGluGlyTrnValGlyTrgGlyCysAsnTrpGlnGluAlaTrnSerIle 799

RESULT 4

US-10-732-563-8
 ; Sequence 8, Application US/10732563
 ; Publication No. US20040132079A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gupta, Shalley K.
 ; APPLICANT: Ghosh, Tarun K.
 ; APPLICANT: Fink, Jason R.
 ; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
 ; FILE REFERENCE: 58183W0003
 ; CURRENT APPLICATION NUMBER: US/10/732,563
 ; CURRENT FILING DATE: 2003-12-10
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 8
 ; LENGTH: 799
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-732-563-8

Alignment Scores:

Pred. No.: 0 Length: 799
 Score: 4141.00 Matches: 799
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 61.59% Indels: 0
 Gaps: 0

US-09-396-985B-3 (1-3811) X US-10-732-563-8 (1-799)

QY 285 ATGAGAGCTGAATTTCTACAAATCCCGACAACTCCCTTCTCAACAGAACAGCTGAC 344
 Db 1 MetGluLeuAsnPheTrpYrIleProAsnLeuProPheSerThrIleAsnLeuAsp 20
 QY 345 CTGAGCTTTAATCCCTGAGGCAATTTAGGCGACTATAGCTTTCTCAAGTTTCCCAAGCTG 404
 Db 21 LeuSerPheAsnProLeuArgHisIleuGlySerTySerPhePheSerPheProGluLeu 40
 QY 405 CAGGTGCGATTTATCCAGGTGGAATCCAGCAATTTGAAGATGGGGCATATCAGAGC 464
 Db 41 GlnValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaTyGlnSer 60
 QY 465 CTAAAGCACTCTCTACCTTAATATTTGACAGAAACCCCATCCAGATTTAGCCCTGGGA 524
 Db 61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaIleuGly 80
 QY 525 GCCTTTTCTGACATATCAAGTTTACAGAAAGTGGTGGTGGAGACAAATCTAGCATCT 584
 Db 81 AlaPheSerGlyLeuSerSerLeuGlnIlyLeuValAlaValGluTrnAsnLeuAlaSer 100
 QY 585 CTAGAGAACTTCCCATTTGACATCTCAAAACTTTGAAGAACTTAAATGTGGCTCACAT 644
 Db 101 LeuGluAsnPheProIleGlyHisIleuLysThrLeuLysGluLeuAsnValAlaHisAsn 120
 QY 645 CTATTCATCTTTCAATTAATCTGAGTATTTTCTATCTGACCAATCTAGACACTTG 704
 Db 121 LeuIleGlnSerPheLysLeuProGluTrpPheSerAsnLeuThrAsnLeuGlnHisIleu 140
 QY 705 GACCTTTTCAGACAAACAGATTTCAAAATTTATTTAGCACAGACTGGCGGTTCTACATCA 764
 Db 141 AspLeuSerSerAsnLysIleGlnSerIleTyCysThrAspLeuArgValIleuHisGln 160

QY 765 ATGCCCCCTACTCAATCTCTCTTAGACCTGTGCCCTGAACCCCTATGAACTTATCCAGCA 824
 Db 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
 QY 825 GGTGCAATTTAAAGAAATTAAGCTTCTCATTAAGCTGACTTTTAAAGAAATATTTGATGTTA 884
 Db 181 GlyAlaPheLysGluIleArgLeuHisIlySerLeuThrLeuArgAsnAsnPheAspSerLeu 200
 QY 885 AATGTAATGAAATCTTGATATTCAGAGTCTGGCGGTTTGAAGTCCATGTTGGTCTTG 944
 Db 201 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 220
 QY 945 GAGAAATTTAGAAATGAGAAACTTGGAAGAAATTTGACAAATCTGCTCTAGAGGCGCTG 1004
 Db 221 GlyIlePheArgAsnGluGlyAsnLeuGluLysPheAspLysSerHisIleuGluGlyLeu 240
 QY 1005 TGCATTTTGAACATTTGAGAAATTCGATTTAGCATCTTATGACTACTACCTCGATGATTT 1064
 Db 241 CysAsnLeuThrIleGluGluPheArgLeuAlaTyLeuAspTyTrpLeuAspAspIle 260
 QY 1065 ATTGACTTATTTAATGTTTGAACAATGTTTCTTCAATTTTCCCTGGGTGAGTGAATTT 1124
 Db 261 IleAspLeuPheAsnCysLeuTrnAsnValSerSerPheSerLeuValSerValTrnIle 280
 QY 1125 GAAAGGTTAAAGACTTTTCTTATTAATTTCCGATGGCAACATTTAGAAATTAATGTTA 1184
 Db 281 GluArgValIlyAspPheSerTyraAsnPheGlyTrpGlnHisIleuGluLeuValAsnCys 300
 QY 1185 AAAATTTGACAGTTTCCACATTTGAAATCTCAAAATCTCTCAAAAGCTTACTTCACTTCC 1244
 Db 301 LysPheGlyGlnPheProThrIleuLysLeuLysSerLeuLysArgLeuThrPheTrnSer 320
 QY 1245 AACAAAGTGGGGAATGCTTTTTCAGAAAGTTGATCTCAAGCCCTGAGTTTCTAGATCTC 1304
 Db 321 AsnLysGlyGlyAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340
 QY 1305 AGTAGAAATGGCTGAGTTTCAAGAGTGTGCTGTTCTCAAAAGTATTTGGGACAAACAGC 1364
 Db 341 SerHisAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrTrnSer 360
 QY 1365 CTAAAGTATTTAGATCTGAGCTTCAATGCTGTTATTTACATGATTTCAAACTTTGGGC 1424
 Db 361 LeuLysTyTrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
 QY 1425 TTGAAACAATAGACATCTCGATTTCCAGCAATTTCAATTTGAAACAAATGAGTGAAGTT 1484
 Db 381 LeuGlnGlnLeuGlnHisIleuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 400
 QY 1485 TCAGTATTCCTATCACTCAGAAACCTCATTTTACCTTGACATTTCTGATCTCACACAGA 1544
 Db 401 SerValPheLeuSerLeuAsnGlnLeuIleTyLeuAspIleSerHisIleThrArg 420
 QY 1545 GTTGCTTTCAATGCAATCTTCAATGCTGTGCTGCAAGTCTGGAAGTCTTGAAGATGGCTGCC 1604
 Db 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValIleuLysMetAlaGly 440
 QY 1605 AATTTCTTCCAGGAAACCTCTTCCAGATATCTTCAAGAGCTGGAACCTTGACCTTC 1664
 Db 441 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuTrnPhe 460
 QY 1665 CTGACCTCTCTCAAGTGTCAACTGAGCAGTGTCTTCCAAACAGCATTTAATCTCACTTCC 1724
 Db 461 LeuAspLeuSerGlnCysGlnLeuGluGlnLeuSerProThrAlaPheAsnSerLeuSer 480
 QY 1725 AGTCTTCAAGTAAATATAGCCCAACACAACTTCTTTTCAATGATACGTTTCTTAT 1784
 Db 481 SerLeuGlnValIleuAsnMetSerHisAsnAsnPhePheSerLeuAspTrpPheProTy 500
 QY 1785 AAGTGTCTGAACCTCCCTCCAGGTTCTTGAATTAAGTCTCAATGCAATTAAGATTTCCAA 1844
 Db 501 LysCysLeuAsnSerLeuGlnValIleuAspTySerLeuAsnHisIleMetTrnSerLys 520
 QY 1845 AAACAGAACTACAGCATTTTCCAGTAGTCTAGCTTTTAAATCTTACTCAGAAATGAC 1904

```

Db      521  LysGInGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
Qy      1905  TTTGGCTTGTACTGTGGAACACAGAGTTTCCGCAATGATCAAGAGACAGAGGAGCTC 1964
Db      541  PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu 560
Qy      1965  TTGGTGAAGTGAACGAATGGAATGTGCAACACCTTCAGATTAAGCAGAGGAGCTGTG 2024
Db      561  LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 580
Qy      2025  CTGAGTTGAATATATACCTGTGACATGAATGAATGAAGACATCATTTGGTGTGGCTCTCAGT 2084
Db      581  LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 600
Qy      2085  GTGGTGAATGATATCGTTGTGAGAGCTGTGGCTTAAAGTTCTATTTTCACTTGAATGCTT 2144
Db      601  ValLeuValValSerValValAlaValAlaValLeuValLysPheLysPheHisLeuMetLeu 620
Qy      2145  CTTCGTGGCTGCATTAAGATATGTAGAGGTGAAGAAACATCTATGATGCTTGTATCTAC 2204
Db      621  LeuAlaGlyCysIleLysIleLysIleLysIleLysIleLysIleLysIleLysIleLys 640
Qy      2205  TCAAGCCAGATGAGAGACTGGGTTAAGATGAGATGAGTGAAGATTTGAAGAAAGGGGTG 2264
Db      641  SerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlyVal 660
Qy      2265  CCTCATTTGAGCTGTGCTTCACTACAGAGACTTATTTCCCGGTGGGCGCATTTGCTGCC 2324
Db      661  ProProPheGlnLeuCysLeuHisIleLysIleLysIleLysIleLysIleLysIleLys 680
Qy      2325  AACATCATTCATGAAGTTTCCATTAAGCCGAAAGGATGATTTGGTGGTGTCCAGAC 2384
Db      681  AsnIleIleHisGlnGlyPheHisIleLysSerArgLysValIleValValSerGlnHis 700
Qy      2385  TTCAATCCAGAGCCCGTGTGATCTTTGATATGATGATGATGCTCAGACCTGGCAGTTTCTG 2444
Db      701  PheIleGlnSerArgTrpCysIlePheGlnLysGlnIleAlaGlnThrTrpGlnPheLeu 720
Qy      2445  AGCAGTGTGTGATGATCATCTTCAATGCTCTGTCAGAGAGGTGAGAGAACCTCTGTCAGG 2504
Db      721  SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeuArg 740
Qy      2505  CAGCAGGTGAGAGTGAACCGCTTCTCAGCAGAGAACCTTACTGTGAGTGGAGAGACAGT 2564
Db      741  GlnGlnValGlnLeuLysArgLeuLeuSerArgAsnThrLysLeuGlnTrpGlnAspSer 760
Qy      2565  GTCTGTGGGCGGCAATCTTGTGAGAGACTCAGAAAGCCCTGTGATGATGAATCA 2624
Db      761  ValLeuGlnArgHisIlePheThrArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 780
Qy      2625  TGGAAATCCAGAAAGAAAGTGGGTGACAGATGCAATTTGGCAGAGAAACATCTATC 2681
Db      781  TrpAsnProGlnGlnLysIleValGlyThrCysAsnThrGlnAlaThrSerIle 799

```

```

US-10-732-796A-8
Alignment Scores:
Pred. No.: 0
Score: 4141.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 61.59%
DB: 16

US-09-396-985B-3 (1-3811) x US-10-732-796A-8 (1-799)
Qy      285  ATGAGAGTGAATTTCTAATAATCCCGACAACTCCCTTCTCAACCAAGACCTGAGAC 344
Db      1  MetGluLeuAsnPheTrpLysIleProAspAsnLeuProPheSerThrLysAsnLeuAsp 20
Qy      345  CTGAGCTTTAATCCCTGAGGAGCAATTTAGGCACTATAGCTTCTTCAAGTTTCCGAACTG 404
Db      21  LeuSerPheAsnProLeuArgHisLeuGlySerLysSerPhePheSerPheProGlnLeu 40
Qy      405  CAGGTGTGATTAATCAGGTGGAATCCAGACATGAAGATGAGGAGCAATACAGAGC 464
Db      41  GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaTrpGlnSer 60
Qy      465  CTAAAGCCACTCTCTACCTTAATATTAATGACAGAAACCCCATCCAGAGTTTACCCCTGGGA 524
Db      61  LeuSerHisLeuSerThrIleLeuThrCylAsnProIleGlnSerIleAlaLeuGly 80
Qy      525  GCTTTTCTGAGCTATGACATTTCAGAGCTGGTGGCTGTGAGACAAATCTAGCATCT 584
Db      81  AlaPheSerGlyLeuSerSerLeuGlnLysLeuValAlaValGlnThrAsnLeuAlaSer 100
Qy      585  CTGAGAGACTTCCCATTTGACATCTCAAAACTTGAAGAACTTAATGAGGCTCACAAT 644
Db      101  LeuGlnAsnPheProIleGlnHisLeuLysThrLeuLysGlnLeuAsnValAlaHisAsn 120
Qy      645  CTATCAATCTTCAATTAATCTGAGATATTTTCTATCTGACCAATCTAGAGCACTTG 704
Db      121  LeuIleGlnSerPheLysLeuProGlnLysPheSerAsnLeuThrAsnLeuGlnHisLeu 140
Qy      705  GACCTTTCCAGCAACAAAGATTCAAGATTTATTTGACAGACTTGGCGGTTCTACATCA 764
Db      141  AspLeuSerSerAsnLysIleGlnSerIleLysCysThrAspLeuArgValLeuHisGln 160
Qy      765  ATGCCCTTACTCAATCTCTCTTGAAGCTGTCGCTGAAACCTTGAACCTTATGACACA 824
Db      161  MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
Qy      825  GGTGCAATTTAAGAAATTTAGGCTTCAATAGCTGACTTAAGAAATAATTTGATAGTTTA 884
Db      181  GlyAlaPheLysGlnIleArgLeuHisLysLeuThrLeuArgAsnAsnPheAspSerLeu 200
Qy      885  AATGTAATGAACCTTGATTAACAAGTCTGGCTGTTTGAAGTCATCGTTTGGTCTG 944
Db      201  AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeu 220
Qy      945  GAGAAATTTGAAGAAATTTAGGCTTCAATAGCTGACTTAAGAAATAATTTGATAGTTTA 1004
Db      221  GlyLysPheArgAsnGlnGlyAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlyLeu 240
Qy      1005  TGCATTTGACCAATTTGAAGAAATTTCCGATTGACATTAAGTACTTACCTCGATGATATT 1064
Db      241  CysAsnLeuThrIleGlnGlnPheArgLeuAlaTrpLeuAspLysTrpLysLeuAspAspIle 260
Qy      1065  ATTGACTTATTTAATGTTTGAACAATGTTTCTTCAATTTCCCTGTGAGTGTGACTATT 1124
Db      261  IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
Qy      1125  GAAAGGTAAAGACTTTTCTTATTTATTTGAGTGAAGCAATTTGAATTAAGTAAATCTGT 1184
Db      281  GlnArgValLysAspPheSerLysAsnPheGlyTrpGlnHisLysLeuGlnLeuValAsnCys 300
Qy      1185  AAATTTGACAGTTTCCCATGAAATCAATCAATCTCTCAAAAGGCTTACTTCACTTCC 1244

```

|||||
Db 301 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 320
Qy 1245 AACCAAGTGGGATGCTTTTTCAGAGTTGATCTTACCAAGCCCTTGAGTTCTGATCTC 1304
Db 321 AsnLysGlyGlnAsnAlaPheSerGluValAspLeuProSerLeuGlnPheLeuAspLeu 340
Qy 1305 AGTGAATGGCTGAGTTTCAAGTGTGCTCTCAAGATGATTTTGGGACAACAGC 1364
Db 341 SerTrpAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
Qy 1365 CTAAAGTATTTAGATCTGAGCTTCAATGAGTGTATTAACATGATGATCAAACTTGTGGC 1424
Db 361 LeuLysTrpLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAspPheLeuGly 380
Qy 1425 TTAAACAACATCAACAATCTGGATTTCCAGATTTCCAAATTTGAAACAATAGAGATTT 1484
Db 381 LeuGlnGlnLeuGlnLysLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 400
Qy 1485 TCAGATATTCCTATCATCTGAGAAACCTCATTTACCTTGACATTTTCTCATCTCACACGA 1544
Db 401 SerValPheLeuSerLeuAspAsnLeuLysLeuAspIleSerHisThrHisThrArg 420
Qy 1545 GTTGCTTTCAATGGCATCTTCAATGGCTGTCTGACATCTGAAAGTCTTGAAATGGCTGGC 1604
Db 421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly 440
Qy 1605 AATCTTTCCAGAAAACCTTCTCCAGATATCTTCAACAGAGCTGAGAAAACCTTCAACCTTC 1664
Db 441 AsnSerPheGlnGlnLysAsnPheLeuProAspIlePheThrGlnLysAsnLeuThrPhe 460
Qy 1665 CTGACCTCTCTCAGTGCATCTGAGAGAGATGTCTCAACAGCATTTAATCTCACTCTCC 1724
Db 461 LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSer 480
Qy 1725 AGTCTTCAAGTACTAATATAGAGCCACAACAATCTTTTCAATGATGATCTTCTTAT 1784
Db 481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 500
Qy 1785 AAGGTCTGAGATCTCCCTCCAGATCTTGTATACAGTCTGCATCACTAATACATCTCCAA 1844
Db 501 LysCysLeuAsnSerLeuGlnValLeuAspLysTrpSerLeuAsnHisIleMetThrSerLys 520
Qy 1845 AAACAGGAATCAAGCATTTTTCAGATGATCTGATCTTAAATCTTAACTCAGATGAC 1904
Db 521 LysGlnGlnLysGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
Qy 1905 TTGTCTGTACTTGTGAACACCAAGTTCCTGCATGGATCAAGAGACCAAGGCAAGCTC 1964
Db 541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnArgGlnLeu 560
Qy 1965 TTGTGTGAAGTTGAACGAATGGAATGTGCACACCTTCAAGTAAAGCAGGAGATCTGTG 2024
Db 561 LeuValGlnValAlaGlnArgMetGlnCysAlaThrProSerAspLysGlnLysMetProVal 580
Qy 2025 CTGAGTTTGAATATCACTGTCAAGATGATTAAGACATCATTTGGTGTGCTCTCAAGT 2084
Db 581 LeuSerLeuAsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeuSer 600
Qy 2085 GTGCTGTAGTATCTGTGTGAGCAGTTGTGCTAATAAGTTCTAATTTTCACTGATGCTT 2144
Db 601 ValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisIleuMetLeu 620
Qy 2145 CTGTGTGCTGATCAATAATATGATGAGTGAAGAAACATCTATGATGCTTTGTATCTAC 2204
Db 621 LeuAlaGlyCysIleLysLeuTyrGlyArgGlyGlnMetIleTyrAspAlaPheValIleLys 640
Qy 2205 TCAAGCCAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2264
Db 641 SerSerGlnAspGlnAspTrpValArgAsnGlnLeuValLysAsnLeuGlnGlnGlyVal 660
Qy 2265 CCTCATTTCAAGCTCTGCTTCACTAAGAGATTTAATCCCGGTGTGGCATTTGCTGCC 2324
|||||

Db 661 ProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAlaIa 680
Qy 2325 AACATCATCATGAGATTTTCCATTAAGCCGAAGAGTGAATTTGTGGTGGTCCACGAC 2384
Db 681 AsnIleIleHisGlnGlnPheHisLysSerArgLysValIleValValValSerGlnHis 700
Qy 2385 TTCATCCAGACCCGCTGTGTATCTTTGAATATGAGATTTGCTCAGACTTGGAGTTTCTG 2444
Db 701 PheIleGlnSerArgTrpCysIlePheGlnTyrGlnIleAlaGlnThrTrpGlnPheLeu 720
Qy 2445 AGCAGTGTGTCTGTATCATCTTCTTCTTCTCAGAAAGTGGAGAAAGACCTGTCTCAGG 2504
Db 721 SerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLysArg 740
Qy 2505 CAGAGGTGAGGTGATGACGCTTCTCAGAGAAACATTAACCTGAGTGGAGAGACAGT 2564
Db 741 GlnGlnValGlnLeuTyrArgLysLeuSerArgAsnThrTyrLeuGlnTrpGlnAspSer 760
Qy 2565 GTCTGTGGGCGGACATCTTCTGAGAGACATCGAAGAAACCTGTGATGGTAAATCA 2624
Db 761 ValLeuGlnLysArgHisIlePheTrpArgArgLeuArgLysAlaLeuLeuAspGlyLysSer 780
Qy 2625 TCGAATCCAGAAAGAACATGCGGTACAGATGCAATTTGCGAGAGAACATCTATC 2681
Db 781 TrpAsnProGlnGlnThrValGlnThrGlyCysAsnTrpGlnGlnAlaTrnSerIle 799
|||||
RESULT 6
US-10-038-854-135
Sequence 135, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Vermet, Corine
APPLICANT: Eiben, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Malyankar, Uriel M
APPLICANT: Shukets, Richard A
APPLICANT: Tobernev, Velizar
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Patturajan, Meera
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gangoli, Esha A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Caeman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Ellerman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glenda
APPLICANT: Mallet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038, 854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258, 928
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259, 415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259, 785
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269, 814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279, 832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279, 833
|||||

```

; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 135
; LENGTH: 661
; TYPE: PRF
; ORGANISM: Mus musculus
; US-10-038-854-135

Alignment Scores:
Pred. No.: 1,49e-53 Length: 661
Score: 656.50 Matches: 199
Percent Similarity: 45.31% Conservative: 115
Best Local Similarity: 28.72% Mismatches: 290
Query Match: 9.76% Indels: 89
DB: 15 Gaps: 17

US-09-396-985B-3 (1-3811) x US-10-038-854-135 (1-661)

QY 192 CCGAGGCTCAGCCCTTACCCGATTCCTTCTGTAATGCTGCCGTTTATC 251
DB 3 ProasprileserysphepheleuValAlaleupheulaser---CyArGAlaThr 21
QY 252 ACG-----GAGGTGTTCTATATATTACTATTCATTCAGATGAG 290
DB 22 ThierserArpGlnLysCyAlleuLysgluValAsnLysThrYrAsnCygluAsn 41
QY 291 CTGAATTTCTCAAAATCCCGACAACCTCCCTTCTTCAACCAAGACTGAGCTGAGC 350
DB 42 LeuGlyLeuAsnGlnIleProGlyThrLeuProAsnSerThrGluCyLeuGluPheSer 61
QY 351 TTTAATCCCTGAGGACTTTGAGCACTATAGCTTTCACTTCCAGAACTGAGGTG 410
DB 62 PheAsnValLeuProThrIleGlnAsnThrThrPheSerArGLeuIleAsnLeuThrPhe 81
QY 411 CTGATTTTACAGGTGGAATCCAGACATTCAGATGAGGCAATTCAGAGCTTACG 470
DB 82 LeuAspLeuThrArGysGlnIleYrTrIleHisGluAspThrPheGlnSerGlnHis 101
QY 471 CACCTCTCTACCTTAATATTGACAGAAACCCATCCAGATTAGCCCTGAGAGCTTT 530
DB 102 ArgLeuAspThrIleuValLeuThrAlaAsnProLeuIlePheMetAlaGluThrAlaLeu 121
QY 531 TCTGACTATCAAGTTTACAGAGCTGCTGCTGAGACAAATTCAGATCTCTAGAG 590
DB 122 SerGlyProLysAlaLeuLysHisLeuPhePheIleGlnThrGlyIleSerSerIleAsp 141
QY 591 AACTCCCATGGACATCTCAAAACTTTGAAAGCTTATGAGGCTCAACAATCTTAT 650
DB 142 PheIleProLeuHisAsnGlnLysThrIleuGlnSerLeuYrLeuGlySerAsnHisIle 161
QY 651 CAATCTTCAATTAACCTGAGTATTTTCTAATCTGACCAATTCAGAGCACTTGACCTT 710
DB 162 SerSerIleLysLeuProLysGlyPheProThr---GluYrLeuLysValLeuAspPhe 180
QY 711 TCCGACAAGATTCAAAGTATTATTGACACAGCTTGCGGGTTCTATCATCAATGCC 770
DB 181 GlnAsnAsnAlaIleHisYrLeuSerLysGluAspMetSerSerLeuGlnGln----- 198
QY 771 CTACTCAATCTCTCTTAAAGCTGCTCAACCTTGAACCTTATTCACCAAGAGTGA 830
DB 199 AlaThrAsnLeuSerLeuAsnGlnLysAsnIleAlaGlyIleGluProGlyAla 218
QY 831 TTTAAAGAAATTAGCTTCATAGCTGACTTAAAGAAATATTGATGATTAAATGTA 890

```

```

DB 219 PheAspSerAlaValPheGlnSerLeu-----AsnPheGlyGlyThrGlnAsn 234
QY 891 ATGAAACTGTGATTCAGAGCTTGCCTGCTTTAGAACTCCATGCTTTGCTTCGGAGAA 950
DB 235 LeuLeuValIlePheLysGlyLeuLysAsnSerThrIleGlnSerLeuThrPheGlyThr 254
QY 951 TTTGAAATGAAAGAACTTGAAAGATTGACCAATCTGCTTGAAGGCGCTGCAAT 1010
DB 255 PheGluAspMetAspAsp---GluAspIleSerProAlaValPheGluGlyLeuCyglu 273
QY 1011 TTGACACTTGAAGAATTCGATTCAGTACTTACACTTACCTCGATGATATTATTGAC 1070
DB 274 MetSerValGluSerIleAsnLeu---GlnLysHisYrPhePheAsnIleSerSerAsn 292
QY 1071 TTATTAAATGTTGACAAATGTTCTTCAATTTCCCTGAGTGCATGACTTGAAGG 1130
DB 293 ThrPheHisCySPheSer----- 298
QY 1131 GTAAAGACTTTTCTTAATTTCCGATGGAACATTTAGAAATTGTAATGTAATTT 1190
DB 299 -----GlyLeuGlnGluLeuAspLeuThrAlaThrHisLeu 310
QY 1191 GGAACAGTTTCCCA-----TTGAAACTCAAACTCTCAAAAGCTTACTTTCACCTCC 1244
DB 311 SerGluLeuProSerGlyLeuValGlyLeuSerThrLeuLysLysLeuValLeuSerAla 330
QY 1245 AACCAAGTGGGAAT-----GCTTTTCAGAACTGATCTTACCAACCTTGAGTT--- 1295
DB 331 AsnLysPheGluAsnLeuCyGlnIleSerAlaSerAsnPheProSerLeuThrHisLeu 350
QY 1295 ----- 1295
DB 351 SerIleLysGlyAsnThrLysArgLeuGluLeuGlyThrGlyCySLeuGluAsnGlu 370
QY 1296 -----CTAGATCTCAGTAGAAATGCTGAGTTTCAAGGTTGCTGTTCTCAA 1343
DB 371 AsnLeuArgGluLeuAspLeuSerHisAspAspIleGluThrSerArpCySAsnLeu 390
QY 1344 AGTGATTTTGGGACACACCACTTAAATATTGATTCAGCTTCAATGCTGTTATTACC 1403
DB 391 GlnLeuArgAsnLeuSerHisLeuGlnSerLeuAsnLeuSerLysYrAsnGluProLeuSer 410
QY 1404 ATGAGTTCAAAAC---TCTTGAGGCTTGAACAATCAGATTCGATTCAGCAATTC 1460
DB 411 LeuLysThrGluAlaPheLysGluCySProGlnLeuGluLeuLeuAspLeuAlaPheThr 430
QY 1461 AATTGAAACAAATGAGTGAATTTTCAGTATCTTCACTCACTCAAGAACTCATTTACCT 1520
DB 431 ArgLeuLysValLysAspAlaGlnSerProPheGlnAsnLeuHisLeuLysValLeu 450
QY 1521 GACATTTCTATACTACACCAAGATGCTTTCAATGGCACTTCAATGCTGCTTCCAGT 1580
DB 451 AsnLeuSerHisSerLeuLeuAspIleSerSerGlnGlnLeuPheAspGlyLeuProAla 470
QY 1581 CTCGAAAGTCTGAAATGCTGCGCAATTTCTTCAGGAAAACTTCCT-----CCAGAT 1634
DB 471 LeuGlnHisLeuAsnLeuGlnGlnLysHisPheProLysGluAsnIleGlnLysThrAsn 490
QY 1635 ATCTTCACAGAGCTGAGAAACTTGACCTTCTGAGACTCTGACGTGAGTGAAGCAG 1694
DB 491 SerLeuGlnThrLeuGlyArgLeuGluIleLeuValLeuSerPheCySAspLeuSerSer 510
QY 1695 TTGTCTCAACAGACTTAACTCACTCTCAAGCTTTCAGGTACTTAAATATGAGCCACAC 1754
DB 511 IleAspGlnHisAlaPheThrSerLeuLysLysMetLeuAsnHisbValAspLeuSerHisAsn 530
QY 1755 AACTCTTTTCAATGATGATGTTCTTATAGAGTGTGAACCTCCAG-----GTT 1808
DB 531 Arg-----LeuThrSerSerSerIleGluAlaLeuSerHisLeuLysGlyIleYr 547
QY 1809 CTTGATTACAGTCTCATCATATGACTTCCAAAAAACAGGAACATACAGCATTTTCCA 1868

```

Db 548 LeuansleuAlaSerAenHleleSerllele-----LeuPro 560
Qy 1869 AGTAGTCTAGCTTTCTTA-----AATCTTACTCAAGAGTCTTGGT 1910
Db 561 SerleuLeuProIleleuSerGlnArgThrIleAsnleuArgGlnAsnProleuAsp 580
Qy 1911 TGTACTGTGAACACAGAGTTCCTGCAATGATCAAGACAGGAGCTCTGGTG 1970
Db 581 CysThrCysSerAenIleTyPheleuGlnUtrPyrIysGluAsnMetGlnIlyleuGlu 600
Qy 1971 GAAGTTGAACGAATGAATGTGCAACCTTCAGATAAGGAGGAGCTGTGCTAGT 2030
Db 601 AspThrGluAsnProIleuCyGluAsnProleuAsnArgIlyValArgleuSerAsp 620
Qy 2031 TTGAATATCACCCTTCAGATGAATAGACCATCATGTGTGTGCGCTTCAGTGTCTT 2090
Db 621 ValThrleuSerCysSerMetAlaAlaValGlyIlePhePheleuIleValPheleu 640
Qy 2091 GTAGTATCTGTGTGAGCAGTTCTGTCTATAGTTCTAT 2129
Db 641 ValPheAlaIleleuLeuIlePheAlaValIlystyrPhe 653
RESULT 7
; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tcherenev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Verneet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Perenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-037-417-107
Alignment Scores:
Pred. No.: 1,49e-53 Length: 661
Score: 656.50 Matches: 199
Percent Similarity: 45.31% Conservative: 115
Best Local Similarity: 28.72% Mismatches: 290
Query Match: 9.76% Indels: 89
DB: Gaps: 17
US-09-396-985b-3 (1-3811) x US-10-037-417-107 (1-661)
Qy 192 CCGAGCCTCAGCCCTTCACCCGATTCCTTGGCTTAATGCTGCGCTTTATC 251
Db 3 ProAspIleSerCysPhePheleuValAlaLeuPheleuAlaSer--CysArgAlaThr 21
Qy 252 ACG-----GAGGTGGTTCCTAATATTAATCTTAATCAATGAG 290
Db 22 ThrSerSerAspGlnIlySerCysIleGlnIlyGlnValAsnIlyThrIlyAsnCyGluAsn 41
Qy 291 CTGAATTTCAAAATCCCGACAACTCCCTCTTCAACCAAGAACTGCACTGAGC 350
Db 42 LeuGlyleuAsnGlnIleProGlyThrIleuProAsnSerThrGlyCysleuGluPheSer 61
Qy 351 TTTAAATCCCTGAGGAGATTAGGAGAGCTATAGCTTCTTGCTTCCAGAACTGAGGTG 410
Db 62 PheAsnValIleuProThrIleGlnAsnThrThrPheSerArgleuIleAsnIlyThrPhe 81
Qy 411 CTGATTTATCAGTGTGTAATCCAGACAAATGAAGATGGGACATATCAGACCTTAAGC 470
Db 82 LeuAspIleuThrArgCysGlnIleTyrrIleHisGlnAspThrPheGlnSerGlnHis 101
Qy 471 CACCTCTTAATCTTAATATTAATGAAGAACTCCATCCAGATTTAGCCTGGAGCCTTT 530
Db 102 ArgleuAspThrIleuValIleuThrAlaAsnProleuIlePheMetAlaGlnThrAlaLeu 121
Qy 531 TCTGCACTATCAAGTTTACAGAGCTGTGCTGGTGGAGCAATATAGCATCTAGAG 590
Db 122 SerGlyProIlyAlaLeuIlySerPhePheIleGlnThrGlyIleSerSerIleAsp 141
Qy 591 AACTCCCATTTGAGCATCTCAAAACTTTGAAGAACTTAATGTGGCTCAAACTTTATC 650
Db 142 PheIleProleuHisAsnGlnIlySerIleuGlnSerleuTyIleuGlnSerAenHisIle 161
Qy 651 CAATCTTCAATTAATCTGAGATTTTCTTAATCTGACCAATCTAGACACTGGACSTT 710
Db 162 SerSerIleIlySerProIlySerGlyPheProThr---GluIlySerIlyValIleAspPhe 180
Qy 711 TCCAGCAACAAGATTCAAATATTTATTAATGACAGACTGGGGTCTACATCAAAATCCC 770
Db 181 GlnAsnAsnAlaIleHisTyIleuSerIlyGlnIlySerPheSerSerleuGlnHis----- 198
Qy 771 CTACTCATCTCTTTAGACTGTCCCTGCAACCTTAATGAATCTTAATCAACAGAGTGCA 830
Db 199 AlaThrAsnIleuSerIleuAsnIlyAsnAspIleAlaGlyIleGlnProGlyAla 218
Qy 831 TTAAAGAAATTAAGCTTCATTAAGCTGACTTTAAGAAATTAATTTGATAGTTAAATGTA 890
Db 219 PheAspSerAlaValPheGlnSerIleu-----AsnPheGlyGlnThrGlnAsn 234
Qy 891 ATGAAACTGTATTCAGAGTCTGGCTGTGTTGAAGTCCATGCTTGGTTCGGGAGAA 950
Db 235 LeuIleuValIlePheIlySerGlyIleuIlyAsnSerThrIleGlnSerIleuThrPleuGlyThr 254
Qy 951 TTGAAGAAATGAAGAACTTGAAAGTTTGAACAATCTGCTCTAGAGGCGCTGTGCAAT 1010

Db 11leHisGluAerThrPheGlnSerHisHisGlnLeuSerThrLeuValLeuThrGlyAsn 111
 Qy 501 CCCATCCAGAGTTAGCCCTGGAGCCCTTTCTGACATACAACTTTACAGAACTGGTG 560
 Db 112 ProLeuIlePheMetAlaGluThrSerLeuAsnGlyProIysSerLeuValSerLeuPhe 131
 Qy 561 GCTTGAGAGCAAACTAGCATCTCTAGAGAACTTCCCATTTGACATCCAAAATCTTGG 620
 Db 132 LeuIleGlnThrGlyIleSerAsnLeuGlnPheIleProValHisAsnLeuGluAsnLeu 151
 Qy 621 AAGAACTTAATGGCTGCACAACTTATCCAACTTTTCAAAATTAACCTGAGATTTTCT 680
 Db 152 GluSerLeuThrLeuGlySerAsnHisIleSerSerIleLysPheProIysAspPhePro 171
 Qy 681 AATGTACCAATCTAGACATTTGACCTTTCCAGCAACAAGATTCAAAGATTATATTC 740
 Db 172 ---AlaArgAsnLeuValLeuAspPheGlnAsnValIleHisIleTyrIleSerArg 190
 Qy 741 ACAGACTTGGGGTTCTACATCAATAGCCCTACATCACTCTCTTATAGACTGCTCCCTG 800
 Db 191 GluAspMetArgSerLeuGlnGln-----AlaIleAsnLeuSerLeuAsnPheAsnGly 208
 Qy 801 AACCTTGAACCTTATTCACAACAGGTGCATTTAAAGAAATTAAGCTTCATTAAGCTGACT 860
 Db 209 AsnAsnValIysGlyIleGluLeuGlyAlaPheAspSerThrValPheGlnSerLeu--- 227
 Qy 861 TTAAGAAATATTTTGAATGTTAAATGTAATGAAACTTGTATTCAAAGCTGAGCTGGCT 920
 Db 228 -----AsnPheGlyIleThrProAsnLeuSerValIlePheAsnGlyLeuGlnAsn 244
 Qy 921 TTAGAAGTCCATCGTTTGGTCTGGAGAAATTTAGAAATTAAGAAACTTGAAGAACTTT 980
 Db 245 SerThrThrGlnSerLeuThrLeuGlyIleThrPheGlnAspIleAspArg---GluAspIle 263
 Qy 981 GACAAATGCTCTAGAGAGGCTGTGCATTTGACATTTGAAGAATTCGATTAAGCATAC 1040
 Db 264 SerSerAlaMetLeuLysGlyLeuGlySerGlyMetSerValGluSerLeuAsnLeuGln-- 282
 Qy 1041 TTAGCATCTACCTCGATGATATTAATTAAGAC---TTATTAATGTTTGAACAAGTTTCT 1097
 Db 283 ---GluHisArgPheSerAspIleSerSerThrThrPheGlnCysPheThrGlnLeuGln 301
 Qy 1098 TCATTTTCCCTGAGTGTGACTATTTGAAGGGTAAAGAACTTTTCTTATTAATTTCCGA 1157
 Db 302 GluLeuAspLeuThrAlaThrHisLeuLysGlyLeuProSer-----Gly 316
 Qy 1158 TGGCAACATTTAGATTAGTTAAC----- 1181
 Db 317 MetLysGlyLeuAsnLeuLeuLysLeuValLeuSerValAsnHisPheAspGlnLeu 336
 Qy 1182 TGTAATTT-----GACAGATTTCCCAATTTG-----AAATCC 1214
 Db 337 CysGlnIleSerAlaAlaAsnPheProSerLeuThrHisLeuTyrIleArgGlyAsnVal 356
 Qy 1215 AAATCTCTCAAAAGGCTTACTTTCACTTCCAAAGGCTGGAGATCTTTTCCAGAGTT 1274
 Db 357 LysLysLeuHisLeuGlyValGlyCysLeuGlnLysLeuGlyAsn----- 371
 Qy 1275 GATCTACCAAGCTTGAAGTTTCTAGATCTCAGTAGAAATTCGCTTGAAGTTTGC 1334
 Db 372 -----LeuGlnThrLeuAspLeuSerHisAsnAspIleGluAlaSerAspArg 387
 Qy 1335 TGTTCCTCAAGTATTTTGGAGCAACAGCCTTAAGTATTTAGATCTGAGCTCAATGCT 1394
 Db 388 CysSerLeuGlnLeuLysAsnLeuSerHisLeuGlnThrLeuAsnLeuSerHisAsnGln 407
 Qy 1395 GTTATTCACATGAGTTCAAC---TTCTGGGCTTGAACAACATGAAATCATCTGAGTTTC 1451
 Db 408 ProLeuGlyLeuGlnSerGlnAlaPheLysGlyCysProGlnLeuGlnLeuLeuAspLeu 427
 Qy 1452 CAG-----CATTCATTTGAACAACATGAGTGAAGTTTCA-----GTATTC 1493
 Db 428 AlaPheThrArgLeuHisIleAsnAlaProGln---SerProPheGlnAsnLeuHisPhe 446

Qy 1494 CTATTCATCGAAGAACTCATTTTAC-----CTTGACATTTTCTGATCTACACAGAGTT 1547
 Db 447 LeuGlnValLeuAsnLeuThrTyrCysPheLeuAspThrSerAsnGlnHis----- 463
 Qy 1548 GCTTTCAATGGCATCTTCAATGGCTTGTCCAGTCTCGAAGCTTGAAGATGCTGGCAAT 1607
 Db 464 -----LeuLeuAlaGlyLeuProValLeuArgHisLeuAsnLeuLysGlyAsn 479
 Qy 1608 TCTTTCCAGAAACATCTCTT-----CCAGATATCTTACAGAGCTGAGAACTTGACC 1661
 Db 480 HisPheGlnAspIleThrIleThrLysThrAsnLeuLeuGlnThrValGlySerLeuGln 499
 Qy 1662 TTCCTGACCTCTCTGAGTGTCACTGATGAGACAGCTGTCTCCAAACAGCATTTAAGTACTC 1721
 Db 500 ValLeuIleLeuSerCysGlyLeuLeuSerIleAspGlnAlaPheHisSerLeu 519
 Qy 1722 TCCAGTCTTCAGGTAATTAATATAGCCACACAACTTCTTT-----TCATTGATACG 1775
 Db 520 GlyLysMetSerHisValAspLeuSerHisAsnSerLeuThrCysAspSerIleAspSer 539
 Qy 1776 TTTCTCTTAT-----AACTGTGAACCTCCCTCCAGTCTTTGAT 1814
 Db 540 LeuSerHisLeuLysGlyIleTyrLeuAsnLeuAlaAlaAsnSerIleAsnIleIleSer 559
 Qy 1815 TACAGTCTCAATGACATTAATGACTTCCAAAAAACAGAACTACAGCATTTTCCAAAGTAT 1874
 Db 560 ProArgLeuLeuProIleLeu-----SerGln 568
 Qy 1875 CTAGCTTTCTTAATCTTACTCAGAAATGACTTTGCTTGTACTTGTGAACACAGACTTTC 1934
 Db 569 GlnSerThrIleAsnLeuSerHisAsnProLeuAspCysSerAsnIleHisPhe 588
 Qy 1935 CTGCAATGATCAAGACACAGAGCAGCTTGTGTGTGAATGTAACGAATGCAATGCA 1994
 Db 589 LeuThrTyrTyrLysGluAsnLeuHisLysLeuGlnGlySerGlnGluThrThrCysVal 608
 Qy 1995 ACACCTTCAGATTAAGCAGGCGATGCTGTGCTGATGTTGAATTCACCTTGCAGATTAAT 2054
 Db 609 AsnProProSerLeuArgGlyValLysLeuSerAspValLysLeuSerCysGlyIle--- 627
 Qy 2055 AAGACATCATCTGCTGTGTGCTGCTCCTCAGTGTCTGTGATCTGTTGTAAGAGTTTCTG 2114
 Db 628 ---ThrAlaIleGlyIlePhePheLeuIleValIlePheLeu---LeuLeuAlaIleLeu 645
 Qy 2115 GTCTAT 2120
 Db 646 LeuPhe 647

RESULT 9
 US-10-038-854-134
 ; Sequence 134, Application US/10038854
 ; Publication No. US20040022781A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Li, Li
 ; APPLICANT: Wolenc, Adam R
 ; APPLICANT: Eisen, Andrew J
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Malyankar, Uriel M
 ; APPLICANT: Shinkets, Richard A
 ; APPLICANT: Tchernev, Velizar A
 ; APPLICANT: Spaderna, Steven K
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Kekuda, Ramesh
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Gusev, Vladimir Y
 ; APPLICANT: Gangoili, Esha A
 ; APPLICANT: Guo, Xiaojia S
 ; APPLICANT: Shenoy, Suresh G
 ; APPLICANT: Raetelli, Luca
 ; APPLICANT: Caeman, Stacie J


```
QY 1548 GCTTTCAATGCATCTTCAATGGCTTGTCCAGTCTCGAAGTCTTGAATAATGGCTGGCAAT 1607
Db 464 -----LeuLeuAlaGlyLeuProValLeuArgHisValLeuAlaLysGlyAsn 479
QY 1608 TCTTCCAGGAAACCTTCCTT-----CAGATATCTTCAACAGACTGAGAACTTGACC 1661
Db 480 HisHegInaRgLyThrIleThrIleThrAspLeuLeuGlnThrValGlySerLeuGlu 499
QY 1662 TTCTGGACCTCTTCTGAGTCTCAATGAGACAGTGTCTCCACAGCATTTAACTCACTC 1721
Db 500 ValLeuIleLeuSerSerCySGlyLeuLeuSerIleAspGlnGlnIleAspHisSerLeu 519
QY 1722 TCCAGTCTCAGTACATAATATATAGCCACACAACTTCCTT-----TCATTGATACG 1775
Db 520 GlyLysMetSerHisValAspLeuSerHisAsnSerLeuThrCyAspSerIleAspSer 539
QY 1776 TTTCCTTAT-----AAGTGTCTGAATCTCTCCAGTTCCTTGAT 1814
Db 540 LeuSerHisLeuLysGlyIleTyLeuAlaSerLeuAlaIleAsnSerIleAsnIleIleSer 559
QY 1815 TACAGTCTCAATCACTAATGACTTCCAAAAACAGAACTACAGCAATTTCCAGTACT 1874
Db 560 ProArgLeuLeuProIleLeu-----SerGln 568
QY 1875 CTAGCTTTCTTAATCTTACTCAGATGACTTGTGCTGTGACTTGTGAACACACAGTTTC 1934
Db 569 GlnSerThrIleAsnLeuSerHisAsnProLeuAspCySerHisValIleHisPhe 588
QY 1935 CTGCAATGATCAACAGACACAGGACAGCTTGTGTGAAGTTGAACAAATGGAATGTGA 1994
Db 589 LeuThrTrpTyLysGlyAlaSerLeuHisValYsLeuGluGlySerGluGluThrThrCyAla 608
QY 1995 ACACCTTCAAGTAAACAGGAGCATGCTGCTGCTGAGTTGAATGACCTGTCAAGTAAAT 2054
Db 609 AsnProGlySerLeuArgGlyValIleYsLeuSerAspValIleYsLeuSerCySGlyIle--- 627
QY 2055 AAGCAATCAATGAGTGGTGGTGGCTCAGTGTGCTGATGATGATGTTGTGACAGTTCTG 2114
Db 628 ---ThrIleAlaGlyIlePhePheLeuIleValIlePheLeu---LeuLeuAlaIleLeu 645
QY 2115 GTCTAT 2120
Db 646 LeuPhe 647

RESULT 10
US-09-950-041-4
; Sequence 4, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kaestlein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OR INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XK1
; CURRENT APPLICATION NUMBER: US/09/950, 041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-950-041-4

Alignment Scores:
Pred. No.: 2,096-48 Length: 784
Score: 603.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 8.98% Indels: 219
DB: 10 Gaps: 38

US-09-396-985b-3 (1-3811) x US-09-950-041-4 (1-784)
QY 306 ATCCCGGACAACTCCCTCTTCAACCAAGAACTTGACCTTAAATCCCTGAGG 365
Db 46 IleProSerGlyLeuThrGlnAlaValIysSerLeuAspLeuSerHisAsnArgIleThr 65
QY 366 CATTTAGGACGTATAGCTTCTTCACTTCCAGAACTGACAGTCTGATTTATCCAGG 425
Db 66 TyIleSerHisSerAspLeuGlnArgCyValAsnLeuGlnAlaLeuValIleThrSer 85
QY 426 TGTGAATCCAGCAATTGAAGATGGGAGATATCAGAGCTTAAGCCACTCTTACCTTA 485
Db 86 AsnGlyIleAsnThrIleGluGlnAspSerPheSerLeuGlySerLeuGlnHisLeu 105
QY 486 ATATTGACAGAAACCCCATCCAGAGTTTAAAGCCCTTGAGACCTTTCTGAGCTATCAAGT 545
Db 106 AspLeuSerTyIleAsnTyIleuSerAsnLeuSerSerTrpPheLysProLeuSerSer 125
QY 546 TTTCAGAGCTG-----GTGGCTGTGGAG 569
Db 126 LeuThrPheLeuAsnLeuLeuGlyAsnProTyLysThrLeuGlyGluThrHisSerLeuPhe 145
QY 570 ACAATCTGACATCTGTAGAGAACTCCCATGACATCTCAAACT----- 617
Db 146 SerHisLeuThrIysLeuGlnIleLeuAlaGlyValGlyAsnMetAspThrPheThrIysIle 165
QY 618 -----TTGAAGAACTTAATGTGGCTCAAACTTT 647
Db 166 GlnArgLysAspPheAlaGlyLeuThrPheLeuGlnGluLeuGluIleAspAlaSerAsp 185
QY 648 ATCCAACTTTCAAAATTAATCTGAGTATTTTCAATCTGACCAATCAAGCACTTGAGAC 707
Db 186 LeuGlnSerTyIleGlu---ProYsSerLeuLysSerIleGlnAsnValSerHisLeuIle 204
QY 708 TTTCCAGCAACAAG-----ATTCAAAGTAT 734
Db 205 LeuHisMetLysGlnHisIleLeuLeuLeuGlnIlePheValAspValThrHisSerVal 224
QY 735 TATTGACAGACTGGGGGTTTACATCAATGCCCTACTCAATCTCTTTAGACCTG 794
Db 225 GluCyLeuLeuIleuArg-----AagThr 232
QY 795 TCCCTGAACCTTGAACCTT-----ATCAACAGGTGCATTTAAGAAATTAAGCTT 848
Db 233 AspLeuAspThrPheHisPheSerGlyLeuSerThrGlyGluThrAsnSerLeu---Ile 251
QY 849 CATTAAGCTACTTTAAGAAAT-----AATTTGATGTTTA---AATGTAATGAA 896
Db 252 LysLysPheThrPheHisGlnValIysIleThrAspIleuSerLeuPheGlnAlaMetLys 271
QY 897 ACTTGT-----ATTCAGGCTGTGGCTGTTTGAAGTCCATCGTTTGTTCTG----- 944
Db 272 LeuLeuAsnGlnIleSerGlyLeuLeuGluLeuGluPheAspAspCyThrLeuAsnGly 291
QY 945 ---GGAGATTTTGAATGAAGAACTTGAAAGTTTGAACAATCTGCTTAGAGGC 1001
Db 292 ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyLysValGlu--- 310
```

```

Qy 1002 CTGTCATTTGACCATTTGAAGAAATTCGATTAAGCA-----TACTTAGACTACTACTC 1055
    |||||
Db 311 -----ThreuthrIleArgIleuHisIleProArgPheTyIleuPheTyr----- 326
Qy 1056 GATGATATTATTGACTTATTAAATTTGTTGACAAATGTTTCTTCAATTTTCCCTGGTGA 1115
    |||||
Db 327 ---AspLeuSerThrIleuTySerIleuThrGluArgValys-----Arg 340
Qy 1116 GTGACTATTGAAAGGGTAAAGACTTTCTTATATATTCCGATGGCAGCATTTAGAAATTA 1115
    |||||
Db 341 IlethrValGluAsnSerIlyValPhe-----Leu 350
Qy 1176 GTTACTGTAAATTTGACAGTTTCCCATTTGAAATCTCAATCTTCGAAAAGGCTTACT 1235
    |||||
Db 351 ValProCysLeuLeuSerGln----- 357
Qy 1236 TTCACCTTCAACAAAGGTGGGAATGCTTTTTCAGAAATTGATCTTACCAAGCTTGAAGTT 1295
    |||||
Db 358 -----HisLeuTySerIleuGluTyr 364
Qy 1296 CTAGATCTCAGTAAAT-----GGCTTGAAGTTTCAAGGTTGCTGTTCT 1340
    |||||
Db 365 LeuAspLeuSerGluAsnLeuMetValGluGluTyrLeuTyAsnSerAlaCys----- 382
Qy 1341 CAAAGTGAATTTGGGACACACGCTTAAAGTATTAGATCTGAGCTTCAATGGTGTAT 1400
    |||||
Db 383 -----GluAspAlaTTrProSerIleuGlnThrIleuIleuArgGlnAsn----- 397
Qy 1401 ACCATGAGTCAAACTTGTGGCTTAGACAACTAGAACATCTGTGATTTCCAGCATTC 1460
    |||||
Db 398 -----HisLeu-----Ala 400
Qy 1461 AATTGAAACAATGAGAGTGTTCAGTATTCCTATACACAGAAACCTGATTTACTT 1520
    |||||
Db 401 SerIleuGluTyThrGlu-----ThreuthrIleuTyAsnSerAlaAsnIle 418
Qy 1521 GACATTTCTCATCTACACACAGAGTTCTTTCAATGCAATCTTCATGAGCTTGCCAGT 1580
    |||||
Db 419 AspIleSerIys----- 422
Qy 1581 CTCGAGTCTTGAATAAGGCTGGCAATCTTTCCAGGAAAATTCCTCCAGATATCTTC 1640
    |||||
Db 423 -----AsnSerPheHisSer-----MetProGluThrCys 432
Qy 1641 ACAGAGCTGAGAACTTGACCTTCTCTGACCTCTCTCAGTGTCACTGAGACAGTGTCT 1700
    |||||
Db 433 GlnTrpProGluTyMetLeuTyIleuAsnLeuSerThrIleuHisSerValThr 452
Qy 1701 -----CCAAACGACATTTAACTCACTCTCCAGTCTTCAAGTAAATATGAGCCAC 1751
    |||||
Db 453 GlyCysIlePro-----LysThrIleuGluIleuAspValSerAsn 466
Qy 1752 AAC-----AAGCTTTTTCATTTGAT----- 1772
    |||||
Db 467 AsnAsnLeuAsnLeuPheSerIleuAsnLeuProGlnLeuTyGluLeuTyIleSerArg 486
Qy 1773 -----AGCTTTCCCT---TATAAGTGTCTGAAGCTCCCTCCAGGTTCTTGATTAC 1817
    |||||
Db 487 AsnIysLeuMetThrIleuProAspAlaSerLeuLeuProMetLeuValLeuIlySle 506
Qy 1818 AGTCTCATCATCATATGACTTCCAAAACAGAACTAGACAGATTTTCCAAAGTATGCTA 1877
    |||||
Db 507 SerArgAsnAlaIleThrThrPheSerIyGluGlnLeuAspSerPhe---HisThrIleu 525
Qy 1878 GCTTTCTTAAATCTTACTCAGATGACTTTCCTTGCTACTTGATGAAACAGACAGTTTCC 1937
    |||||
Db 526 LysThrIleuGlnAlaGlyGlyAsnAsnPheIleCysSerCysGluPheLeuSerPheThr 545
Qy 1938 CAATGATCAAGACGACAGGAGCTCTTGCTGGAAGTT-----GAACGA 1982
    |||||
Db 546 Gln-----GluGlnGlnAlaLeuAlaIysValIleuIleAspTrpProAlaAsn 561
Qy 1983 ATGGAATGTGCAACACTTCAGATTAAGACAGGAGCATGCTGTGCTGAGTTGAATATCACC 2042

```

```

Db 562 TyIleuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581
Qy 2043 -----TCTGAGATGAATTAAGACCATCATTTGCTGTGTGCGCTCCAGTGTCTGTA 2093
    |||||
Db 582 ValSerGluCysHisArgThrAlaLeuValSerIlyMetCysValAlaLeuPheLeu 601
Qy 2094 GTATCTGTGTAGACAGTTCTGTGTCTATAGTTCTAT-----TTTCACTGTATGCTTCT 2147
    |||||
Db 602 IleuLeuThrGlyValIleuLeuCysHisArgPheHisGlyLeuTrpTyIleuTyMetCys 621
Qy 2148 GCTGGCTGCAATTAAGTATGTAGA-----GGTGAACATC---TAT 2186
    |||||
Db 622 TrpAlaTrpLeuGlnAlaIlySerGlyProArgIlyAspAlaProSerArgAsnIleCysTyr 641
Qy 2187 GATGCCCTTTGTATCTATCTCAAGCCAGATGAGACCTGGGTGAAGATGAGCTGTAAAG 2246
    |||||
Db 642 AspAlaPheValSerTySerGluArgAspAlaTyTrpValGluAsnLeuMetValGln 661
Qy 2247 AATTAGAAAGAGGGGTGCTCCATTTCACTGTGCTGCTTCACTACAGACACTTATTTCC 2306
    |||||
Db 662 GluLeuGluAsnPheAsnProProPheIlyLeuCysLeuHisIlyAspArgAspPhePro 681
Qy 2307 GGTGTGGCAATGCTGTCCCAATCATCATGAAAGTTTCCATTAAGCCGAAAGTGATT 2366
    |||||
Db 682 GlyIysTrpIleIleAspAsnIleIle---AspSerIleGluTySerHisIlyThrVal 700
Qy 2367 GTTGTGTGTCCCAAGCACTTCATCAAGCCGCTGGTGTATCTTTGAATATGAAATGCT 2426
    |||||
Db 701 PheValIleuSerGluAsnPheValIlySerGluTrpCysIlyTyrgIleuAspPheSer 720
Qy 2427 CAGACCTGGCAGTGTCTTGAGAGTCGTGCTGTATCATCTTCATTTCTCCGACAGAGTG 2486
    |||||
Db 721 HisPheArgLeuPheGluGluAsnAspAlaAlaIleuIleuLeuGluProIle 740
Qy 2487 GAGAAAGCCCTGTCTCAGACAGAG---GTGAGCTGTACCGCTTCTCAGACAGACAT 2543
    |||||
Db 741 GluIlySerAlaIleProGlnArgPheCysIlyLeuArgIlyIleMetAsnThrIlyThr 760
Qy 2544 TACTGTGAGTGGAGAGACAGTGTCTGGGCGGACATCTTCTGAGACAGCACTAGAAA 2603
    |||||
Db 761 TyIleuIlyTrpProMetAspGluAlaGlnArgGluIlyPheTrpValAsnLeuArgAla 780
Qy 2604 GCCCTG 2609
    |||||
Db 781 AlaIle 782

RESULT 11
US-10-456-947-46
; Sequence 46, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456,947
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147,447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-456-947-46
Alignment Scores:

```

Pred. No.:	2.09e-48	Length:	764
Score:	603.50	Matches:	2330
Percent Similarity:	41.88%	Conservative:	1388
Best Local Similarity:	27.03%	Mismatches:	2822
Query Match:	8.9%	Indels:	219
DB:	15	Gaps:	38

US-09-396-985B-3 (1-3811) x US-10-456-947-46 (1-784)

Qy	306	ATCCCGGACAACTCCCTCTCTCAACCAAGAACTCGACCTTAGCTTTAAATCCCTGAGG	365
Db	46	IIleProSerGIyLeuThrGIuAlaValIlySerLeuAspLeuSerAsnAspArgIIleThr	65
Qy	366	CATTAGGACAGCTTAAGCTTCTTCAGTTTCCAGAACTCGACGTCGTGAAATTATTCACGAG	425
Db	66	TYrIIleSerAsnSerAspLeuGIuArgCysValAsnLeuGIuAlaLeuValLeuThrSer	85
Qy	426	TGTGAAATCCAGACAATTGAAGTGGGACATATACAGACCTTAGCCACTCTTACCTTA	485
Db	86	AsnGIyIIleAsnThrIIleGIuGIuAspSerPheSerSerLeuGIySerLeuGIuHISLeu	105
Qy	486	ATATTGACAGGAAACCCCATCCAGAGTTTAGCCCTGGAGACCTTTCTTGACATAACAGT	545
Db	106	AspLeuSerTYrAsnTYrLeuSerAsnLeuSerSerSerTYrPheIysProLeuSerSer	125
Qy	546	TTACAGAGCTG-----GTGGCTGTGAG	569
Db	126	LeuThrPheLeuAsnLeuLeuGIuAsnProTYrIyThrIIleuGIyGIuThrSerIleuPhe	145
Qy	570	ACAAATTCAGACATCTCTAGAGAACTCCCATTTGACATCTCAAACT-----	617
Db	146	SerHISLeuThrIyLeuGIuIIleuArgValGIyAsnMetAspThrPheThrIySile	165
Qy	618	-----TGAAAGAACTTAATGTGGCTCACAAATCTT	647
Db	166	GIuArgIyAspPheAlaGIyLeuThrPheLeuGIuGIuLeuGIuIIleAspAlaSerAsp	185
Qy	648	ATCCAAATCTTTAAATTAACCTGAGTATTTTCTAATCTGACCAATCTGACAGCACTTGAGC	707
Db	186	LeuGIuSerTYrGIu---ProIySerLeuIySerIIleGIuAsnValSerHISLeuIIe	204
Qy	708	CTTTCCAGCAACAAG-----ATTCAAGTATT	734
Db	205	LeuHISMetIySleGIuHISIIleLeuLeuLeuGIuIIlePheValAspValThrSerSerVal	224
Qy	735	TATTGCACAGACTTCGGGTTTCAATCAATGCCCCCTAATCTCTTTAAGACTCG	794
Db	225	GIuCYySleuGIuLeuArg-----AspThr	232
Qy	795	TCCCGCAACCCCTATGAACTTT-----ATCCAAACAGGCGATTTAAAGAAATTAGGGCT	848
Db	233	AspLeuMetThrPheHISPheSerGIuLeuSerThrGIuThrAsnSerIeu---IIe	251
Qy	849	CATAAGCTGACTTTAAGAAAT-----AATTTGATAGTTTA---AATGTAATGAAA	896
Db	252	IySlySPheThrPheArgAsnValIySileThrAspGIuSerLeuPheGIuValMetIyS	271
Qy	897	ACTTGT-----ATTCAAGGTCTGGCTGGTTTGAAGATCCATCGTTTGGTTCTG-----	944
Db	272	LeuLeuAsnGIuIIleSerGIyLeuLeuGIuLeuGIuPheAspAspCYyThrIleuAsnGIy	291
Qy	945	---GGAGAAATTTAGAAATGAAGAAACTTGAAAGATTTGACAAATCTGCTTAGAGGGC	1000
Db	292	ValGIyAsnPheArgIaSerAspAsnAspArgValIIleAspProGIyIySValGIu---	310
Qy	1002	CTGTGCAATTTGACCAATTGAAGAAATTCGATTAGCA-----TACTTAGACTTAACCTC	1055
Db	311	-----ThrLeuThrIIleArgArgLeuHISIIleProArgPheTYrLeuPheTYr-----	326
Qy	1056	GATGATATTATTAGCTTATTATTATGTTTGACAAATGTTTCTTCAATTTCCCTGGTAGCT	1111
Db	327	---AspLeuSerThrIleuIySerLeuThrGIuArgValIyS-----Arg	340

OY		1116	GTCACATTTGAAAGGGTAAGAAGCTTTCCTATAATTGTGGATGGCAACTTGAATTA	1175
Dd		341	IleThrValIglubnsSerLysValPhe-----Leu	350
OY		1176	GTTAATCGTAAATTTGGACAGTTTTCCACATTGAAAACAATCTCCTCAAAGGCCTTACT	1235
Dd		351	ValProCysLeuLeuSerGln-----	357
OY		1236	TTCACITTCCAACAAAGGTGGAAATGCTTTTCAGAAAGTGATTCACCAGCCTTAGCTT	1295
Dd		358	-----HisLeuSerLeuGlutlTy	364
OY		1296	C TAGATCTCACGTAGAAAT-----GCCGTGAGTTCCAAGGTTCGTCTTCT	1340
Dd		365	LeuAspLeuSerGluAbnMetValIgluglutlTyLeuLysAsnSeraLaCys-----	382
OY		1341	CAAAAGTATTTGGGACAAACAGCCTTAAGATTTATTCATCTGAGCTTCATNGGNTATT	1400
Dd		383	----GluAspAlaTrpProSerLeuGlnThrLeuLeuArgGlnAsn-----	397
OY		1401	ACCATGAGTTCAAACTTCCTGGCGCTTAGAACCATAGAACATCTGGATTTCCAGCATTCC	1460
Dd		398	-----HisLeu-----Ala	400
OY		1461	AATTGTAACAAATGAGTGAGTTTCAGTATTCCTATCACTCAGAAAACTCATTTACTCT	1520
Dd		401	SerLeuGlnLysThrArgLglin-----ThrLeuLeuThrLeuLysAbnLeuThrAsnIle	418
OY		1521	GACATTTCTCAATCTCACACAGAGTTGCTTCAATGACATCTTCATNGGCTTGTCCAGT	1580
Dd		419	AspLisSerLys-----	422
OY		1581	CTCGAAGCTTGAAMAATGCGTCGCAATCTTTCACAGAAAACTTCCTCCAGATATCTTC	1640
Dd		423	-----AsnSerPheHisSer-----MetProGluThrCys	432
OY		1641	ACAGAGCTGAGAACTTGACCTTCCTGGACCTCTCTCAIGTCACTGAGACAGCTGTCT	1700
Dd		433	GlnTrpProGluLysMetLysTYrLeuAbnLeuSerThrArgIleHisSerValThr	452
OY		1701	-----CCAAAGACATTTAACTCACTCTCCAGCTCTCCAGACACTTAATATGAGCAC	1751
Dd		453	GlyCysIlePro-----LysThrLeuGluIleLeuAspValSerAsn	466
OY		1752	AAC-----AACTCTTTTCATTGGAT-----	1772
Dd		467	AsnAsnLeuAbnLeuPheSerLeuAsnLeuProGlnLeuLysGluLeuTYrIleSerArg	486
OY		1773	-----ACGTTTCT--TATTAAGTGTCAACTCCCTCCAGGTTCTTGAATAC	1817
Dd		487	AsnLysLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValLeuLysIle	506
OY		1818	AGTCTCAATCAATTAAGACTTCCAAAAACAGAACTTACAGACTTTTCCAAAGTAAGCTA	1877
Dd		507	SerArgAsnAlaIleThrTrpSerLysGlnGlnLeuAspSerPhe--HisThrLeu	525
OY		1878	GCTTTCCTTAATCTTACTCAGAAATGACTTGTCTTGTACTTGTAAGACACAGAGTTTCTGT	1937
Dd		526	LysThrLeuGlnWalaglLyglYAsnAspHeliLeysSerCysGlnLeuLeuSerPheThr	545
OY		1938	CAATGATCAAGACCAAGGAGCAGCTTGTGTGAAGTT-----GAAACA	1982
Dd		546	Gln-----GluGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsn	561
OY		1993	ATGGAATGTGACAACTTTCAGATTAAGCAGGGACGCTGTGCTGAAGTTGAATATACAC	2042
Dd		562	TyrLeuCysAspSerProSerHisValArgLygInGlnValGlnAspValArgLeuSer	581
OY		2043	-----TGTCAAGATGAATTAAGACATCATGTCGGTGCGGTGCTCCAGTGTCTTGTGA	2093
Dd		582	ValSerGluCysHisArgThrAlaLeuValSerGlyMetCysCybaAlaLeuPheLeuLeu	601
OY		2094	GTAATCTGTGTGAGACAGTTCTGTGCTTAAAGTTCTAT-----TTTCACTGATGCTTCTT	2147


```

Db      252  LysylSerPheThrPheArgAsnValLysIleThrAspGlnSerLeuPheGlnValMetLys 271
Qy      897  ACTTGT-----ATTCAAGGTCGGCGGTGTTTAGAAGTCCATCGTTGGTTGG----- 944
Db      272  LeuLeuAsnGlnIleSerGlyLeuLeuGlnLeuGlnPheAspSerGlyThrLeuAsnGly 291
Qy      945  ---GGAAATTAGAAATGAAAGAACTGGAAAGTTTGAACAATCGCTGAGAGGC 1001
Db      292  ValGlyAsnPheArgAlaSerAspAsnAspArgValIleAspProGlyLysValGln--- 310
Qy      1002  CTGTGCAATTGTGACCATTTGAAGAATCCGATTAGCA-----TACTTAGACTACTACCTC 1055
Db      311  -----ThrLeuThrIleArgArgLeuHisIleProArgPheGlyLeuPheGly----- 326
Qy      1056  GATGATATTATGACTATTATTAATTGTTTGAACAATGTTTCTCATTTTCCCTGGTAGT 1115
Db      327  ---AspLeuSerThrLeuGlySerLeuThrGlnArgValLys-----Arg 340
Qy      1116  GTGACTATTGAAAGGGTAAAGACTTTTCTATATTAATTCCGATGGCAACATTAGAAATTA 1175
Db      341  IleThrValGlnAsnSerLysValPhe-----Leu 350
Qy      1176  GTTAACTGTAAATTGGACAGTTTCCACATTTGAACCTCAATCTCAAAAGGCTTAAT 1235
Db      351  ValProCysLeuLeuSerGln----- 357
Qy      1236  TTCACTTCCAAAGGCGGAATCGTTTTCAGAAAGTTGATCTTACCAAGCTTGAGTTT 1295
Db      358  ----- 364
Qy      1296  CTAGATCTCAGTAGAAT-----GGCTTGAGTTTCAAGGTTGCTGTCTT 1340
Db      365  LeuAspLeuSerGlnAsnLeuMetValGlnGluLysLeuLysAsnSerAlaCys----- 382
Qy      1341  CAAGATGATTTGGACACACAGCTTAAGATTATTAATCTGACCTTCAATGCTGTTAAT 1400
Db      383  -----GluAspAlaTrpProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 397
Qy      1401  ACCATGAGTTCAAACTTCTGGGCTTAGAACAATAAGCACTTGAGATTCCAGCATTC 1460
Db      398  -----HisLeu-----Ala 400
Qy      1461  AATTGAAACAATAGAGTAGTTTTCAGTATCTTATCACTCAGAAACCTCATTTACTT 1520
Db      401  SerLeuGlnLysThrGlyGlu-----ThrLeuLeuThrLeuLysAsnLeuThrAsnIle 418
Qy      1521  GACATTTCTCACTACTACACACAGAGTTGCTTCAATGCGCATCTTCAATGCTGTCCAGT 1580
Db      419  AspIleSerLys----- 422
Qy      1581  CTCGAAGCTTGAATAATGCGTGGCAATTCCTTCCAGGAAACCTTCCAGATATCTTC 1640
Db      423  -----AsnSerPheHisSer-----MetProGlnThrCys 432
Qy      1641  ACAGAGCTGAGAAATGACCTTCCTGGACCTCTCTCAGTGTCAACGAGACAGTGTCT 1700
Db      433  GlnTrpProGlnLysMetLysTyrLeuAsnLeuSerThrArgIleHisSerValThr 452
Qy      1701  -----CCAGACGATTTAACTCACTCTCCAGTCTTCAGTACTAATATATAGCCAC 1751
Db      453  GlyCysIlePro-----LysThrLeuGlnIleLeuAspValSerAsn 466
Qy      1752  AAC-----AAGCTTTTTCATTGGAT----- 1772
Db      467  AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGlnLeuTyrIleSerArg 486
Qy      1773  -----ACGTTTCTCT-----TATAAGTGTGGAAGCTCTCCAGGTTCTTGATTAC 1817
Db      487  AsnLysLeuMetThrIleuProAspAlaSerIleuLeuProMetLeuValLeuLysIle 506
Qy      1818  AGTCTCAATCACTAATGACTTCCAAAACAGGAACTACAGCAATTTTCCAGTAGTCTA 1877

```

```

Db      507  SerArgAsnAlaIleThrThrPheSerLysGlnLeuAspSerPhe---HisThrLeu 525
Qy      1878  GCTTCTTAAATCTTACTCAGAAATGACTTGTGCTGACTTGTGTAACACCAAGATTCTCTG 1937
Db      526  LysThrLeuGlnAlaGlyGlnAsnAsnPheIleCysSerCysGlnPheLeuSerPheThr 545
Qy      1938  CAATGATCAACGACACAGGACGAGCTTGTGGAAAGTT-----GAACGA 1982
Db      546  Gln-----GluGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsn 561
Qy      1983  ATGGAATGTGCAACACTTCAATTAAGCAGGAGATCGCTGTGTGAGTTGAAATACACC 2042
Db      562  TyrLeuCysAspSerProSerThrIleValArgGlyGlnGlnValGlnAspValArgLys 581
Qy      2043  -----TGTCAATGAAATAAGACCATCATTTGATGGTGTGCGGATCTCCAGTGGCTTGA 2093
Db      582  ValSerGlnCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeuPheLeuLeu 601
Qy      2094  GATCTGTGTGTACAGCTTGTGCTGTATTAAGTTCTAT-----TTTCACTGATGCTTCTT 2147
Db      602  IleLeuLeuThrGlyValLeuLysCysHisArgPheHisGlyLeuTrpTyrMetLysMet 621
Qy      2148  GCTGGCTGCATTAAGTAGTGTAGA-----GTTGAAAATC-----TAT 2186
Db      622  TrpAlaTrpLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTyr 641
Qy      2187  GATGCTTTGTTTATCTACTACAGCCAGAGATGAGATCGGGGTGAAGATGAGTAGTAAG 2246
Db      642  AspAlaPheValSerLysSerGlnArgAspAlaTyrTrpValGlnAsnLeuMetValGln 661
Qy      2247  AATTGAAAGAAAGGGTGCCTCCATTTGACGCTTGTGCTTCACTTACAGAGACTTATTC 2306
Db      662  GlnLeuGlnAsnPheAsnProProPheLysLeuCysLeuHisValArgAspPheIlePro 681
Qy      2307  GGTGTGCACTTCTCTGCCAATCATTCATGAAGTTTCCATTAAGCCGAAAGGATGATT 2366
Db      682  GlyLysTrpIleLeuAsnIleIle---AspSerIleGlnLysSerHisLysThrVal 700
Qy      2367  GTTGTGTGTGCCAGACTCATCTCAGAGCCGCTGGTGTATCTTGAATATGATGTGCT 2426
Db      701  PheValLeuSerGlnAsnPheValLysSerGlnTrpCysLysTyrGlnLeuAspPheSer 720
Qy      2427  CAGACCTGGCAGTTTCTGAGCAGCTCGTGTGATCATCTTCAATGCTCTGACAGAAAGTG 2486
Db      721  HisPheArgLeuPheAspGlnAsnAsnAspAlaIleIleuIleLeuLeuGlnProIle 740
Qy      2487  GAGAAACCTGCTCAGGACAGAG---GTGAGCTGTACCGCTTCTCAGACGAAACACT 2543
Db      741  GlnLysLysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThr 760
Qy      2544  TACTGTGAGTGGGAGGACAGTGTCTCGGGCGGACATCTTCTGAGACGACTCAGAAA 2603
Db      761  TyrLeuGlnTrpProMetAspGlnAlaGlnArgGlnGlyPheTrpValAsnLeuArgAla 780
Qy      2604  GCCCTG 2609
Db      781  AlaIle 782

RESULT 13
US-10-732-563-4
; Sequence 4, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tatum K.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 58183W0003
; CURRENT APPLICATION NUMBER: US/10/732,563
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4

```

LENGTH: 784
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-732-563-4

Alignment Scores:

Pred. No.: 2,61e-48 Length: 784
 Score: 602.50 Matches: 233
 Percent Similarity: 41.88% Conservative: 128
 Best Local Similarity: 27.03% Mismatches: 282
 Query Match: 8.96% Indels: 219
 DB: 16 Gaps: 38

US-09-396-985B-3 (1-3811) x US-10-732-563-4 (1-784)

```

QY 306 ATCCCGCAACCTCCCTTCACACCAAGAACTGGACCTGACTTATATCCCTGAGG 365
    |||||
DB 46 ILeProSerGlyLeuThrGluAlaValIleSerLeuAspLeuSerAsnAsnArgIleThr 65
QY 366 CATTAGGACGCTATAGCTTCTTCAGTTTCCAGAACTGACGGTGGATTATTCAGG 425
    : : : : :
DB 66 TyrlleSerAsnSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValLeuThrSer 85
QY 426 TGTGAATTCAGACAAATTGAAGATGGGCATATCAGACCTTAAGCCACTTACCTTA 485
    |||||
DB 86 AsnGlyIleAsnThrIleGluGlnAspSerPheSerSerLeuGlySerLeuGlnHisLeu 105
QY 486 ATATTGACAGAAACCCATCCAGAGTTTACGCCCTGGAGCCTTTCTGACTATCAAGT 545
    |||||
DB 106 AspLeuSerIleAsnTyrlleSerAsnLeuSerSerIlePheIlePheThrIleAsn 125
QY 546 TTACGAGAGCTG-----GTGGCTGTGGAG 569
    |||||
DB 126 LeuThrPheLeuAsnLeuLeuGlnAsnProIleTyrlleThrLeuGlnIleThrSerLeuPhe 145
QY 570 ACAATCTAGACATCTTGAAGAACTCCCATTTGACATCTCAAAACT----- 617
    |||||
DB 146 SerHisLeuThrIleGlnLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrIle 165
QY 618 -----TTGAAGAACTTAATGTGGCTCACATCTT 647
    |||||
DB 166 GlnArgIleAspPheAlaGlyLeuThrPheLeuGlnIleGlnIleAspAlaSerAsp 185
QY 648 ATCCATCTTTCAATCTGATGATATTTTCTATCTGACCAATCTGACAGCACTGGAC 707
    : : : : :
DB 186 LeuGlnSerIleTyrlle---ProIleSerLeuIleSerIleGlnAsnValSerHisLeuIle 204
QY 708 CTTTCCAGCAACAAG-----ATTCAAGTATT 734
    |||||
DB 205 LeuHisMetIleGlnHisIleLeuLeuLeuGlnIlePheValAspValIleThrSerSerVal 224
QY 735 TATTGCACAGACTGGCGGTTCTACATCAAAATGCCCTACTCAATCTCTTTAGACCTG 794
    |||||
DB 225 GlnCysLeuGlnLeuArg-----AspThr 232
QY 795 TCCCTGAACCTATGAACCTT-----ATCCACAGGCTGATTAAGAATTAAGGCTT 848
    |||||
DB 233 AspLeuAspThrPheHisPheSerGlnLeuSerThrGlyGlnIleThrAsnSerLeu---Ile 251
QY 849 CATATGACTGATTAAGAAT-----AATTTGATAGTTTA---AATGTAATGAA 896
    |||||
DB 252 LysIlePheThrPheArgAsnValIleThrAspGlnSerLeuPheGlnValMetIle 271
QY 897 ACTGT-----ATTCAAGTCTGCTGGCTGTTAAGATCCATCGTTGGTCTG----- 944
    |||||
DB 272 LeuLeuAsnGlnIleSerGlyLeuLeuGlnIleGlnPheAspAspCysThrLeuAsnGly 291
QY 945 ---GGAGATTATTAAGAAAGAACTTGAAAAAGTTGACCAATCGCTGAGAGGC 1001
    |||||
DB 292 ValGlyAsnPheArgIleSerAspAsnAspArgValIleAspProGlyIleValGln--- 310
QY 1002 CTGTGCAATTGACCATTAAGAAATTCGATTAGCA-----TACTTAGACTTACTACTC 1055
    |||||

```

```

DB 311 -----ThrLeuThrIleArgArgLeuHisIleLeuProArgPheTyrlleuPheTyrlle 326
QY 1056 GATGATATATTTAGCTATTTATTTGATGACAAAGTTTCTTATTTTCCCTGGTAGT 1115
    |||||
DB 327 ---AspLeuSerThrLeuTyrlleSerLeuThrGluArgValIle-----Arg 340
QY 1116 GTGACTATTTGAAGGATTAAGAACTTTCTTAATTTCCGATGGCAACATTGAAATTA 1175
    : : : : :
DB 341 IleThrValGlnAsnSerIleValPhe-----Leu 350
QY 1176 GTTAACTGTAAATTTGACAGTTTCCCACTGAACCTCAATCTCCAAAAGGCTTACT 1235
    |||||
DB 351 ValProCysLeuLeuSerGln----- 357
QY 1236 TTCACTTCCAAACAAAGTGGGAATGCTTTTCAAGATGATCTACAGCCTTGAGTTT 1295
    |||||
DB 358 -----HisLeuIleSerLeuGlnIleTyrlle 364
QY 1296 CTAGATCTCAGTAGAAT-----GGCTTGAGTTTCAAAAGTTGCTGTTCT 1340
    |||||
DB 365 LeuAspLeuSerGlnAsnLeuMetValGlnGlnIleTyrlleuIleAsnSerAlaCys----- 382
QY 1341 CAATGATATTTGGACACACCAAGCTTAAGATTATGATCTGACCTTCAATGCTGTTATT 1400
    : : : : :
DB 383 ---GlnAspAlaIleProSerLeuGlnThrLeuIleLeuArgIleAsn----- 397
QY 1401 ACATGAGTTCAAACTTCTGGGCTTAGAACAACTAACAATCGATTTCCAGATTCC 1460
    |||||
DB 398 -----HisLeu-----Ala 400
QY 1461 AATTGAACAAATGATGAGATTTTTCAGTATTTCTATCACTGACAAACCTCATTTACTT 1520
    : : : : :
DB 401 SerLeuGlnIleTyrlleGlnIle-----ThrLeuLeuThrLeuIleAsnLeuThrAsnIle 418
QY 1521 GACATTTCTCATCTACACACCAAGTGTCTTCAATGCAATCTCAATGCTGTCCAGT 1580
    |||||
DB 419 AspIleSerIle----- 422
QY 1581 CTGAAATCTTGAAGAAATGGCTGGCAATCTTCCAGGAAACCTTCCAGATATCTTC 1640
    |||||
DB 423 -----AsnSerPheHisSer-----MetProGlnThrCys 432
QY 1641 ACAGAGCTGAGAAACTGACCTTCTGAGACTCTGCTCAGTGTCAACAGAGAGAGTTCCT 1700
    : : : : :
DB 433 GlnIleProGlnIleGlnMetIleTyrlleAsnLeuSerThrArgIleHisSerValIleThr 452
QY 1701 -----CCAAAGCATTTAATCTCACTCTCAGTCTTCAAGTACTTAATATGAGGCAC 1751
    |||||
DB 453 GlyCysIlePro-----LysThrLeuGlnIleLeuAspValSerAsn 466
QY 1752 AAC-----AAGCTTTTTCATTTGATGAT----- 1772
    |||||
DB 467 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuIleGlnLeuTyrlleSerArg 486
QY 1773 -----ACGTTTCTT-----TATTAAGTGTGAACTCCCTCCAGGTTCTGATTAC 1817
    |||||
DB 487 AsnIleLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValLeuIle 506
QY 1818 AGTCTCAATCAATATGACTTCCAAAACAGAGAACTACAGCAATTTTCCAAAGTACTTA 1877
    |||||
DB 507 SerArgAsnAlaIleThrThrPheSerIleGlnIleAsnAspPhe---HisThrLeu 525
QY 1878 GCTTTCTTAATCTTACTAGATGACTTGTGCTTGTACTTGTGAACACAGAGTTTCTG 1937
    |||||
DB 526 LysThrLeuGlnIleGlyIleAsnAsnPheIleCysSerCysGlnPheLeuSerPheThr 545
QY 1938 CAATGATCAAGACACAGGACGCTCTTGGTGAAGTT-----GAACGA 1982
    |||||
DB 546 Gln-----GlnGlnGlnAlaLeuAlaIleValIleLeuIleAspIleAspProAlaAsn 561
QY 1983 ATGGAATGTGCAACACTTCAATTAAGACAGGAGATCGCTGTGATTTGAATATCACC 2042
    |||||
DB 562 TyrlleuIleAspSerProSerHisValArgGlyGlnGlnIleValGlnAspValArgLeuSer 581

```



```

QY 1236 TTCACTTCCAAAGAGTGGAAATGCTTTTCAGAAATGATCTACCAAGCTTGAGTTT 1295
DB 358 -----HleuLeuYSerLeuGlnThr 364
QY 1296 CTAGATCTCAGTAGAAT-----GGCTTGAGTTTCAAGGTTGCTGTCTT 1340
DB 365 LeuAspLeuSerGluAsnLeuMetValGluGlnThrLeuYAsnSerAlaCys----- 382
QY 1341 CAAGTAGATTTGGGACACACAGCTTAAGATTAGTTCAGAGCTTCAAGGTATTAT 1400
DB 383 -----GluAspAlaThrProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 397
QY 1401 ACCATGAGTTCAAACTTGTGGCTTAGAACAACATAGACATGTGATTTCAGACATTCC 1460
DB 398 -----HisLeu-----Ala 400
QY 1461 AATTGAAAACAATGAGTAGAGTTTTCAGTATTCCTATCAGTACAGAAACCTGATTACCTT 1520
DB 401 SerLeuGlnThrGlnGlu-----ThrLeuLeuThrLeuYAsnLeuThrAsnIle 418
QY 1521 GACATTTCTCATCTACACACAGAGTTGCTTCAATGAGCATCTTCATAGCGTTGCCAGT 1580
DB 419 AspIleSerIys----- 422
QY 1581 CTCGAAGCTTGAAATGGCTGGCAATCTTCCAGAAAATTCTTCAGATATGCTTC 1640
DB 423 -----AsnSerPheHisSer-----MetProGlnThrCys 432
QY 1641 ACAGAGCTGAGAACTTGACCTTCCTGACCTCTCTCAGTGTCACTGGACAGCTGTCT 1700
DB 433 GlnThrProGlnYMetLeuYThrLeuAsnLeuSerThrArgGlnIleHisSerValThr 452
QY 1701 -----CGAACAGCATTTAACTCACTCTCCAGTCTTCAGGTAATTAATAGCCAC 1751
DB 453 GlyCysIlePro-----LysThrLeuGlnIleLeuAspValSerAsn 466
QY 1752 AAC-----AACTCTTTTCATGGAT----- 1772
DB 467 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuYSerGlnLeuYThrIleSerArg 486
QY 1773 -----ACGTTTCTCT--TATAAGTGTGAATCCCTCCAGGTTCTTGATTAC 1817
DB 487 AsnYsLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValLeuYIle 506
QY 1818 AGTCTCAATCACTAATGACTTCCAAAAACAGAACTACAGCAATTTCCAAAGTAGCTTA 1877
DB 507 SerArgAsnAlaIleThrThrPheSerYsGlnGlnLeuAspSerPhe--HisThrLeu 525
QY 1878 GCTTTCTTAATCTTACTCAGATGACTTGTGCTGATCTTGTAACACACAGATTTCCTG 1937
DB 526 LysThrLeuGlnAlaGlyGlyAsnAsnPheIleCysSerYsGlnPheLeuSerPheThr 545
QY 1938 CAATGATCAAGACACAGAGCAAGCTTGTGAGT-----GAACGA 1982
DB 546 Gln-----GluGlnGlnAlaLeuValLeuIleAspThrProAlaAsn 561
QY 1983 ATGGAATGTGCACACCTTCAGATAGAGGCAATGCTGTGCTGAGTTGAATATACACC 2042
DB 562 TyrLeuCysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSer 581
QY 2043 -----TGTGATGATGAATAGAACCATCATGTTGGTGGTGGTCCATGAGTCTTGTA 2093
DB 582 ValSerGlnCysHisArgThrAlaLeuValSerGlnMetCysValAlaLeuPheLeuLeu 601
QY 2094 GTATCTGTGTAGAGAGTTGTGCTATAGATTAT-----TTTCACTGATGCTTCTT 2147
DB 602 IleLeuLeuThrGlnGlyValLeuCysHisArgPheHisGlnLeuThrPryGlyMetLeuMet 621
QY 2148 GCTGGCTGCAATTAAGTATGTAGA-----GGTAAAAATC---TAT 2186
DB 622 TrpAlaThrLeuGlnAlaYsArgYsProArgYsAlaProSerArgAsnIleCysThr 641

```

```

QY 2187 GATGCTTTGTATTACTCAAGCCAGATGAGAGCTGGGTAAAGATTAGCTTAAG 2246
DB 642 AspAlaPheValSerTyrSerGlnArgAspAlaTyrThrValGlnAsnLeuMetValGln 661
QY 2247 AATTAAAGAAAGGGGCTCTCCATTTACAGTCTGTGCTTCACTACAGAGCTTTATCCC 2306
DB 662 GlnLeuGlnAsnPheAsnProProPheYsLeuCysLeuHisYsArgAspPheIlePro 681
QY 2307 GGTTGGCATTGTGCTGCACATCATCATCAATGAGTTTCCATTAAGCCGAAAGGATT 2366
DB 682 GlyYsThrPheIleIleAspAsnIleIle--AspSerIleGlnYsSerHisYsThrVal 700
QY 2367 GTTGTGTGTCCAGCACTTCATCCAGAGCCGTGTGATCTTTGAATAGAGATTGCT 2426
DB 701 PheValLeuSerGlnAsnPheValYsSerGlnThrCysYsThrYsGlnLeuAspPheSer 720
QY 2427 CAGACTGGCAGTTTCTGACAGACTGCTGTGATATCATCTTCATTTGCTTCGACAGAGCT 2486
DB 721 HisPheArgLeuPheAspGlnAsnAsnAspAlaAlaIleLeuIleLeuGlnProIle 740
QY 2487 GAGAGACCCGTGCTCAGCAGCAG--GTGGAGCTGTACCGCTTCACAGAGACACT 2543
DB 741 GlnYsYsAlaIleProGlnArgPheCysYsLeuArgYsIleMetAsnThrYsThr 760
QY 2544 TACCTGAGTGGGAGAGCAGATGTCCTGGGCGGACACATCTTGGAGACGACTCAGAAA 2603
DB 761 TyrLeuGlnThrProMetAspArgAlaGlnArgGlnGlnYsThrValAsnLeuArgAla 780
QY 2604 GCCCTG 2609
DB 781 AlaIle 782

RESULT 15
US-10-741-600-1390
; Sequence 1390, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARIGIL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1390
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1390

Alignment Scores:
Pred. No.: 2,61e-48 Length: 784
Score: 602.50 Matches: 233
Percent Similarity: 41.88% Conservative: 128
Best Local Similarity: 27.03% Mismatches: 282
Query Match: 8,96% Indels: 219
DB: 17 Gaps: 38

US-09-396-985b-3 (1-3811) x US-10-741-600-1390 (1-784)
QY 306 ATCCCGGACAACTCCCTTCACACCAAGACCTGAGCTTAATCCCTGAGG 365
DB 46 IleProSerGlnYsThrGlnAlaValYsSerLeuAspLeuSerHisAsnAlaGlnThr 65
QY 366 CATTTAGGACATAGCTTCTTCACTTCCAGAACTGCAAGGTGCTGATTTATCCAGG 425
DB 66 TyrIleSerHisSerAspLeuGlnArgCysValAsnLeuGlnAlaLeuValLeuThrSer 85
QY 426 TGTGAATCCAGACATTTGAAGATGGGCAATATCAGAGCTTAAGCCACTCTTACCTTA 485
DB 86 AsnGlyIleAsnThrIleGlnGlnAspSerPheSerSerLeuGlnYsLeuGlnHisLeu 105

```

QY	486	ATATTGACAGAAACC	CCATCCAGATT	TAGCCCTGGAGCCTTTTCTGACAT	TCAAGT	545
Db	106	AspLeuSer	TrpAsn	TrpLeuSer	AsnLeuSer	125
QY	546	TTACAGAACTG	-----	GTGGCTGGAG	569	
Db	126	LeuThr	PheLeuAsn	LeuLeuGln	AsnPro	145
QY	570	ACAATTCAGACATCTCT	GAGAACTTCCCACTTGACATCTCAAAACT	-----	617	
Db	146	SerHis	LeuThr	TrpLeuGln	HisLeuArg	165
QY	618	-----	TTGAAAGACTTAACTGTGCTCACAATCTT	647		
Db	166	GlnArg	TrpAsn	PheLeu	AsnLeuGln	185
QY	648	ATCCAACTCTTTCAAAT	TTCAGATTTTCTATCTGACCAATCTTACAGACACTGGAC	707		
Db	186	LeuGln	SerTrpArg	TrpLeuSer	TrpLeuGln	204
QY	708	CTTTCCACCAACAAG	-----	ATTCAAAGTAT	734	
Db	205	LeuHis	Met	TrpLeuGln	HisLeuVal	224
QY	735	TATTCACAGACACTTGC	GGGCTTTCATCATCAAAATGCCCTACTCAATCTCTTTAGACCTG	794		
Db	225	GlnCys	LeuGln	LeuArg	-----	232
QY	795	TCCCTGAAACCCATTA	ACTT-----	ATCCACAGCTGCATTTAAAGAAATTAAGCTT	848	
Db	233	AspLeu	AsnThr	PheHis	SerGln	251
QY	849	CATAGACTGACTTTAAGA	AAAT-----	AATTTGATAGTTTA--	AATGTAATGAA	896
Db	252	LysTrp	SerPhe	ThrPhe	ArgAsn	271
QY	897	ACTGT-----	ATTCAAGTCTGCTGCTGTTAGAACTCAATCGTTGGTCTG	944		
Db	272	LeuLeu	AsnGln	His	SerGln	291
QY	945	---GGAGAAATTAGAA	ATAGAAAGAACTTGGAAAGTTTGACAAATCTGCTTAGAGGC	1001		
Db	292	ValGln	AsnPhe	ArgAla	SerAsp	310
QY	1002	CTGTGCAATTTGACAT	TTCAGAAATTCGATAGCA-----	TACTTAGACTTACATCTC	1055	
Db	311	-----	ThrLeu	ThrHis	LeuHis	326
QY	1056	GATGATATTAATTA	CTTAATTTAGTTTGACAAATGTTTCTTCAATTTCCCTGGTGA	1115		
Db	327	---AspLeu	SerThr	LeuTrp	SerLeu	340
QY	1116	GTGACTATTTGAAAG	GTAAAGACTTTTCTTATTAATTCGATGCAACATTTAGAAATTA	1175		
Db	341	HisThr	ValGln	AsnSer	TrpVal	350
QY	1176	GTTTACTGTAAATTT	GGACAGTTTCCACATTTGAAACTCAATCTCTCAAAAGCTTACT	1235		
Db	351	ValPro	CysLeu	LeuSer	Gln-----	357
QY	1236	TTACATTCACAAAG	GTGGAGTCTTTTCAGAGTTGATCTTACAGAGCTTGAGTTT	1295		
Db	358	-----	HisLeu	TrpSer	LeuGln	364
QY	1296	CTAGATCTCAGTAAAT	-----	GGCTTGAGTTTCAAAAGTTGCTGTTCT	1340	
Db	365	LeuAsp	LeuSer	GlnAsn	MetVal	382
QY	1341	CAAACTGATTTTGG	CAACAACGCTTAAGTATTTAGATCTGAGCTTCAATGCTGTATT	1400		
Db	383	-----	GlnAsp	AlaTrp	ProSer	397
QY	1401	ACCATGAGTTTCAAA	CTTTCTTGGGCTTAGAACAATCT			

Db 398 -----HisLeu-----Ala 400

1461 AATTGAAACAAATGATGATTTCAGTATTCCTATCACTGACGAAACCTATTACCT 1520

401 SerLeuGluYsthrGlu-----ThrLeuLeuThrLeuYsnLeuThrAsnLe 418

1521 GACATTTCCTACTACTACACACAGATTCTTTCAATGGCATCTTCAATGGCTGTCCAGT 1580

419 AspIleSerLys----- 422

1581 CTCGAAGCTTGAAAGGCTGGCAATTCCTTCCAGAAACCTCTCCAGATATCTTC 1640

423 -----AsnSerPheHisSer-----MetProGluThrCys 432

1641 ACAGAGCTGAGAACTTGACCTTCCAGACCTCTCAGTGTCACTCACTGAGACAGTTGCT 1700

433 GlnTrpGluGluYsnMetLysTyLeuYsnLeuSerThrArgIleHisSerValThr 452

1701 -----CCAGACGATTTTACTCACTCCAGTCTTGAGTAAATATGAGCCAC 1751

453 GlyCysIlePro-----LysThrLeuGluIleLeuAspValSerAsn 466

1752 AAC-----AACTCTTTTCAATGGAT----- 1772

467 AsnAsnLeuAsnLeuPheSerLeuAsnLeuProGlnLeuYsnLeuTyrIleSerArg 486

1773 -----AGTTTCCCT-----TATTAAGTGTCAACTCCCTCCAGGTTCTTGATTAC 1817

487 AsnLysLeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValLeuLysIle 506

1818 AGTCCATATCAATATGACTTCCAAAAACAGAACTACAGACTTTTCCAAAGTACTTA 1877

507 SerArgAsnAlaIleThrLysPheSerLysGluIleLeuAspSerPhe--HisThrLeu 525

1878 GCTTTCTTAATCTTACTAGATAGACTTTGCTGTGTGTGAACACAGAGTTCTCTG 1937

526 LysThrLeuGluAlaArgLysLysAsnAsnPheIleCysSerCysGluPheLeuSerPheThr 545

1938 CAATGATTCAGAGACCAAGACAGACTCTGGTGGAGATT-----GAACGA 1982

546 Gln-----GluGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsn 561

1983 ATGGAATGTGCACACCTTCAGATTAACAGAGGCAAGCTGTGCTGAATTAATGACCC 2042

562 TyrLeuCysAspSerProSerHisValArgLysGlnGlnAlaGlnAspValArgLeuSer 581

2043 -----TGTCAAGTAAATTAAGACCACTTGTGTGTGCTGCTCCAGTGTCTTGTGA 2093

582 ValSerGluCysHisArgThrAlaLeuValSerLysMetCysValaLeuPheLeuLeu 601

2094 GATCTGTGTGAGACAGTTCTGGTGTATTAAGTTCAAT-----TTTCAACGTGATCTCTT 2147

602 IleLeuLeuThrGlyValLeuCysHisArgPheHisValLeuTyrLeuTyrMetLysMet 621

2148 GCTGGCTGCATAAAGTATGTAGA-----GGTGAACCAATC-----TAT 2186

622 TrpAlaTrpLeuGlnAlaLysArgLysTrpArgLysValaProSerArgAsnIleCysTyr 641

2187 GATGCTTTGTTATCTACTCAAGCCAGAGATGAGACTGGGTAAAGATGAGTACTGAAG 2246

642 AspAlaPheValSerLysSerGluArgAspAlaTyrTrpValGluAsnLeuMetValGln 661

2247 AATTTAAGAAAGAGGGTCCCTCACTTTCAGCTGCTGCTCACTACAGACTTATATCCC 2306

662 GluLeuGluAsnPheAsnProProPheLeuLeuCysHisLysLysValAspAspPheIlePro 681

2307 GGTGGAGCCATGTGCTGCCACATGATCCATGAAGGTTTCCATTAAGCCGAAAGGATAT 2366

682 GlyLysTrpIleIleAspAsnIleIle-----AspSerIleGluYsnSerHisLysThrVal 700

2367 GTTGAGTGTCCACAGACTTATCATCAGACCCGCTGTGTATCTTTGAATATGAAATGCT 2426

```
Db      701 PheValLeuSerGluAsnPheValIysSerGluTrpCysLysTyrGluLeuAspPheSer 720
Qy      2427 CAGACCTGCGACGTTCTGAGCAGTGTGCTGTATCATCTTCATTGCTCGACAGAGGTG 2486
Db      721 HisPheArgLeuPheAspGluAsnAsnAlaAlaIleLeuIleLeuLeuGluProIle 740
Qy      2487 GAGAGACCTGCTCAGCGCAGCAG--GTGAGCTGTACCGCCCTTCTCAGCAGGACACT 2543
Db      741 GluLysLysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThr 760
Qy      2544 TACCTGAGTGGAGAGCAGTGTCTCTGGGGCGGCACATCTTCTGAGACGACTCAGAAA 2603
Db      761 TyrLeuGluTrpPrometAspGluAlaGlnArgGluGluPheTrpValAsnLeuArgAla 780
Qy      2604 GCCCTG 2609
Db      781 AlaIle 782
```

Search completed: March 30, 2005, 04:40:43
Job time : 224.708 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_nbp model

Run on: March 30, 2005, 03:00:48 ; Search time 119.022 Seconds
(without alignments)
16418.453 Million cell updates/sec

Title: US-09-396-985B-46
Perfect score: 5177
Sequence: 1 cctccctgcagcagcgagcagat.....ccttaactcgaagcagaag 2951

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1407402 segs, 331100923 residues
Total number of hits satisfying chosen parameters: 2814804

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+np model -DEV=xlh
-O=/cgn2_1/USFPO.spool/US09396985/runat_28032005_155745_21245/app_query.fasta_1.85098
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09396985@cgn_1 1.3955@runat_28032005_155745_21245
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PTC_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PTCUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result Query

SUMMARIES

No.	Score	Match Length	DB	ID	Description
1	2772.5	53.6	837	10	US-09-950-041-26
2	2675.5	51.7	799	10	US-09-950-041-8
3	2675.5	51.7	799	16	US-10-128-166-7
4	2675.5	51.7	799	16	US-10-732-563-8
5	2675.5	51.7	799	16	US-10-732-796A-8
6	579.5	11.2	661	13	US-10-114-893-10
7	579.5	11.2	661	15	US-10-038-854-134
8	567.5	11.0	661	15	US-10-038-854-135
9	567.5	11.0	661	15	US-10-037-417-107
10	559	10.8	1032	10	US-09-954-987B-192
11	559	10.8	1032	14	US-10-272-502A-31
12	559	10.8	1032	15	US-10-407-952-32
13	546	10.5	1059	10	US-09-954-987B-187
14	546	10.5	1059	15	US-10-407-952-30
15	546	10.5	1059	17	US-10-153-267-30
16	541	10.5	1041	9	US-09-168-978-3
17	541	10.5	1041	9	US-09-978-295A-498
18	541	10.5	1041	9	US-09-978-697-498
19	541	10.5	1041	9	US-09-978-192A-498
20	541	10.5	1041	9	US-09-999-832A-498
21	541	10.5	1041	10	US-09-978-189-498
22	541	10.5	1041	10	US-09-978-608A-498
23	541	10.5	1041	10	US-09-978-585A-498
24	541	10.5	1041	10	US-09-978-191A-498
25	541	10.5	1041	10	US-09-978-403A-498
26	541	10.5	1041	10	US-09-978-564A-498
27	541	10.5	1041	10	US-09-999-833A-498
28	541	10.5	1041	10	US-09-981-915A-498
29	541	10.5	1041	10	US-09-978-824-498
30	541	10.5	1041	10	US-09-918-585A-498
31	541	10.5	1041	10	US-09-999-834A-498
32	541	10.5	1041	10	US-09-978-423A-498
33	541	10.5	1041	10	US-09-978-193A-498
34	541	10.5	1041	10	US-09-999-830A-498
35	541	10.5	1041	10	US-09-978-757A-498
36	541	10.5	1041	10	US-09-978-187B-498
37	541	10.5	1041	10	US-09-978-643B-498
38	541	10.5	1041	10	US-09-978-375A-498
39	541	10.5	1041	10	US-09-978-298A-498
40	541	10.5	1041	10	US-09-978-188A-498
41	541	10.5	1041	10	US-09-978-681A-498
42	541	10.5	1041	10	US-09-978-194A-498
43	541	10.5	1041	10	US-09-999-829A-498
44	541	10.5	1041	10	US-09-978-299A-498
45	541	10.5	1041	10	US-09-978-544A-498

ALIGNMENTS

RESULT 1
US-09-950-041-26
Sequence 26, Application US/09950041
Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Kock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Liu, Yong-Jun
TITLE OR INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: EX0724XX1
CURRENT APPLICATION NUMBER: US/09/950,041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293

PRIOR FILING DATE: 1997-05-07
 PRIOR APPLICATION NUMBER: 60/072,212
 PRIOR FILING DATE: 1998-01-22
 PRIOR APPLICATION NUMBER: 60/076,947
 PRIOR FILING DATE: 1998-03-05
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 26
 LENGTH: 837
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-950-041-26
 Alignment Scores:
 Pred. No.: 1,96e-269 Length: 837
 Score: 2772.50 Matches: 554
 Percent Similarity: 79.56% Conservative: 100
 Best Local Similarity: 67.40% Mismatches: 162
 Query Match: 53.55% Indels: 7
 Gaps: 5
 US-09-396-985b-46 (1-2951) x US-09-950-041-26 (1-837)

226 CTGGCTAGAGCTGATCATGCACTG---TTCTTCTCTGCTGACACACAGAACTTG 282
 6 LeuIaGlyThrLeuIleProAlaMetAlaPheLeuSerCyValArgProGluSerTrp 25
 283 AATCCCTGCATAGAGGTGTTCTTAATTATCTTACCAATGCAATGCATGACAACTCAGC 342
 26 GluProCyValGlu--ValProAsnIleThrTyGlnCyMetGluLeuAsnPheTyr 44
 343 AAATCCCTGCATGACATCTCTTCTTCAACCAAGAAACATAGATCTGAGCTTCAACCCCTTG 402
 45 LysIleProAsnPheLeuProPheSerThrIlyAsnLeuAsnLeuSerPheAsnProLeu 64
 403 AAGATCTTAAAAAGCTATAGCTTCTTCCAAATTTTTCAGAACTTCAAGTGCATTTATTC 462
 65 ArgIleLeuGlySerTyrSerPhePheSerPheProGluLeuGlnValLeuAspLeuSer 84
 463 AGGTGGAATTTGAAACAAATTGAAAGACAAAGACATGCGACTTACACCACTCTTCAAC 522
 85 ArgCySerGluIleGlnThrIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuSerThr 104
 523 TTGATCTGACAGGAAACCTATCCAGAGTTTTCACAGGAAGTTTCTGAGTAACA 582
 105 LeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSer 124
 583 AGTTTGAACAATCTGGTGGCTGTGGAGACAAATTTGGCTCTAGAAAGCTTCCATT 642
 125 SerLeuGlnIlyLeuValAlaValGlnThrAsnLeuAlaSerLeuGluAsnPheProIle 144
 643 GACAGCTTATTAACCTTAAAGAACTCAATGTGGTCAATTTTATATCTCTGTAAG 702
 145 GlyIlyLeuIlySerIlyLeuIlyGluLeuAsnValAlaHisAsnLeuIleGlnSerPheIly 164
 703 TTACCTGATATTTTTCATCTGACGAACCTAGTACATGTGATCTTCTTATATCAT 762
 165 LeuProGluTyrPheSerHisLeuThrAsnLeuGluIlyHisLeuAsnLeuSerSerHisIly 184
 763 ATTCAAACTATTAATGTCAACGACTTACAGTTTCTACGTGAAAATCCCAAGTCAATGTC 822
 185 IlegInserIleTyrCyThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeu 204
 823 TCTTTAGCATGCTCTTGAACCAATTAATCTTCAATTAAGACCAAGCTTTCAGGAATT 882
 205 SerLeuAsnLeuSerLeuAsnProMetAsnPheIleGlnProGlyAlaPheIlyGluIle 224
 883 AAGCTCATGAGTGAAGTAAAGTAAATTTTATATAGCTCAAAATATATGAAAACTTGC 942
 225 ArgLeuHisIlySerLeuThrLeuArgAsnAsnPheAspSerLeuAsnValMetIlySerHis 244
 943 CTTCAAAACTGGCTGTTTACACGCTCATCGGTGATCTTGGAGAAATTTAAAGATGAA 1002

245 IlegIlyLeuAlaGlyLeuGlnValHisArgLeuValLeuGlyIlyPheArgAsnGlu 264
 1003 AGAAATCTGGAATTTTGTGAACCTCTATCATGGAAGAACTATGATGACATGAT 1062
 265 GlyAsnLeuIlySerPheAspIlySerAlaLeuGlnGlyLeuCySerLeuThrIleGlu 284
 1063 GAGTTCAAGTTAACATATACAAATGATTTTTCAGATGATTTGTAG--TTCCATTGC 1119
 285 GluPheArgLeuAlaTyrLeuAspIlyTyrLeuAspHisIleIleAspLeuPheAsnCy 304
 1120 TTGGCGAATGTTTCTGCAATGCTCTGGCAGGTGATCTTAAATAATCTCAAGATGTT 1179
 305 LeuThrAsnValSerSerPheSerLeuValSerValThrIleGlnArgValIlyAspPhe 324
 1180 CTTAAATTTCAAAATGCAATCTTATCATATGATTAAGATGCAACTAAC--CGTTTCCA 1238
 325 SerTyrAsnPheGlyTyrGlnHisLeuGlnLeuValAsnCyIlySerPheGlyGlnPhePro 344
 1239 ACTCTGATCTACCCCTTCTTAAAGATTGACCTTAACTATGAAACAAGGCTCATAGT 1298
 345 ThrLeuIlySerLeuIlySerLeuIlyArgLeuThrPheThrSerHisIlyGlyIlyAsnAla 364
 1299 TTTAAAAAGTGGCCCTTACCAAGTCTCAGCTATCTAGATTTTATGTAAGAAATGCACTGAGC 1358
 365 PheSerGluValAspLeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSer 384
 1359 TTTTAAAGTGGCTGTTCTTATCTGATTTTGGGAAACAACGCGCTGAGACCTTAGACTC 1418
 385 PheIlyGlyCySerGlnSerAsnPheGlyThrThrSerLeuIlySerIlyLeuAspLeu 404
 1419 AGCTTCAATGGTGCATATTATAGTGCACAAATTTGAGGTCTAGAAAGCTGCAGAC 1478
 405 SerPheAsnGlyValIleThrMetSerSerAsnPheLeuIlyLeuGlnGluHis 424
 1479 CTGATTTTTCAGACCTCTTCTTAAAGAGTCAACAATTTCTCAGCTTCTTATCTCT 1538
 425 LeuAsp-PheGlnHisSerSerAsnLeuIlyGlnMetSerGlnPheSerValPheLeuSerIle 444
 1539 TGAAGACTACTTACTTACCTTGCATCTCTTATACCTTACACCAAAATGACTTCAGTGTAT 1598
 444 ValArgAsnLeuIleTyrLeuAspIleSerHisIlyHisIlyThrArgValAlaPheAsnGlyIle 464
 1599 ATTCTTGGCTGACAGCTCTCAACATTTTAAATGCTGGCAATCTTTCAGAACAA 1658
 464 ePheAsnGlyLeuSerSerLeuGlnValLeuIlyMetAlaGlyAsnSerPheGlnGluAs 484
 1659 CACCTTTCAAAATGCTTTTGCAAAACACAAACCTTGCAATTCCTGATCTTAAATG 1718
 484 nPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerGlnCy 504
 1719 TCAATTGGAACAAATATCTGGGGGGTATTGACACCTCTCATAGACTTCAATTATTA 1778
 504 GlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAs 524
 1779 TATAGTCAACAACATATATGTTTGGATTCATCCCATTAATTAACAGCTGATTTCCCT 1838
 524 nMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyrIlySerCySerLeuAsnSerIle 544
 1839 CAGCACTTGTGATGTCAGTTTCAATGCGATAGACATCT--AAAGAAATCTGCACAA 1895
 544 uGlnValLeuAspIlySerSerLeuAsnHisIleMetThrSerIlySerIlyGlnIlyLeuGlnHis 564
 1896 TTTTCCAAAGAGTCTACCTTCTTCAATCTTCAATCAATTCGATGCTTGTATATGTA 1955
 564 sPheSerSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCySerHisCySerGln 584
 1956 ACATCAAGAAATCTCTGCAAGTGGTCAAGAAACAGAACAGATTTCTGTGATGTTTGAACA 2015
 584 uHisGlnSerPheLeuGlnIlyPheIlySerGlnArgGlnLeuLeuValGluValGluArg 604
 2016 AATGACATGTGCAACACTGTAGAGATGAATACCTCTTATGTTGGATTTTAAATATTC 2075
 604 gMetGluCyAlaIleThrProSerAspIlySerGlnIlyMetProValLeuSerLeu--AsnIle 623

Qy	2076	TACCGTTAAATGTAACAAGACATCATGAGTGTGACATGGCAGTGGATTC	2135
Db	623	ethTCySgImetAnbYsthrIleIGLyAlSeRvAlIeUsErVAlIeUvAlSe	643
Qy	2136	CACGTGACCATTTCTGATATACCACTTCTATTTTCCCTGATACTTATTTGCTGGCTGTAA	2199
Db	643	rValVAlAlvAlIeUvAlTyrIlybPheTyRphenIstIeUmetIeUeUAlAGLyCybI	663
Qy	2196	AAAGTACAGCAGAGGAAAGACATTTATGATGACATTTGTGATCTTACTGAGTCAGATGA	2255
Db	663	eIyErTydIyArGgLyGuAmIleTyArSPAlArPheVAlIleTyRSeSerGIaSPGI	683
Qy	2256	GGACCTGGGTGAAGAATGAGCTGGTAAAGATTTTGAAGAAGAGCGCCGCTTCACT	2315
Db	683	uASpTTrAlArGbsnGluIeUvAlLybAmIeUdIuGIuGlyAlPrOpRopheGInIe	703
Qy	2316	CTGCCTTCACTPACAGAGACTTATTCCTGTGTAGCCATTCCTGCCAATCATCAGGA	2375
Db	703	uCyIeUenIstYrArGAsPheIleProGlyValAlAlleAlAlaenIleIleAGI	723
Qy	2376	AGGCTTCCACAAGACCGGAAAGCTTATTTGGTAGTGTCTAGACATTTATTCAGACCG	2435
Db	723	uGlyPhehIstbYsSeRArGlybValIleValVAlSeRGIhISpHeIleGIInSeRAr	743
Qy	2436	TTGGGTGATCTTTGAATATGAGATTGTCCAACATGAGAGTTTCTGACAGACCGCTCG	2495
Db	743	gTrPyAlIlePheGInIyrgIuIleAlAGInThrTrpGInPheUsSeRArGAlAGI	763
Qy	2496	CATCATCTTCATTGTCTCTTGAGAAAGTTGAGAAAGCTCCTGCTGAGCAGCAGTGAATT	2555
Db	763	YIleIlePheIleValIeUgInLybValGluIyErhIeUenArGInGInValGluIe	783
Qy	2556	GTAATCGCTTTCTTACGACAAACACCTACTGGAATGGAGACATCTCTGGGGAGGCA	2615
Db	783	uTyArGLeUeUsErArGvAnThrTyRLeUGInTrpGInbSPSeRValIeUGLyArGhI	803
Qy	2616	CATCTTCTGAGAGACTTAAAAAATGCCCTATTGGATGGAAGAAAGCTCGAATCTTGAGCA	2675
Db	803	sIlePheTrpArGArGLeUArGlybAlaIeUeUAspGIySeRTrpAsnProGInGI	823
Qy	2676	AACA 2679	
Db	823	yThr 824	
RESULT 2			
US-09-950-041-8			
Sequence 8, Application US/09950041			
Publication No. US20030032090A1			
GENERAL INFORMATION:			
APPLICANT: Hardiman, Gerard T.			
APPLICANT: Rock, Fernando L.			
APPLICANT: Bazan, J. Fernando			
APPLICANT: Kaestlein, Robert A.			
APPLICANT: Ho, Stephen W.K.			
APPLICANT: Liu, Yong-Jun			
TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS			
FILE REFERENCE: DKO724XK1			
CURRENT APPLICATION NUMBER: US/09/950, 041			
PRIOR APPLICATION NUMBER: 09/728,540			
PRIOR FILING DATE: 2000-11-28			
PRIOR APPLICATION NUMBER: 60/207,558			
PRIOR FILING DATE: 2000-05-25			
PRIOR APPLICATION NUMBER: 09/073,363			
PRIOR FILING DATE: 1999-06-05			
PRIOR APPLICATION NUMBER: 60/044,293			
PRIOR FILING DATE: 1997-05-07			
PRIOR APPLICATION NUMBER: 60/072,212			
PRIOR FILING DATE: 1998-01-22			
PRIOR APPLICATION NUMBER: 60/076,947			
PRIOR FILING DATE: 1998-03-05			
NUMBER OF SEQ ID NOS: 45			

```

; SOFTWARE:PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-8

Alignment Scores:
Pred. No.: 1,13e-259
Score: 2675.50
Percent Similarity: 79.82%
Best Local Similarity: 67.51%
Query Match: 51.68%
DB: Gaps: 10
      Indels: 5
      Matches: 3

US-09-396-985B-46 (1-2951) x US-09-950-041-8 (1-799)

QY 325 ATGGATCAGAAACTCAGCAAAAGTCCCTGATGACATTCCTTCTTCAACCAAGACATAGAT 384
   ||:::|||||
Db 1 MetGluLeuAenPheTyrlYsIleProkAspAenLeuProPheSerThrlYsAenLeuAep 20

QY 385 CTGAGCTTCAACCCCTTGAAGATCTTAAAAAGCTTACTTCTCCAAATTTTTCAGAACTT 444
   ||:::|||||
Db 21 LeuSerPheAenProLeuArlgHIsleuAlySerTyrlSerPhePheSerPheProGluLeu 40

QY 445 CAGTGGCTGGAATTTATCCAGGNGTGAATTTGAAACAATTGAAGACAGAGCTGAGTGC 504
   |||
Db 41 GluValLeuAenPheSerArlgCysGluIleGlnThrIleGluAspGlyAlaTyrlGlnSer 60

QY 505 TTACACACACCTCTCAAACTTGATACAGCAAGAAACCTATCCAGAGTTTTCACAGGA 564
   |||
Db 61 LeuSerHIsleuSerThrlLeuIleLeuThrlGlyAenProIleGlnSerLeuAlaGluGly 80

QY 565 AGTTCTCTGGACTTAACAAGTTTAGACACAATCTGCGTGGCTGAGAGAAATTTGGCTCT 624
   ||:::|||||
Db 81 AlaPheSerGlyLeuSerSerLeuGlnIlyLeuValAlaValaGluThrAsnLeuAlaSer 100

QY 625 CTAGAAGAAGCTTCCCTATTTGAGACAGCTTATTAACCTTAAAGAAACATCATGTGCTCAAT 684
   |||
Db 101 LeuGluAenPheProIleGlyHIsleuAlySerThrlLeuAlyGluLeuAenValAlaHIsAen 120

QY 685 TTTATACATTCCTGTAAAGTTACTGCATATATTTTTCATCTGACGAAACCTAGTACATGTG 744
   |||
Db 121 LeuIleGlnSerPheAlyLeuProGluTyrlPheSerAenLeuThrlAsnLeuAlyHIsleu 140

QY 745 GATCTTTCTTATTAATACTAATATCAAACTTATTAAGTGTCAACGACTTACAGTTTCTAGTGA 804
   |||
Db 141 AspLeuSerSerAenAlyIleGlnSerIleTyrlCysThrAenLeuAlyValIleuHIsGln 160

QY 805 AATCCACAAGCAATCTCTCTTGAACATGCTTTGAACCCCAATGATGACTTCATCAAGAC 864
   |||
Db 161 MetProLeuAenAenLeuSerLeuAenAlySerLeuAenAenProMetAenPheIleGlnPro 180

QY 865 CAAGCTTTTCAGGAATTAAGCTCCATGAACCTGACTCTPAAGAGTAAATTTTAAATAGCTCA 924
   |||
Db 181 GlyAlaPheAlyGluIleArlGlnHIsIlySerLeuThrlAenAlyAenAenAenAenAenLeu 200

QY 925 AATTAATTAAGAAACCTGGCTTCAAAACCTGGCTGTTTAAACGTCATCGGTGATCACTTG 984
   |||
Db 201 AsnValMetCylsThrCysIleGlnGlyLeuAlyGlyLeuGluValAlaHIsArlGlyLeuValIleu 220

QY 985 GGAGAATTTTAAGATGAAGAAAGAAATCTGGAATTTTGAACCTCTATCATGAGAGACTA 1044
   |||
Db 221 GlyIleuPheArlGlnAenGluGlyAlyAsnLeuAlyIlyAlyPheAenAlyAlySerAlyAenGluGlyLeu 240

QY 1045 TGTGATGTGACCATTTGATGAGTTCAAGTTAAACATATTAACAATGATTTTTCAGATGATTT 1104
   |||
Db 241 CysAenLeuThrIleGlnGluPheArlGlnAlyAlyTyrlLeuAenAlyTyrlTyrlLeuAenAlyAly 260

QY 1105 GTTAAAG---TTCCATGGCTGGCGAATATTTCTGGAATGTCTCTGGCAGAGTCTATCTATA 1165
   |||
Db 261 IleAspLeuPheAenCysLeuThrAenValAlySerPheSerLeuValAlySerValThrIle 280

```

QY	1162	AAATATCTAGAAAGATGTTCTTAACATTTCAAAATGGCAATCTCTTAATCAATATTAAGATGT	1221
Db	281	GIATGATValVAspPheSerTyrAsnHegLITrgGlnIstLeuValAlaCys	300
QY	1222	CAGCTAAG-CAGTTTCCAACTCTGGATGTATACCTCTTCTTAAAGTTTCACTTTAACTATG	1280
Db	301	LysPheGlyGlnPheProThrLeuLysLeuLysSerLysValGlyLeuThrPheThrSer	320
QY	1281	AACAAAGGCTATACGTTTAAAAAAGTGGCCCTCAAGTCTCAGCTATCTAGATTT	1340
Db	321	AsnLysGlyGlyAlaAsnAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu	340
QY	1341	AGTAGAAATGCATGACGTCTTAAGTGGTGGCTGTTCTTATTTGATTTTGGGAAACAACGC	1400
Db	341	SerArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer	360
QY	1401	CTAGAGACCTTAGACCTCAGCTTCAATGGTGCATTTATGAGGCGCAATTCATGGGT	1460
Db	361	LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAspPheLeuLys	380
QY	1461	CTAGAAAGCTGCACACCTGGATTTTTCAGACACTCTTAAAAAAGGTCAAGATTT	1520
Db	381	LeuGlnGlnLeuGlnLysLeuAsp-PheGlnIstSerAsnLeuLysGlnMetSerGlnPh	400
QY	1521	CTCAGCGTTCTTATCCCTTGAAAAGCTATTAACCTGACATCTCTTAATCAACACCA	1580
Db	400	SerValPheLeuSerLeuAspArgAsnLeuIleTyrLeuAspIleSerIstThrIstThrX	420
QY	1581	AATGACCTTCATGGTATATTTCTTGGCTGACACGCTGCACACATTAATAAAGGCTGG	1640
Db	420	GValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaG	440
QY	1641	CAATCTTTCAAAAGACAACACCCTTTCAAAATGCTTTTGCAAAACAACAACCTTGACATT	1700
Db	440	YAsnSerPheGlnGlnLysAsnPheLeuProAspIlePheThrGlyLeuAspAsnLeuThrPh	460
QY	1701	CCTGGATCCCTCTAATATGTCATTGGAAACAATATCTTGGGGGGATTTATGACACCTTCA	1760
Db	460	LeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnLeuSerLeuSe	480
QY	1761	TAGATCTCAATTAATAATATGAGCGACAACAATCTATTTGTTGATTCATCCCATTA	1820
Db	480	rSerLeuGlnValLeuAsnMetSerIstAsnAsnPhePheSerLeuAspThrPheProTyr	500
QY	1821	TAACCAAGCTGATTTCCCTCAGACACTCTTGATTTGCACTTGCATGCAATGACAGACT--	1878
Db	500	rLysCysLeuAsnSerLeuGlnValLeuAspLysrSerLeuAsnIstIleMetThrSerLys	520
QY	1879	-AAAGGAATCTGCACAATTTTCCAAAGATGTAGCTTTCTTCAATCTTATCAATTC	1937
Db	520	sLysGlnGlnLeuGlnIstPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAlaAs	540
QY	1938	TGTTGCTTGTAATGTGAACATCAAAATTCCTGAGAGGGGCAGAAACAAGACACTT	1997
Db	540	pPheAlaCysThrCysGlnLysGlnSerPheLeuGlnIstPheLysAspGlnAlaGlyLe	560
QY	1998	CTTGGTGAATGTTGAACAATGACATGTGCAACCTGTGAGAGATGAATACCTCTTAGT	2057
Db	560	uLeuValGlnValGlnLysGlnMetGlnCysAlaIstThrProSerAspLysGlnGlyMetPro	580
QY	2058	GTTGGATTTTAATAATTCCTACCTGTTATATGTACAAGACATCATCAGTGTGTAGTGT	2117
Db	580	IleuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLe	599
QY	2118	CAGTGTGATGTGGATATGCACGTGTAGCATTTTGATATACCACCTCTATTTTACACTGAT	2177
Db	599	uSerValLeuValIstSerValAlaAlaValLeuValTyrLysPheTyrPheIstLeuMe	619
QY	2178	ACTTATGTGCTGTGTAATAAAGATCAAGCAGAGAAAGAAAGCATCTATGATGTGCTGAT	2237
Db	619	rLeuLeuAlaGlyCysIleLysTyrGlyArgGlyLeuAsnIleTyrAspAlaPheValIst	639
QY	2238	CTACTCGACTCGAATGTAGAGACTGGGTGAGAAATGAGCTGTAAAGAAATTTAGAGAAAG	2297

[illegible]


```

Oy 505 TTACACACCTCTGAACTGTATCTGACAGAAACCTATCCAGATTTTCCACAGA 564
Db 61 LeuSerHisLeuSerThrLeuIleuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
Oy 565 AGTTCTCTGAGACTAACAGTTTAGACAATCTGTGTGCTGTGAGACAAATTTGGCTCT 624
Db 81 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGluThrAsnLeuAlaSer 100
Oy 625 CTAGAAAGCTTCCTTATTTGACAGCTTAACTTAAAGAACTCAATGTGGCTCACAT 684
Db 101 LeuGluAsnProIleGlyHisLeuSerThrLeuGlyGluLeuAsnValAlaHisAsn 120
Oy 685 TTATACATCTCTGATTAAGTCACTGCAATATTTTCCATCTGACGAACCTAGTACATGT 744
Db 121 LeuIleGlnSerPheLeuSerProGluTyrPheSerAsnLeuThrAsnLeuGlnHisLeu 140
Oy 745 GATCTTTCTTAACTATATTAATCAACTATTACTGCAACGACTTACAGTTTCTACGTGA 804
Db 141 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValIleGln 160
Oy 805 AATCCACAAGTCATCTCTTTAGACATGTCTTTGAAACCCAAATTGACTTCAATCAAGAC 864
Db 161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
Oy 865 CAAGCCTTTGAGGAAATTAAGCTCCATGCACTGAAGCTTAAGATTTTAAATAGCTCA 924
Db 181 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLeuArgAsnAspPheAspSerLeu 200
Oy 925 AATATTAATGAAACCTGCTTCAAAACCTGGCTGTTTACAGTTCATCGGTATCTTG 984
Db 201 AsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHisArgLeuValLeu 220
Oy 985 GGAAGATTTAAAGTGAAGAAATCTGAAAATTTTGAACCTTCATCATGGAAGACTA 1044
Db 221 GlyIleuPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGlnGlyLeu 240
Oy 1045 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1104
Db 241 CysAsnLeuThrIleGluGlnPheArgLeuAlaTyrLeuAspTyrTyrLeuAspPheIle 260
Oy 1105 GTTAAG--ATTCATTTGCTGGCAATGTTTCTGCAATGTCTCTGGCAGGTGATCTATA 1161
Db 261 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
Oy 1162 AAATATCTAGAAAGTGTCTTAAACATTTCAATGGCAATCTTATCAATTAAGATGT 1221
Db 281 GluArgValLysAspPheSerTyrAsnPheGlyTyrGlnHisLeuGluLeuValAsnCys 300
Oy 1222 CAACTAAG-CAGTTTCCAACTCTGATCACTCCCTTTCTTAAAGTTTGAACCTTAAGTATG 1280
Db 301 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysAspGlyThrPheThrSer 320
Oy 1281 AACAAAGGCTCTATCAGTTTAAAGAGTGCCCTTACCAAGTCAAGCTATCTAGATCTT 1340
Db 321 AsnLysGlyGlyAsnAlaPheSerGluValAsnLeuProSerLeuGlnPheLeuAspLeu 340
Oy 1341 AGTGAAGATGCACTGAGCTTATAGTGTGGCTGTCTTATTTGATTTGGGAACAACAAC 1400
Db 341 SerTrpAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
Oy 1401 CTGAGACACTTGAACCTCAGCTTCAATGGCCCACTTGAATGAATGGCAATTTAGGGT 1460
Db 361 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
Oy 1461 CTAGAAAGCTGACAGCACTGATTTTTCAGACACTTAACTTAAAGAGTCAAGATTT 1520
Db 381 LeuGlnGlnLeuGluHisLeuAsp-PheGlnHisSerAsnLeuLysGlnMetSerGluPhe 400
Oy 1521 CTGAGCGTTTATTCCTTGAAGAAAGCTATTTACCTTGAACATCTTATTAACCAACA 1580
Db 400 eSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThrAr 420

```

```

Oy 1581 AATTGACTGCGATGATATTTCTTGGCTTGACCAAGCTCTCAACATTTAAATAGGCTGG 1640
Db 420 gValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaG 440
Oy 1641 CAATTTCTTGAACAAACACCTTTCAAAATGCTTTTGAACAAACAAACCTTGACATT 1700
Db 440 yAsnSerPheGlnGluAsnPheLeuProAspIlePheThrCylLeuArgAsnLeuThrPh 460
Oy 1701 CCTGATCTCTTAAAGTCAATTTGGAACAAATATCTTGGGGGATATTTGACACCTTCCA 1760
Db 460 eLeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSe 480
Oy 1761 TAGACTCAATTTATTAATAGAGTCAACAACATCTATTTGTTTGGATTCATCCCATTA 1820
Db 480 rSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTy 500
Oy 1821 TAACCAAGCTGATTCCTCTGACGACTCTTGATTTGCAAGTTTCAATGCAATGACATCT 1878
Db 500 rLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLy 520
Oy 1879 -AAAGAAATCTGCAATTTTCCAAAGACTTACGCTTCTTCAATCTTAAACAATTC 1937
Db 520 sLysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAs 540
Oy 1938 TGTGCTTGTATATGTGAACATCAGAAATTCCTGACAGTGGTCAAGGAACAGACAGTT 1997
Db 540 pPheAlaCysThrCysGlnHisGlnSerPheLeuGlnTrpIleLysAspGlnAsGlnLe 560
Oy 1998 CTGTGTAATGTTGAACAAATGACATGTGCAACACCTGTAGAGATGAATACCTTCCTAGT 2057
Db 560 uLeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnLysMetProVa 580
Oy 2058 GTTGAGATTTAAATATCTACCTGTATATGTACAAACAATCATCATGTGTGATGCT 2117
Db 580 lLeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLe 599
Oy 2118 CAGTGTATGTGGTATCCACTGATGATTTCTGATTAACACTTCTATTTTCACTGAT 2177
Db 599 uSerValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMe 619
Oy 2178 ACTTATTTGCTGCTGTAAAGTACAGCAGAGAGGAAGAAATCTATGATGATTTGTGAT 2237
Db 619 tLeuLeuAlaGlyCysIleLysTyrGlyArgGlyGluAsnIleTyrAspAlaPheValIl 639
Oy 2238 CTACTGAGTCAAGATAGAGACTGGGTGAGAAATGACTGTGAAGAAATTTGAAGAGAG 2297
Db 639 eTyrSerSerGlnAspGluAspTrpValArgAsnGluLeuValLysAsnLeuGluGlu 659
Oy 2298 AGTGCCCGCTTCACTGCTGCTTCACTGACAGACTTATTCCTGTGAGGCATTTGC 2357
Db 659 yValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAl 679
Oy 2358 TGCCCAATCATCCAGGAAGGCTTCCACAAAGACCGGAAGTTATTTGTGATGCTTAG 2417
Db 679 aAlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValValSerGl 699
Oy 2418 ACACTTATTCAGAACCGCTGTGTATCTTTGAATATGAATGCTTAAACATGGCAGTT 2477
Db 699 nhIAspIleGlnSerArgTrpCysIlePheGluTyrGluHisAlaGlnHisTrpGlnPh 719
Oy 2478 TCTGAGACGCGCTGACATCATCTTCACTTGTGCTTGAAGAGTTGAGAAGTCCCGCT 2537
Db 719 eLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLe 739
Oy 2538 GAGGACAGAGTGAATTTGATGCGCTTTTACAGAAACACCTTACGTAATGGAGAGA 2597
Db 739 uArgGlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGluTrpGluAs 759
Oy 2598 CAATCTCTGGGAGGACATCTTCTGAGAAAGCTTAAATGAAGCCCTATTTGATGAGAA 2657
Db 759 pSerValLeuGluLysArgHisIlePheThrParArgLeuArgLysAlaLeuLeuAspGlyLy 779
Oy 2658 AGCCTGAATCTGAGCAACA 2679

```

```

Db      779 sSerTrpAsnProGluGlyThr 786
      ||:::|||||||
RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 58183WO003
; CURRENT APPLICATION NUMBER: US/10/732,563
; FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-563-8

Alignment Scores:
Pred. No.:      1,13e-259      Length:      799
Score:          2675.50        Matches:     532
Percent Similarity: 79.82%      Conservative: 97
Best Local Similarity: 67.51%    Mismatches: 155
Query Match:    51.68%         Indels:      5
                        Gaps:      3

US-09-396-985B-46 (1-2951) x US-10-732-563-8 (1-799)
Qy      325 ATGATACAGAACTCAGCAAGTCCCTGATGACATCTCTTCAACCAAGATACATGAT 384
      ||:::|||||||
Db      1 MetIuLeuAsnProGlyThr 20
      ||:::|||||||
Qy      385 CTGAGCTTCAACCCCTGATGATCTTAAAGCTATGATCTTCAATTTTTCAGACTT 444
      |||||
Db      21 LeuSerPheAsnProGlyThr 40
      |||||
Qy      445 CAGTGGTGTGATTTATCCAGGTGTGAATTTGAACCAATTTGAAGCAAGCATGGCATGGC 504
      |||||
Db      41 GluValLeuAsnProGlyThr 60
      |||||
Qy      505 TTACACACCTCTCAAACTTATCTGACAGCAAACTTATCCAGATTTTCCCGAGCA 564
      |||||
Db      61 LeuSerHisLeuSerTrpLeuHisLeuThrGlyAsnProGlyLeuValAlaLeuGly 80
      |||||
Qy      565 AGTTCTCTGGACTTAACAAGTTTGAACAATCTGGGCTGTGAGACAAATTTGGCCCT 624
      |||||
Db      81 AlaPheSerGlyLeuSerSerLeuGlnValAlaValGlnThrAsnLeuHisSer 100
      |||||
Qy      625 CTGAAAGCTTCCCTATTGACACAGCTTAACTTAAAGAACTCAATGTGGCTCACAAT 684
      |||||
Db      101 LeuGlnAsnProGlyLeuHisLeuThrGlyLeuValAlaHisAsn 120
      |||||
Qy      685 TTTATACATCTCTGAATGATCTGACATTTTTCGAATCTGACGAACCTGATCATGTG 744
      |||||
Db      121 LeuIleGlnSerPheLeuProGlyThrPheSerAsnLeuThrAsnLeuGlnHisLeu 140
      |||||
Qy      745 GATCTTCTTATATATATATCAATCTTACTGTCACAGACTTCTAGACTTTCTACGGTGA 804
      |||||
Db      141 AsnLeuSerSerAsnHisIleGlnSerIleGlyThrAsnProGlyValLeuHisGln 160
      |||||
Qy      805 AATCCACAGATCAATCTCTCTTGAACAATGTCTTTGAACCCCAATGTGACTTCAAGAC 864
      |||||
Db      161 MetProLeuLeuAsnLeuSerLeuAsnProGlyLeuAsnProGlyLeuHisGln 180
      |||||
Qy      865 CAAGCTTTCAGGGAATTAAGTCAATGATGATCTGATGATGATGATGATGATGATGAT 924
      |||||
Db      181 GlyAlaPheLeuGlyIleArgLeuHisIleValLeuThrLeuArgAsnAsnPheAsnSerLeu 200

```

```

Qy      925 AATATATGAAAACTTGCCCTCAAAAACCTGGCTGTTTACACGTCATCGATGATCTTG 984
      |||||
Db      201 AsnValMetLeuSerThrCysIleGlnGlnValAlaGlyLeuGlnValHisValArgLeuValLeu 220
      |||||
Qy      985 GAGAAATTTAAAGATGAAGAAATCTGGAAATTTTGAACCTCTATCATGGAAGACTA 1044
      |||||
Db      221 GlyGluPheArgAsnGlnGluValAsnLeuGlnValPheAsnProGlyLeuValGlnGlyLeu 240
      |||||
Qy      1045 TGTGATGTGACCTTGAATGAGTTCAGGTTTAACTATTAACAATGATTTTTCAGATGATTT 1104
      |||||
Db      241 CysAsnLeuThrIleGlnGluPheArgLeuValAlaValLeuAsnProGlyThrLeuAsnProGly 260
      |||||
Qy      1105 GTTAAG--TTCCATTTGCTGGCGAATGTTTCTGACATGTCTCGACAGGTGATGATATA 1161
      |||||
Db      261 IleAsnLeuPheAsnGlyLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
      |||||
Qy      1162 AAATATCTAGAGATGTTCTCTTAAACATTTCAATGGCAATCTTATCATCATTAAGTGT 1221
      |||||
Db      281 GluArgValIleAsnProGlyThrAsnProGlyThrGlnHisLeuGlnValLeuValAsnGly 300
      |||||
Qy      1222 CAACATAAG-CAGTTTCAACCTGAGATCTACCTCTTCTTAAAGTTGACTTAACTATG 1280
      |||||
Db      301 LysPheGlyGlnPheProThrLeuValLeuValSerLeuValArgLeuThrPheThrSer 320
      |||||
Qy      1281 AACAAAGGCTCTATCAGTTTAAAGAGCCCTACCAAGTCCAGCTATCTAGATCTT 1340
      |||||
Db      321 AsnIleGlyGlyAsnAlaPheSerGlyValAlaPheLeuProSerLeuGlnPheLeuAsnPro 340
      |||||
Qy      1341 AGTGAAGATGCACTGAGCTTATGATGCTGCTGTTCTTATTTGATTTGGGAACAAACAGC 1400
      |||||
Db      341 SerArgAsnGlyLeuSerPheLeuGlyCysGlySerGlnSerAsnProGlyThrThrSer 360
      |||||
Qy      1401 CTGACACACTTATGACCTCAGCTTCAATGGGCGCATCATTTATGATGATGATGATGATGATGAT 1460
      |||||
Db      361 LeuValSerTrpLeuAsnProGlyThrAsnGlyValIleThrMetSerSerAsnProGly 380
      |||||
Qy      1461 CTGAAGAGCTGACAGCACTGATTTTTCAGCACTGATCTTAAAGGCTCAGAAAT 1520
      |||||
Db      381 LeuGlnGlnLeuGlnHisLeuAsnProGlyThrIleSerValLeuGlnMetSerGlnPro 400
      |||||
Qy      1521 CTGAGCGTTTATTCCTTGAAGAACTTATCTTACATCTTATTTCTAATACACCA 1580
      |||||
Db      400 eSerValPheLeuSerLeuArgAsnLeuIleValLeuAsnProGlyThrIleThrIleThrIle 420
      |||||
Qy      1581 AATTTGACTCGATGATATTTCTTGGCTTGAACAGCTTCAACAACAATTAATTAATGCTGG 1640
      |||||
Db      420 GlyAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuValMetAlaGly 440
      |||||
Qy      1641 CAATTTCTTCAAGACACACCTTCAATGCTTTTGAACAACAACAATTTGACATTT 1700
      |||||
Db      440 ValAsnSerPheGlnGlnAsnProGlyThrIlePheThrGlnLeuValGlnMetLeuThrPro 460
      |||||
Qy      1701 CTGGAATCTTCTTGAATGTCATTTGAACAACAATTTCTTGGGGGCTATTTGACACCTTCCA 1760
      |||||
Db      460 eLeuAsnProGlyLeuGlnHisLeuGlnGlnLeuSerProThrAlaPheAsnSerLeu 480
      |||||
Qy      1761 TAGACTTCAATTAATTAATTAATGATGACCAATGATTAATTTTGGATTCACCCATTA 1820
      |||||
Db      480 rSerLeuGlnValLeuAsnMetSerHisAsnAsnProGlyThrPheProGly 500
      |||||
Qy      1821 TAAACAGCTGATATCTCCCTGACAGCTCTTGAATGCTTGAATGCTGATGACATCT-- 1878
      |||||
Db      500 rLysCysLeuAsnSerLeuGlnValLeuAsnProGlyThrLeuValHisIleLeuThrSerIle 520
      |||||
Qy      1879 -AAAGCAATCTGCAACATTTTCCAAAGAGCTTGAAGCTTTTCAATTTTCAATTAATTC 1937
      |||||
Db      520 rLysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsn 540
      |||||
Qy      1938 TGTTCCTTGTATATGCAACAATGATGATGATGATGATGATGATGATGATGATGATGAT 1997
      |||||
Db      540 rPheAlaCysThrCysGlnHisGlnSerPheLeuGlnThrProGlyValAsnProGlnValLeu 560
      |||||
Qy      1998 CTGTTGTAATGTTGAACAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2057

```

Db	560	uLeuValGluValGluArgMetGluCysAlaThrProSerLeuArgGlnGlyMetProVa	580
Qy	2058	GTGGATTATTAATAATTTACCTGTTATATGTACAAGACAATCATCATGCTGTCAGTGT	2117
Db	580	lleuSerLeu---AenIleThrCysGluMetAsnIlyThrIleIleGlyValSerValle	599
Qy	2118	CAGTGTATTTGTGGTATTCACCTGTAGCATTTTCTGATATACCACTCTTATTTTCACCTGAT	2177
Db	599	uSerValIleuValValSerValIleValIleValIleuValIlyTrysPheTrypPheHISleuMe	619
Qy	2178	ACTATTTGCTGGCTGTATAAAAGTACAGCAGAGGAGAAAGCATCTATGTATGATTTGTGAT	2237
Db	619	tleuenuIlaGlyCysIleIlyTrysGlyArgGlyGluIuSnnIleTrysApAlaIleValIli	639
Qy	2238	CTACTCGAGTCAGATGAGATGAGACCTGGGTGAGAAATAGCTGTGTAAGAATTTAGAGAAG	2297
Db	639	eTysSerSerGlnAepGluAmpTrpValArgAsnIleuValIlySnnIleuGluGluGlu	659
Qy	2298	AGTGGCCCCGCTTTACCTCTGCTGCTTACATACAGAGACTTTATCTCTGGTGTAGCCATTGC	2357
Db	659	yValIProProPheGlnIleuCysIleuHISTrysArgSpheIleIleProGlyValAlaIleAl	679
Qy	2358	TGCCAACAATCATCCAGGAAGGCTTCCACAAGAGCCGGAAGGTTATTTGGTAGTGTCTAG	2417
Db	679	AlaAsnIleIleHISGlnGlyPheHISLysSerArgIlySnnIleValIleValIleValSerGlu	699
Qy	2418	ACACTTATTTACAGAGCCCTGTGGTGTATCTTTGAATATGAGATTTGCTCAAAATGGCAGTT	2477
Db	699	nHISpheIleGlnSerArgTrpCysIleIlePheGluTrpGluIleAlaGlnIleThrTrpGlnPh	719
Qy	2478	TCTGAGCAGCGCGCTCTGCGATCATTTTCATTGTCTTGGAGAAAGTTGGAAGTCCCTGCT	2537
Db	719	eIeuSerSerArgAlaGlyIleIlePheIleValIleuIlnIlySnnIleuValGlnIlySnnIleu	739
Qy	2538	GAGCAGACAGGTGGAATGTATTCGCTCTTAGACAGAAACCTACCTCGAATGGAGGAGA	2597
Db	739	uArgGlnIlnIlnValGluIleuTrysArgIleuIleuSerArgSnnIlyTrysGluIlnTrpGluAs	759
Qy	2598	CAATCTCTGGGGAGGACACATCTTCTGGAGAAAGCTTAAAAATGCGCTTATTTGATGGAAA	2657
Db	759	pSerValIleuGlyArgHISIleIlePheTrpArgArgIleuArgIlySnnIleuIleuAmpGlyLy	779
Qy	2658	AGCCTCGAATCTGTGACAAACA	2679
Db	779	sSerTrpAsnProGluGlyThr	786
RESULT 5			
US-10-732-796A-8			
; Sequence 8, Application US/10732796A			
; Publication No. US20040197865A1			
; GENERAL INFORMATION:			
; APPLICANT: Gupta, Shalley K.			
; APPLICANT: Ghosh, Taron K.			
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines			
; FILE REFERENCE: 58182US004			
; CURRENT APPLICATION NUMBER: US/10/732,796A			
; CURRENT FILING DATE: 2003-12-10			
; NUMBER OF SEQ ID NOS: 23			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 8			
; LENGTH: 799			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-732-796A-8			
Alignment Scores:			
Pred. No.: 1,13e-259			
Score: 2675.50			
Percent Similarity: 79.82%			
Best Local Similarity: 67.51%			
Query Match: 51.68%			
Length: 799			
Matches: 532			
Conservative: 97			
Mismatches: 155			
Indels: 5			

DB:	16	Gaps:	3
DB:	US-09-396-985B-46 (1-2951) x US-10-732-736A-8 (1-799)		
OY	325 ATGATGACGAAACTCAGCAAAAGTCCCGATGACATTCCTTTCTTCAACCAAGACATAGAT	384	
DB	1 MetGluLeuAenPheTyTylgATleProAspAsnLeuProPheSerThrTylAsnLeuAsp	20	
OY	385 CTGAGCTTCAACCCCTTGAGAGATCTTAAAAAGCTATAGCTTCTCCATTTTTCAGACTT	444	
DB	21 LeuSerPheAenProLeuArgHileuGlySerTylSerPhePheSerPheProGluLeu	40	
OY	445 CAGTGGCTGGATTTATCCAGGTGTGAATTAACAATTGAAGCAAGCAGTCGATGCG	504	
DB	41 GluValLeuAspLeuSerArgCysGluHileuGlnThrIleGluAspGlyAlaTylIleSer	60	
OY	505 TTACACCAACCCCTCAAACTGATATCTAGCAGGAAGACCCCTATCCAGAGTGTTCGCCAGA	564	
DB	61 LeuSerHileuSerThrIleuHileuThrGlyAsnProIleGlnSerIleuAlaLeuGly	80	
OY	565 AGTTTCTCTGGACTTAACAGTTTAAAGACATCTGGTGGCTGTGGAGACAAATGGCGCTT	624	
DB	81 AlaPheSerGlyLeuSerSerIleuGlnIleuValAlaValIleGluThrAsnLeuAlaSer	100	
OY	625 CTAGAAAGCTTCCCTATTTGACACGCTTATTAACCTTAAAGAAATCTAATGTGGCTCAACAT	684	
DB	101 LeuGluAsnPheProIleGlyHileuHileuThrLeuIleuSerGlyLeuAsnValAlaHileuAsn	120	
OY	685 TTTATACATCTCTGTAAGTTACCTCGCAATATTTTCCATCTGACGAACCTAGTACATGTG	744	
DB	121 LeuIleGlnSerPheIleuPheProGluTyrPheSerAsnLeuThrAsnLeuGluHileu	140	
OY	745 GATCTTTCTTATTAACCTATTTCAAACTATTACTGTCAACGACTTCAAGTTTCTACGTGAA	804	
DB	141 AspLeuSerSerAsnIleGlnSerIleTyrCysThrAspLeuArgValLeuHileuGln	160	
OY	805 AATCCACAGTCATCTCTTTAGACATAGCTTTGAACCCCAATTTGACTTCATTCAGAC	864	
DB	161 MetProLeuLeuAsnLeuSerIleuAspLeuSerIleuAsnProMetAsnPheIleGlnPro	180	
OY	865 CAACCCCTTTCAGGAAATTAAGCTCCAGTAAGTCACTTAAGAGGTAAATTTTAATAGTCA	924	
DB	181 GlyAlaPheIleuSerGluIleArgLeuHileuLeuThrLeuAlaGlnAsnLeuPheAspIleu	200	
OY	925 AATATTAATGAACCTGCTTCAAAACCTGGCTGGTTTACGTCGATCGGTGATCTTG	984	
DB	201 AsnValMetCysThrCysIleGlnGlyLeuAlaIleIleuGluValHileuArgLeuValIleu	220	
OY	985 GGAGAAATTTAAAGATGAAGAGATCTGGAAATTTTGAACCCCTTATCATGGAAGACTA	1044	
DB	221 GlyIleuPheArgGlnGluGlyAsnLeuGlnIleuPheAspIleuSerAlaLeuGlnGlyIleu	240	
OY	1045 TGTGATGTGACCAATGATGAGTTACAGGTGAACATATACAAATGATTTTTCAGATGATTT	1104	
DB	241 CysAsnLeuThrIleGluGluPheArgLeuAlaTyrIleuSerIleuGlyLeuAspAspIle	260	
OY	1105 GTTAAG--TTCCATCTCTGGCAAAAGTTTCTGCAATGTCTCTGGAGAGGTATCTATA	1161	
DB	261 IleAspLeuPheAsnCysIleuThrAsnValSerSerPheSerIleuValSerValThrIle	280	
OY	1162 AATATATCTAGAGATGTCTTAAACATTTCAATGCGAATCTTATCAATCATTAAGATGT	1221	
DB	281 GlyTyrGlyIleuPheProThrIleuHileuLeuSerIleuIleuAspIleuValAsnIleu	300	
OY	1222 CAACTAAG-CAGTTTCAACCTCGGAGCTACCCCTTCTTAAAGTTTGAAGCTTAACTATG	1280	
DB	301 LysPheGlyGlnPheProThrIleuHileuLeuSerIleuIleuAspIleuThrPheThrSer	320	
OY	1281 AACCAAAAGGCTCATCAGTTTAAAAAAGTGCGCCCTTACCAAGTCTCAGACTCTTGAATCTT	1340	
DB	321 AsnIleuSerGlyGlnAlaIlePheSerGluValAlaAspLeuProSerIleuGluPheLeuAspLeu	340	
OY	1341 AGTAGAAATGACTGAGCTTTAGTGTGGCTGTTCTTATTTCTGATTTGGGAACAACAGC	1400	

```

Db      341 SerArgAnGlyLeuSerPheLeuGlyCysCysSerGlnSerAspPheGlyThrThrSer 360
Qy      1401 CTGAGACACTTAAGACCTTCAGCTTCAATGTCGCCATCATATGATGCGCAATTCATGGCT 1460
Db      361 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAspPheLeuGly 380
Qy      1461 CTGAAGAGCTGCAGCAGCTGATTTTTCAGACCTCACTTAAATAAAGGCGCAGAGATT 1520
Db      381 LeuIuGlnLeuGluHisLeuAsp-PheGlnHisSerAsnLeuLysGlnMetSerGluPh 400
Qy      1521 CTCAGCGTTCTTAATCCCTTGAAGAGCTTACCTTACCTTCACTCTTATACTAACCCAA 1580
Db      400 eSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisThrAr 420
Qy      1581 AATTGACTTGATGATATTTCTTGGCTTGACCAAGCTTCAACACTTAAATAAGCTGG 1640
Db      420 gValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGl 440
Qy      1641 CAATTCTTCAAGACAAACACCTTTCAAATGTCCTTTCGAAACAAACAACTTGACATT 1700
Db      440 yAsnSerPheGlnGlnLeuAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPh 460
Qy      1701 CTGGAATCTCTTAATGTCATTAATGTCGAAACAATATCTTGGGGGCTATTTGACACCTTCCA 1760
Db      460 eLeuAspLeuSerGlnCysGlnLeuGlnLeuSerProThrAlaPheAsnSerLeuSe 480
Qy      1761 TAGACTTCATTAATTAATAGATGCACAAATCATATGTTTGGATTCATCCCATTA 1820
Db      480 rSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTy 500
Qy      1821 TAAACAGCTGATATCCCTCAGACACTCTTGATTCAGATTGACATGCATAGACATCT-- 1878
Db      500 rLysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLy 520
Qy      1879 -AAAGGAATACTGCAACATTTTCCAAAGAGTCTAGCCTTCTTCAATCTTACTTAAACATTC 1937
Db      520 sLysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAs 540
Qy      1938 TGTGCTGTTGATATGTCGAACATCGAATAATTCCTCAGAGGCTCAGAGAAAGAACGCTT 1997
Db      540 pPheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleTyrLeuAspGlnArgGlnLe 560
Qy      1998 CTGAGTGAATGTTGAACAATGATGATGTCGAACACCTTAGAGATGAATACCTCCTTAGT 2057
Db      560 uLeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVa 580
Qy      2058 GTTGGATTTTAATAATCTTACCTGTTATATGTATACAAAGCAATCATCACTGTGTCAGTGT 2117
Db      580 lLeuSerLeu---AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLe 599
Qy      2118 CAGGTGATTTGTCGATTCAGTACATTTCTGATATACACATTCCTATTTTCACTCGAT 2177
Db      599 uSerValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMe 619
Qy      2178 ACTTATTCCTGCTGTAAATAAGTACAGCAGAGAGAAAGCATCTATGATGATTTGAT 2237
Db      619 tLeuLeuAlaGlyCysIleLysTyrGlyArgGlyLysGlnAsnIleTyrAspAlaPheValI 639
Qy      2238 CTATCTGAGTCAGATGAGAGCTGGGTGAGAAATGAGCTGTGTAAGATTTTGAAGAAG 2297
Db      639 eTyrSerSerGlnAspGlnAspTyrValArgAsnGluLeuValLysAsnLeuGlnGlu 659
Qy      2298 AGTGGCCCGCTTACCTCTGCTCCTTCACTACAGAGACTTTATCTCTGTGTAGGCATTGC 2357
Db      659 yValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGlyValAlaIleAl 679
Qy      2358 TGGCAACATCATCCAGAGAGCTTCCACAAGAGCGGAGAGGTTATGTGAGTGTAG 2417
Db      679 aAlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValSerG 699
Qy      2418 ACACTTATTCAGAGCCGTTGGTGTATCTTTGAATATGAGATTGCTCAACATGGCAGTT 2477

```

```

Db      699 nHisPheIleGlnSerArgTyrPyrCysIlePheGlnTyrGluIleAlaGlnThrTrpGlnPh 719
Qy      2478 TCTGAGACCGCGCTCGGCATCATCTTCAATGTCCTTGAAGAGGTTGAGAAATCCCTGCT 2537
Db      719 eLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLe 739
Qy      2538 GAGCAGCAGAGTGGAATTGATGCGCTTCTTACAGAAACACCTTACCTGGAATGGAGGA 2597
Db      739 uArgGlnGlnValGluLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrGluAs 759
Qy      2598 CAATCTCTGGGAGAGGCATCTTCTGAGAGAAACATTTAAATAGCCCTATTTGATGAAA 2657
Db      759 pSerValLeuGlyArgHisIlePheThrPargArgLeuArgValaLeuLeuAspGlyLy 779
Qy      2658 AGCCTGGAATCTGAGCAACA 2679
Db      779 sSerTrpAsnProGlnGlyThr 786

RESULT 6
US-10-114-893-10
; Sequence 10: Application US/10114893
; Publication No. US20020193567A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Collins-Racle, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Metberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Bowman, Michael R.
; APPLICANT: Carlin-Duckett, McKeough
; APPLICANT: Kelleher, Kerry S.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6000-10A
; CURRENT FILING DATE: 2002-04-02
; EARLIER APPLICATION NUMBER: 09/413,232
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-114-893-10

Alignment Scores:
Score: 1,38e-48 Length: 661
Percent Similarity: 579.50 Matches: 185
Best Local Similarity: 47.54% Conservative: 124
Query Match: 28.46% Mismatches: 305
DB: 11.19% Indels: 37
Gaps: 16

US-09-396-985b-46 (1-2951) x US-10-114-893-10 (1-661)
Qy      289 TGCATAGAGGTAGTCTCTAATATTACCTTACCAATGCATGATGAGAAACTCAGCAAGTC 348
Db      28 CysIleGlnLysGlnAlaAsnLysThrTyrAsnGlnLysLeuGlnLysLeuSerGluIle 47
Qy      349 CTGATGACATCTCTTCTTCAACCAAGACATAGATGTGAGCTTCAACCCCTTGAAGATC 408
Db      48 ProAspThrLeuProAsnThrThrGluPheLeuGlnPheSerPheAsnPheLeuProThr 67
Qy      409 TTAATAAGCTATAGCTTCTCCCAATTTTTCAGAACTTCAGAGGCTGATTTATCCAGGTGT 468
Db      68 lIleHisAsnArgThrPheSerArgLeuMetAsnLeuThrPheLeuAspLeuThrArgCys 87
Qy      469 GAAATTGAACAATTGAAGCAAGGACATGCGCTTACACCACTCTCAAACTTGATA 528

```

Db 88 GlnleasentripLeuHsIgluAspThrPheGlnSerHisIglInLeuSerThrLeuVal 107
 Qy 529 CTGACAGAAACCCATCCAGAGTTTCCCAGAGATTTCTCGACATAACAAGTTTA 588
 Db 108 LeuThrGlyAsnProLeuIlePheMetCysIgluThrSerLeuAsnGlyProLysSerLeu 127
 Qy 589 GACATCTGTGGCTGTGAGACAAATGGCTCTTCAAGAGCTTCCCTTATGACAG 648
 Db 128 LysHisLeuPheLeuIleGlnThrGlyLeSerAsnLeuGlnPheIleProValHisAsn 147
 Qy 649 CTATTAACCTTAAAGAACTCAATGTGGCTCAATTTTATACATCTCTGTAAGTACT 708
 Db 148 LeuGlnSerLeuGlnSerLeuTyrlLeuGlySerAsnHisIleSerSerIleLysPhePro 167
 Qy 709 GCATATTTTCCATCTGACAGACCTTACATGAGTCTTCTTATATATATATCA 768
 Db 168 LysAspPhePro--AlaArgAsnLeuLysValLeuAspPheGlnAsnAlaIleHis 186
 Qy 769 ACTATTACTGTCAACAGCTTACAGTTTCTACGTGAAATCCACAACTCATCTCTTTA 828
 Db 187 TyrIleSerArgGluAspMetCysSerLeuGln-----AlaIleAsnLeuSerLeu 204
 Qy 829 GACATGTCTTGAACCCAAATGACTTCAATCAAGACCAAGCTTTCAAGGAATTAAGCTC 888
 Db 205 AsnPheAsnGlyAsnAsnValLysGlyIleGlnLeuGlyAlaPheAspSerThrValPhe 224
 Qy 889 CATGACGACTCAAGAGTAAATTTTATAGCTCAATATATATGAAGAACTGGCTTCA 948
 Db 225 GlnSerLeuAsnPheGlyLysThrProAsnLeuSerValIlePheAsnGly--LeuGln 243
 Qy 949 AACCTGGCTGTGTTACACGTCATCGATCTTGTGAGAGATTTAAAGATGAAGAGAT 1008
 Db 244 AsnSerThr-----ThrGlnSerLeuThrPheGlnLysThrPheGlnAspIleAspAsp 260
 Qy 1009 CTGAAATTTTGAACCTCTATCATGAGAGACTATGATGATGACCATGATGATTC 1068
 Db 261 GluAspIle--SerSerIleMetLeuLysGlyLeuGlyMetSerValIgluSerLeu 279
 Qy 1069 AGCTTAACATATACAATGATTTTTCAGAT--GATATGTGATGCTTCATGCTGGCG 1125
 Db 280 AsnLeu--GlnGlnHisArgPheSerAspIleSerSerThrThrPheGlnCysPheThr 298
 Qy 1126 AATGTTCTGCAATGCTCTGGACAGTGTATCTATTAATAATCTAGAAGATGTCCTTAA 1185
 Db 299 GlnLeuGlnGlnLeuAspLeuThrAlaThrHisLeuLysGlyLeuProSerGlyMetLys 318
 Qy 1186 CATTT-----CAATGGCAATCCTTATCAATCAT-----TAG 1217
 Db 319 GlyLeuAsnLeuLeuLysLeuValLeuSerValAsnHisPheAspGlnLeuGlyGln 338
 Qy 1218 ATGTCACTAAGACAGTTTCCAACTCTGATCTACCCCTTTCTTAAAGTTTACCTTAACT 1277
 Db 339 IleSerIleAlaAsnPheProSerLeuThrHisLeuTyrlLeuArgGlyAsnValLysLys 358
 Qy 1278 ATGAACAAGAGGTATATCATGTTTAAAAAAGTGCCCTACCAAGCTCATGATCTTAT 1337
 Db 359 LeuHisLeuGlyValIgluGlyLeuGlnLys-----LeuGlyAsnLeuGlnThrLeuAsp 376
 Qy 1338 CTTAGTAGAAATGACCTGAGCTTATGAGTGAGCTGTTCTTATTTGATTGGAAACAAC 1397
 Db 377 LeuSerHisAsnAspIleGluAlaSerThrCysCysSerLeuGlnLeuLysAsnLeuSer 396
 Qy 1398 AGCTTGAGACACTTACAGCTCATGCTCATAGTGGCAT--ATTAGAGTGGCAATTTG 1454
 Db 397 HisLeuGlnThrLeuAsnLeuSerHisAsnIleProLeuGlyLeuGlnSerGlnAlaPhe 416
 Qy 1455 ATGGGTCTAGAAGAGCTGACACCTGAGATTTTCAAGACCTCTTAAAGAGGTCAAC 1514
 Db 417 LysGlnCysProGlnLeuGlnLeuLeuAspLeuAla-PheThrArgLeuHisIleAsnAl 436
 Qy 1515 AGAATCTGACAGCTTCTTATCCCTTGAAGAACTTATACCTTGACATCTTATATCA 1574
 Db 436 AProGlnSerProPheGlnLeuLeuHisPheLeuGlnValLeuLeuLeuThrTyrlCysPhe 456

Qy 1575 CACCAAAATGACTTCGATGGTATATTTCTTGCTTGACAGCTCAACATTAATAAT 1634
 Db 456 eLeuAspThrSerAsnGlnHisLeuLeuAlaGlyLeuProValLeuArgHisLeuAsnLe 476
 Qy 1635 GGCTGGCAATTTCTTCAAGACCAACCTT-----TCAAAATGCTTTTGCAACACAC 1688
 Db 476 LysGlyAsnHisPheGlnAspGlyThrIleThrLeuThrAsnLeuGlnThrValIgl 496
 Qy 1689 AAATTTGACATCTCTGATCTCTTAAATGTCATTTGGAACAATATCTTGGGGGTATT 1748
 Db 496 YSerLeuGlnValLeuLeuLeuSerSerCysGlyLeuLeuSerIleAspGlnAlaPhe 516
 Qy 1749 TGACACCTTCATGACCTTCAATATTAATATGATGACACAAATCTATTTG-----TT 1802
 Db 516 eHisSerLeuGlyLysMetSerHisValAspLeuSerHisAsnSerLeuThrCysAspSe 536
 Qy 1803 TTGTGATTTCA--TCCATTTATTAACAGCTGTATTTCCCTGACACCTTGTGATTTG 1859
 Db 536 rIleAspSerLeuSerHisLeuLysGlyIleTyrl-----LeuAsnLeuAlaI 552
 Qy 1860 CAATGCAATGAGACATCTTAAAGAAATATGCAACATTTTCCAAAGAGCTAGCTTCTT 1919
 Db 552 aAsnSerIleAsnIleIleSerProArgLeuLeuProIleLeuSerGlnGlnSerThrI 572
 Qy 1920 CAATCTTACTAACAATCTGTGCTTGTATATGTAATGAAATTCCTGAGTGGGT 1979
 Db 572 eAsnLeuSerHisAsnProLeuAspCysThrCysSerAsnIleHisPheLeuThrTyrl 592
 Qy 1980 CAAGAAACAGAAAGAGTCTTGTGATGTTGAACAATGACATGTGCCAACCTGTAGA 2039
 Db 592 rLysGlnAsnLeuHisLysLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 612
 Qy 2040 GATGCAAT-----ACCTCCTTAGTGTGATTTTAATATCTTACCTGTATAT 2087
 Db 612 rLeuArgGlyValLysLeuSerAspValLysLeuSerCysGlyIleThrAlaIleGlyI 632
 Qy 2088 GTACAAACAAATCAATGCTGTGTCAGTGCAGTGCAGTGTGATGATCACTGAGCAT 2147
 Db 632 ePhePheLeuIleValPheLeuLeuLeuLeuAlaIleLeuLeuPheAlaValLysTy 652
 Qy 2148 TCTGATATACACTTCTATTTTTCACCTG 2175
 Db 652 rLeuLeuArgTrpLysTyrlGlnHisIle 661

RESULT 7
 US-10-038-854-134
 : Sequence 134, Application US/10038854
 : Publication No. US20040022781A1
 : GENERAL INFORMATION:
 : APPLICANT: Spytek, Kimberly A
 : APPLICANT: Li, Li
 : APPLICANT: Wolenc, Adam R
 : APPLICANT: Verneel, Corine
 : APPLICANT: Eissen, Andrew J
 : APPLICANT: Liu, Xiaohong
 : APPLICANT: Malysankar, Uziel M
 : APPLICANT: Shinkets, Richard A
 : APPLICANT: Tchernev, Velizar
 : APPLICANT: Spaderna, Steven K
 : APPLICANT: Gorman, Linda
 : APPLICANT: Ketkuda, Ramesh
 : APPLICANT: Paturajan, Meera
 : APPLICANT: Gusev, Vladimyr Y
 : APPLICANT: Gangolli, Baha A
 : APPLICANT: Guo, Xiaojia S
 : APPLICANT: Shenoy, Suresh G
 : APPLICANT: Rastelli, Luca
 : APPLICANT: Casman, Stacie J
 : APPLICANT: Boldog, Ferenc
 : APPLICANT: Burgees, Catherine E
 : APPLICANT: Edinger, Shlomit R
 : APPLICANT: Ellerman, Karen

```

; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT FILING DATE: US/10/038, 854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 134
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-854-134

Alignment Scores:
Pred. No.: 1,38e-48 Length: 661
Score: 579.50 Matches: 185
Percent Similarity: 47.54% Conservative: 124
Best Local Similarity: 28.46% Mismatches: 305
Query Match: 11.19% Indels: 37
DB: Gaps: 16

US-09-396-985b-46 (1-2951) x US-10-038-854-134 (1-661)
QY 289 TGCATAGAGTAGTTCCTAATATTATTAACCTACCATGATGATGACAGAACTGACGAAAGTC 348
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 349 CCGATGATTCCTCTTCTTCAACCAAGAAACATAGATCTGAGCTTCAACCCCTTGAAAGTC 408
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 409 TTAAGAGCTAGCTTCCATTTCTTCAAGATTTTTCAGAACTTCAAGTGGCTGATTTTCAAGGTC 468
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 469 GAAATGGAACATTTGAAGACAGAGCATGAGCTGATGACCAACCTTCAAACTTGATA 528
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 529 CTGACAGAAACCCATATCCAGAGTTTTCGCCAGGAAGTTTCTCGACATAAGTTTA 588
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 589 GACATCTGATGCTGGAGAGCAAAATTTGGCTCTAGAAAGCTTCCATTAGGACAG 648
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 649 CTTATACCTTTAAAGAACTCAATGTGCTGACATTTTATATCAATTCCTGTAGTTACT 708
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

DB 148 LeuGluAsnLeuGluSerLeuTyrLeuGlySerAsnHisIleSerSerIleLysPhePro 167
QY 709 GCATATTTTCCAAATGACGAGCAACCTAGTACAGTGGAGCTTTCTTATCTATATTCAA 768
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 168 LysAspPhePro--AlaArgAsnLysValLeuAspPheGlnAsnAlaIleHis 186
QY 769 ACTATTTCTGCAACGATTCACGATTTCTAGTGAAGATTCACAGCAATCTCTCTTTA 828
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 187 TyrIleSerArgGluAspMetArgSerLeuGln-----AlaIleAsnLeuSerLeu 204
QY 829 GACATGCTTTTGAACCCCAATGATCTTCATCAAGCAACCCCTTCAAGGAATTAAGTC 888
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 205 AsnPheAsnGlyAsnAsnValLysGlyIleGlnLeuGlyAlaPheAspSerThrValPhe 224
QY 889 CATGAACCTGACCTGAGAGGTAATTTTAATAGCTCAAACTTAATGAAGAACTGCTGCA 948
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 225 GlnSerLeuAsnPheGlyGlyThrProAsnLeuSerValIlePheAsnGly---LeuGln 243
QY 949 AACCTGGCTGTTTACACGTCGATCGGTTATCTTGGAGAAATTTAAAGTGAAGAGAAAT 1008
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 244 AsnSerThr-----ThrGlnSerLeuThrLeuGlyThrPheGlnAspIleAspAsp 260
QY 1009 CTGGAATTTTGAACCCCTGATCATGAGAAAGCACTATGTGATGACCATGATGACTTC 1068
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 261 GlnAspIle---SerSerAlaMetLeuLysGlyLeuGlySerGlnMetSerValGlnSerLeu 279
QY 1069 AGGTTACATATACAAATGATTTTTCAGAT---GATATGTGTAAGTCCATGCTGGCG 1125
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 280 AsnLeu---GlnGluHisArgPheSerAspIleSerSerThrThrPheGlnCysPheThr 298
QY 1126 AATGTTTCTGCAATGTCTGAGAGGTGTATTAATAATATGATAGATGTTCTTAA 1185
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 299 GlnLeuGlnGlnLeuAspLeuThrAlaThrHisLeuLysGlyLeuPheProSerGlyMetLys 318
QY 1186 CATTT-----CAATGSCAATCTTATCATGAT-----TAG 1217
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 319 GlyLeuAsnLeuLeuLysLysValLeuSerValAsnHisAspPheArgGlnCysGln 338
QY 1218 ATGTCAACTAAGCAAGTTCCACGCTGAGATCTACCCCTTGAAGTTGATGACTTAACT 1277
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 339 IleSerAlaAlaAsnPheProSerLeuThrHisLeuLysIleArgGluAsnValLysLys 358
QY 1278 ATGAACAAAGGCTCTATCACTTTTAAAGAGGAGCTTCAACATGCTCACTATGAT 1337
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 359 LeuHisLeuLysValGlyCysLeuGlnLys-----LeuLysAsnLeuGlnThrLeuAsp 376
QY 1338 CTTATGTAAGAAATGACCTGAGCTTTAGTGTGGCTGTTCTTATTTCTGATTTGGAAACAAC 1397
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 377 LeuSerHisAsnAspIleGluAlaSerAspCysSerSerLeuGlnLeuLysAsnLeuSer 396
QY 1398 AGCCTGACACTTGAACCTCAGCTTCAATGAGTGGCCATC--ATTATGAGTGGCAATTC 1454
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 397 HisLeuGlnThrLeuAsnLeuSerHisAsnGlnProLeuLysGlnSerGlnAlaPhe 416
QY 1455 ATGGGCTTAAGAGAGCTGACGACCTGATTTTTCAGACACTTAAATTAAGAGGTCAC 1514
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 417 LysGlnCysProGlnLeuGlnLeuLeuAspLeuAla-PheThrArgLeuHisIleAsnAl 436
QY 1515 AGAATTTGACAGGCTTTTATCCCTTGAAAGCTTATCTTACCTTGACATCTTATACATA 1574
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 436 ArgGlnSerProPheGlnLeuAsnLysHisPheGlnValLeuAsnLeuThrGlyCysPhe 456
QY 1575 CACCAAAATTTGACTGATGATATTTCTTGGCTTGACCAAGTCAACATTAATAAAT 1634
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 456 GluAspPheThrSerAsnGlnHisLeuLeuAlaGlyLeuProValLeuArgHisLeuAsnLe 476
QY 1635 GAGCTGCAATTTCTTCAAGAACAAACCCCTT-----TCAATGTCTTTGCAACACAAAC 1688
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 476 LysArgGlyAsnHisPheGlnAsnArgLysThrIleThrLysPheAsnLeuGlnThrValGln 496
QY 1689 AAATTTGACATTCCTGATCTTTTAAATGTCATTTGAAACAATATCTTGGGGGGGTAT 1748
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 496 YserLeuGlnValLeuLeuLeuSerSerCysGlyLeuLeuSerIleAspGlnGlnAlaPhe 516

```



```
Dh 189 SerIegIuaepMetSerSerLeuGln-----AlaThrAenLeuSerLeuAenLeu 206
Qy 835 TCCTTGAACCAATTTGACTTCATTCACAGACCAACCTTTCGGGAATTAAGCTCCAGAA 894
Dh 207 AenGlyAenAerIleAglYIleGluProGlyAlaPheAerSerAlaValPheGlnSer 226
Qy 895 CTGACCTAAGAGGTAATTTAATAGCTCAATATTAATGAAGAACTTGCTCCAAACCTG 954
Dh 227 Leu-----AenPheGlyGlyThrGlnAenLeuValIlePheGlyGlyLeu 242
Qy 955 GCTGGTTACACGTCATCGGTGATCTTGGAGAAATTAAGATGAAGAAATCTGGAA 1014
Dh 243 LysAenSerThrIleGlnSerLeuTrpLeuGlyThrPheGluAerMetAspArgLys 262
Qy 1015 ATTTTGAACCTTCATCATGGAAGAACTATGATGATGACCATGATGATTCAGGTTA 1074
Dh 263 Ile---SerProAlaValPheGluGlyLeuGlyGluMetSerValGluSerIleAenLeu 281
Qy 1075 ACATATACAAATGATTTTTCAGATGATGTTAAGTTCCATGCTTGGCGAATGTTTCT 1134
Dh 282 GlnIyehIstYrPhePheAenIleSerSerAenThrPheIstCySPheSerGlyLeuGln 301
Qy 1135 GCAATGCTCTGGCAGGTGATCTATAAATATCTAGAAGATGTTCTTAACATTTCC-- 1191
Dh 302 GluLeuAerLeuThrAlaThr-----HisLeuSerGluLeuProSerGlyLeuVal 318
Qy 1192 -----NAATGGCAATCCTTTATCATC 1212
Dh 319 GlyLeuSerThrLeuValLeuValLeuSerAlaAenLysPheGluAenLeu----- 336
Qy 1213 ATTAGATGTCAACTAGACAG-----TTTCAACTCTGATCTACACCTTCTTAAAAAGT 1265
Dh 337 -----CysGlnIleSerAlaSerAenPheProSerLeuThrHisLeuSerIleGlyGly 354
Qy 1266 TTGACTTTAAGTAAACAAGGCTATATCAATTTAAAAAAGTGGCCCTTCAAGTCTC 1335
Dh 355 AenThrLysArgLeuGluLeuGlyThrGlyCysLeuGluAen-----LeuGluAenLeu 372
Qy 1326 AGCATCTAGATCTTAGTAGAAGAAATCACTGAGCTTAAGTGAGCTGTCTTATTTGAT 1385
Dh 373 ArgGluLeuAerLeuSerHisAerAerPheIleGluThrSerAerCysAenLeuGlnLeu 392
Qy 1386 TTGGGAACAACAGCCTGAGACACTTAAAGCCTTCAATGAGTGCATATTAGT 1445
Dh 393 ArgAenLeuSerHisLeuGlnSerLeuAenLeuSerGlyArgGlnProLeuSerLeuLys 412
Qy 1446 GCCAAT--TTCATGGCTTAGAAGAGCTGACGACCTGGAATTTTTCAGACCTACTTT 1502
Dh 413 ThrGluAlaPheLysGlyCysProGlnLeuGluLeuAerLeuAla-PheThrArgLe 432
Qy 1503 AAAAAGGTCACAGAAATCTCAGCCTTCTTATCCTTGAAAAGTCACTTACCTTGACAT 1562
Dh 432 uLysValLysAerAlaGlnSerProPheGlnAenLeuHisLeuLeuLysValLeuAenLe 452
Qy 1563 CTCCTATACTAAACCAAAATTTGACTGATGATTTCTTGGCTTGAACGACCTGAA 1622
Dh 452 uSerHisSerLeuAerPheIleSerSerGlnLeuPheAerGlyLeuProAlaLeuGly 472
Qy 1623 CACATTAATAATGGCTGCAATTTCTTCAAGACAAACCTT-----TCAATGTCTT 1676
Dh 472 nHisLeuAenLeuGlnGlyAenHisPheProLysGlyAenIleGlnLysThrAenSerLe 492
Qy 1677 TGCAAAACAACAACCTTGACATCTCTGATCCTTCAATATTTGAATGGAACAAATTC 1736
Dh 492 uGlnThrLeuGlyArgLeuGluIleLeuValLeuSerPheCysAerLeuSerSerLeuAs 512
Qy 1737 TTGGGGGGTATTTGACACCTTCATAGACTCAATATTAATTAATGATCAACAATCT 1796
Dh 512 pGlnHisAlaPheThrSerLeuLysMetMetAenHisValAerLeuSerHisAerAlaArgLe 532
Qy 1797 ATTTGTTTTGAT-----TCAATCCATTTAATCAACGCTGATTTCTCAGACACTCT 1847
Dh 532 uThrSerSerSerIleGluAlaLeuSerHisLeuLysGlyIleTy-----Le 548
```

```
Qy 1848 TGATTCAGATTTCAATGCGATATAGACATCTAAAGAAATCTGCAACATTTTCCAAAGAG 1907
Dh 548 uAenLeuAlaSerAenHisIleSerIleIleLeuProSerLeuAerProIleLeuSerGly 568
Qy 1908 TCATGCTTCTTCAATCTTATCTTAACAATTCCTGTGCTGTATATATGAAATCAGAAAT 1967
Dh 568 nGlnArgThrIleAenLeuArgLysnProLeuAerCysThrCysSerAenIleTyRph 588
Qy 1968 CTCGCACTGGGTCAAGAACAGACATCTTGGTGAATGTTGAACAAATGACATGTGC 2027
Dh 588 eLeuGluTrpTyLysGlyLysAenMetGlnLysLeuGluAerThrGluAerThrLeuCysGly 608
Qy 2028 AACACCTGTAGATGAAT-----ACCTCCTTATGTTGATTTTAATTAATTC 2075
Dh 608 uAenProProLeuLeuArgGlyValArgLeuSerAerAerValThrLeuSerCysSerMetAl 628
Qy 2076 TACCTGTATATATGACAAACAATCATCACTGTGTGACGTGTCAGTGTGATTTGCTATC 2135
Dh 628 aAlaValGlyIlePhePheLeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePh 648
Qy 2136 CACTGTAGCATTTCTGATATACCACTTCATTTTTCACCTG 2175
Dh 648 eAlaValLysTyRphLeuAerGlyTrpLysTyRglnHisIle 661

RESULT 9
US-10-037-417-107
Sequence 107, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Rameesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: PatluraJan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Verne, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malysankar, Uriel M
APPLICANT: Kothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eisen, Andrew J
TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305,060
```



```

PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 107
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus
US-10-037-417-107

Alignment Scores:
Pred. No.: 2,23e-47      Length: 661
Score: 567.50           Matches: 181
Percent Similarity: 45.99%      Conservative: 129
Best Local Similarity: 26.85%    Mismatches: 314
Query Match: 10.96%             Indels: 51
DB:                               Gaps: 16

US-09-396-985b-46 (1-2951) x US-10-037-417-107 (1-661)

QY 241 ATCATGCACTGTTCTTC--TCCTGC--CTGACACGAGAGCTTGATCCCTGCATA 294
D 10 LeuValAlaLeuPheLeuAlaSerCysArgAlaThrThrSerSerAspGlnLysCysIle 29
QY 295 GAGTAGTCTCTATATTATCTACCAATGCATGCATGACGAAAGCTCAGCAAGTCCCTGAT 354
D 30 GlnLysGlnValAlaLysThrThrAsnGlnLysGlnLysGlnLysGlnLysGlnLys 49
QY 355 GACATCTCTCTTCAACCAAGACATAGATCTGAGCTTCAACCCCTTGAAGATCTTAAA 414
D 50 ThrLeuProAsnSerThrGlnCysLeuGlnPheSerPheAsnValLeuProThrIleGln 69
QY 415 AGCTATAGCTTCTCCAAATTTTTCAGAACTTCAGTGGCTGATTTATCCAGGTGAAATT 474
D 70 AsnThrThrPheSerArgLeuIleAsnLeuThrPheLeuAspLeuThrArgGlnIle 89
QY 475 GAAACAATTGAAGCAAGGATGGCATGGCTTACACCACTCTCAAACTTGATCTGACA 534
D 90 TyrTrpIleHisGlnAspThrPheGlnSerGlnHisArgLeuAspThrLeuValLeuThr 109
QY 535 GGAACCCCTATCCAGATTTTCCCAAGAAATTTCTGAGCTTCAACAAGTTTGAACAT 594
D 110 AlaAsnProLeuIlePheMetAlaGlnThrAlaLeuSerGlnProLysAlaLeuLysHis 129
QY 595 CTGGTGGCTGTGAGACAAATTTGGCTCTCTAGAAAGCTTCCCTATTTGACAGCTTATA 654
D 130 LeuPhePheIleGlnThrGlyIleSerSerIleAspPheIleProLeuHisAsnGlnLys 149
QY 655 ACCTTAAGAACTCAATGTGGCTCACAATTTTATCACTTCTTAAAGTTACCTGCATAT 714
D 150 ThrLeuIleSerLeuIleGlnLysSerAsnHisIleSerSerIleLysLeuProLysGln 169
QY 715 TTTTCCATCTGACGAACCTAGTACATGATGATCTTTCTTATCTATCTTAAACATAT 774
D 170 PheProThr---GlnLysLeuLysValLeuAspPheGlnAsnAsnAlaIleHisTyrLeu 188
QY 775 ACTGTCAACGACTTACAGTTTCTACGTGAATTCACAGTCAATCTCTTTAGACATG 834
D 189 SerLysGlnAspMetSerSerLeuGlnGln-----AlaThrAsnLeuSerLeuAsnLeu 206
QY 835 TCTTTGAACCAATGATGATCTTCAAGACCAAGCCCTTCAAGGAATTAAGCTTCATGAA 894
D 207 AsnIleLysAsnAspIleAlaGlnLysGlnProGlnAlaPheAspSerAlaValPheGlnSer 226
QY 895 CTGACTCTAAGAGGATATTTTATAGCTCAAAATATATGAAGAACTTGCTTCAAAACCTG 954
D 227 Leu-----AsnPheGlnGlyThrGlnAsnLeuValIlePheLysGlnLeu 242
QY 955 GCTGGTTTACACGTTCATCGGTGATCTTGGAGAAATTTAAAGATGAAGAAATCTGAA 1014

```

```

D 243 LysAsnSerThrIleGlnSerLeuTrpLeuGlyThrPheGlnLysAspAspGlnAsp 262
QY 1015 ATTTTGAACCCCTATCAATGAGAGCACTATGCAATGCAATGATGATGAGTTA 1074
D 263 Ile---SerProAlaValPheGlnGlyLeuGlnCysGlnLysSerValGlnSerIleAsnLeu 281
QY 1075 ACATATACAAATGATTTTTCAGATGATGATTTTAACTTCACTTGGCGCAATGTTTCT 1134
D 282 GlnLysHisTyrPhePheAsnIleSerSerAsnThrPheHisCysPheSerGlnLeuGln 301
QY 1135 GCAATGTCTCTGCGAGGTGATCTATATAATCTAGACAGATGCTCTTAAACATTC-- 1191
D 302 GlnLeuAspLeuThrAlaThr-----HisLeuSerGlnLeuProSerGlnLeuVal 318
QY 1192 -----AAATGGCAATCCCTATCAATC 1212
D 319 GlnLeuSerThrLeuLysLysLeuValLeuSerAlaAsnLysPheGlnAsnLeu----- 336
QY 1213 ATTAGATGTCAACTAAGCAG-----TTTCAACTCTGGATCTACCCCTTCTTAAAAGT 1265
D 337 -----CysGlnIleSerAlaSerAsnPheProSerLeuThrHisLeuSerIleLysGln 354
QY 1266 TTGACTTTAATCTATGAACAAAGGCTTATGATTTTAAAAAAGTGGCCCTACCAAGTCTC 1325
D 355 AsnThrLysArgLeuGlnLeuGlyThrGlnCysLeuGlnAsn-----LeuGlnAsnLeu 372
QY 1326 AGCTATGATCTTGTATGAATAATGCATGAGCTTATGCTGGCTGCTTCTTATTCGAT 1385
D 373 ArgGlnLeuAspLeuSerHisAspAspIleGlnThrSerAspCysCysAsnLeuGlnLeu 392
QY 1386 TTGGAAACAAACAGCCCTGAGACACTTACAGCTTCAAGCTTCAAGTGGCATATTAAGT 1445
D 393 ArgAsnLeuSerHisLeuGlnSerLeuAsnLeuSerGlyThrAsnGlnProLeuSerLeuLys 412
QY 1446 GCCAAT--TTCAATGGCTTAAAGAGCTGCAGACCTGATATTTTACAGACTCTACTT 1502
D 413 ThrGlnAlaPheLysGlnCysProGlnLeuGlnLeuLeuAspLeuAla--PheThrArgLe 432
QY 1503 AAAAAGGATCACAGAAATCTCAGGCTTATCCCTTGAAGAAAGTACTTATCTTGACAT 1562
D 432 CysValLysAspAlaGlnSerProPheGlnAsnLeuHisLeuLeuLysValLeuAsnLe 452
QY 1563 CTTTATATCAACCAACCAAAATTTGATCTGATGATTTCTTGGATCTTCAAGCACTTCAA 1622
D 452 userHisSerLeuLeuAspIleSerSerGlnGlnLeuPheAspGlyLeuProAlaLeuGln 472
QY 1623 CACATTAATAAATGGCTGGCAATTTCTTCAAGAACACACCTT-----TCAATGTCTT 1676
D 472 nHisLeuAsnLeuGlnGlnLysAsnHisPheProLysGlnAlaIleLysThrAsnSerLe 492
QY 1677 TGCAAACACAAACCTGACATTCCTGATCCTTCTTAATGTCAATTTGGAACAAATATC 1736
D 492 uGlnThrLeuGlnArgLeuGlnIleLeuValLeuSerPheCysAspLeuSerSerIleAs 512
QY 1737 TTGGGGGGTATTTGACACCTCCATAGACTTCAATATTAATTAATGATGCACAAATCT 1796
D 512 pGlnHisAlaPheThrSerLeuLysMetMetAsnHisValAspLeuSerHisAsnArgLe 532
QY 1797 ATGTGTTTGGAT-----TCATCCATTTAATCAACAGCTGATTTCCCTCAGCACTCT 1847
D 532 uThrSerSerSerIleGlnAlaLeuSerHisLeuLysGlnIleLys-----Le 548
QY 1848 TGATTCAGTTCATATTCGATAGACATCTAAGAAATCTGCAACATTTTCCAAAGAG 1907
D 548 uAsnLeuAlaSerAsnHisIleSerIleIleLeuProSerLeuAspProIleLeuSerGln 568
QY 1908 TCTAGCCTTCTTAATCTTAACTTCAATCTTGGCTGTGATGATGATGACAGAAAT 1967
D 568 nGlnArgThrIleAsnLeuArgGlnAsnProLeuAspCysThrCysSerAsnIleTyrPhe 588
QY 1968 CTGCAAGTGGGTCAAGAAACAGAGAGATTTTGTGGAATGTTGAACAAATGACATGTGC 2027
D 588 eleuGlnTrpTyrLysGlnAsnMetGlnLysLeuGlnAspThrGlnAspThrLeuCysGln 608

```

```

Qy 2028 AACACCTGTAGATGAAT-----ACCTCTTACTGTGATTTTAAATATTC 2075
Db 608 uasnpProleuLeuarglyValArgLeuSerAspValThrLeuSerCysSerMetAl 628
Qy 2076 TACCTGTTATATGACAAAGACATCATAGTGTCTAGTGTGATGATTTGATGATC 2135
Db 628 aalavalGlyIlePhePheLeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePh 648
Qy 2136 CACTGTAGACATTTCTGATATACCACTTCTATTTTACCTG 2175
Db 648 eaIaValIeYrPheLeuArgTrpIyTrpGlnHisIle 661

RESULT 10
US-09-954-987B-192
; Sequence 192, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; APPLICANT: Hermann Wagner
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; FILE REFERENCE: C1041/7016 (AMS)
; CURRENT APPLICATION NUMBER: US/09/954,987B
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233,035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263,657
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/291,726
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300,210
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 192
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-954-987B-192

Alignment Scores:
Pred. No.: 1,99e-46 Length: 1032
Score: 559.00 Matches: 253
Percent Similarity: 38.61% Conservative: 157
Best Local Similarity: 23.82% Mismatches: 353
Query Match: 10.80% Indels: 300
DB: 10 Gaps: 42

US-09-396-985B-46 (1-2951) x US-09-954-987B-192 (1-1032)
Qy 211 ATGCGCTGCC-----TGGCTCTGCGCTAGACCTGTGATCATG-----GCA 249
Db 4 MetProGlnSerTrpIleLeuThrCysPheCysLeuLeuSerSergIyThrSerAla 23
Qy 250 CTGTTCTTCTCTGCTGACACACGAAAGCTTGAATCCCTGCATAGAGTGCTTCAT 309
Db 24 IlePheHisIyValaAsenIySerArgSerIyTr--ProCysAspGluIleArgHisAsn 42
Qy 310 -----ATTACCTTACCATGATGATGATGACAAAGCTCAGCAAGTCCGATGACATTCT 363
Db 43 SerLeuValIleAlaGluCysAsnHisArgGlnLeuHisIleGluValProGlnThrIleGly 62
Qy 364 TCTTCAACCAAGACATGATCTGAGCTTCAACCCCTTGAGAGATCTTAAAAAGCTATAGC 423
Db 63 LysTrpValThrAsnIleAspLeuSerAspAsnAlaIleThrHisIleThrIleGluSer 82
Qy 424 TTCTCCAAATTTTTCAGAACTTCAGTGGCTGATTTATCCAGGTGTGAATTGAA----- 477
Db 83 PheGlnIySLeuGlnAsnLeuThrIySileAspLeuAsnHisAsnAlaIyGlnGlnHis 102
Qy 478 -----ACATTTGAAGCAAGGATGGCATGGCTTACACAC 513

```

```

Db 103 ProAsnGluAsnIyAsnGlyMetAsnIleThrGlnGlyAlaLeuLeuSerLeuArgAsn 122
Qy 514 CTCTCAACTGTACTAGACAGAAACCTATCCAGAGTTTTC-----CCAGGA 564
Db 123 LeuThrValLeuLeuLeuGlnIyAspAsnGlnLeuIyThrIleProAlaGlyLeuProGln 142
Qy 565 AGTTTCTGAGATACAAAGTTTAGCAATCTGCTGCTGTGGAGCAAAA----- 615
Db 143 SerLeuSgIuLeuSerLeuIleGlnAsnAsnIlePheGlnValThrIyAsnAsnThr 162
Qy 616 -----TGGCCTCTCTAGAAACCTTCCCTATTTGA----- 645
Db 163 PheGlyLeuArgAsnLeuGluArgLeuIyLeuGlyTrpAsnCySerIyPheIySAsn 182
Qy 646 -----CAGCTTATACCTTAAAGAACTTCAT 672
Db 183 GlnThrPheIyValGlnAspGlyAlaPheIyAsnLeuIleHisIleuIyValLeuSer 202
Qy 673 GNGGCTCACAAT-----TTTATACATTCCTGTAGCTTACCTGCA----- 711
Db 203 LeuSerPheAsnAsnLeuPheIyTrpValProProIyLeuProSerSerLeuArgIySLeu 222
Qy 711 ----- 711
Db 223 PheLeuSerAsnAlaIySileMetAsnIleThrGlnGluAspPheIySgIyLeuGluAsn 242
Qy 711 ----- 711
Db 243 LeuThrLeuLeuAspLeuSerGlyAsnCySProArgCySerIyAsnAlaProPheProCys 262
Qy 711 ----- 711
Db 263 ThrProCysIySgIuAsnSerSerIleHisIleHisProLeuAlaPheGlnSerLeuThr 282
Qy 712 -----TATTT 717
Db 283 GlnLeuLeuIyTrIeAsnLeuSerSerThrSerLeuArgThrIleProSerThrTrpPhe 302
Qy 718 TCCAACTGACGACCTAGTATGATGATCTTTCTTATACAT--ATTCAACATATT 774
Db 303 GluAsnLeuSerAsnLeuIySgIuLeuHisIleGlnIyPheAsnIyTrIeValGlnGluIle 322
Qy 775 ACTGTACAGACTTACAGTTCTTACGGAAGAAATCCAAAGTCAATGCTCTTACAGATG 834
Db 323 AlaSergIy-----AlaPheLeuThrIySLeuProSerLeuGlnIle--LeuAspLeu 339
Qy 835 TCTTTGAACCAATGATGATTCATTTCAAGACCAAGCCTTTCAAGGAAATTAGCTCAGTAA 894
Db 340 SerPheAsn-----PheGlnIyTrIySgIuIyTrIeGlnIlePheIleAsnIle----- 354
Qy 895 CTGACTTAAGAGTAAATTTTATAGCTCAAAATATATGAAGAACTTCCCTTCAAAACCTG 954
Db 355 -----SerSerAsnPheSerIyS-----LeuAspSerLeu 364
Qy 955 GCTGTTTACAGCCATGCGTGTGATCTTGAGAAATTTAAGATGAAGAAAGAAATCTGAA 1014
Db 365 LysIyLeuAsnHisLeuArgGlyTrpValPheArgGluLeuIySAsnIySAsn----- 381
Qy 1015 ATTTTTACCCCTCTATCATGAGAAAGCATATGATGTGACCATGTGATGAGTTACAGTTA 1074
Db 382 ---PheGlnHis-----LeuGlnSerLeuProAsnLeuAlaThrIleAsnLeuGlyIle 398
Qy 1075 ACATATACAAATGATTTTTCAGATGATATTGTTAAGTTCATGCTTGGCAATGTTTCT 1134
Db 399 AsnPheIleGluIySile-----AspPheIyAlaPheGlnAsnPheSerIySLeuAsp 416
Qy 1135 GCATGCTCTGCGAGGTGATATCTATAAATATCTGAAGATGTCTTAACATTTTGAA 1194
Db 417 ValIleIyTrIeSerGlyAsnArgIleAlaSerValLeuAspGlyThrAspIyTrSerSer 436
Qy 1195 TGGCAATCTT-----ATC 1208

```

Db 437 TTPARGENARGLEUArglyProLeuSerThrAspAspArgLupheAspProHleVal 456
 QY 1209 AATGATAGATGACCTAAGACAGTTT-----CCAACT 1241
 Db 457 AsnGheTyrHisSerThrLysProLeuLleLysProGlnCysThrAlaTyrGlyLysAla 476
 QY 1242 CTGGATCTACCCCTT----- 1256
 Db 477 LeuSerLeuSerLeuAsnAsnLlePheLleLleGlyLysSerGlnPheGlnGlyPheGln 496
 QY 1257 ---CTTAAAGTTTGACTTTTACTATGACAAAGGGCTTACGTTTAAAAAGTG-- 1310
 Db 497 AspLleAlaCysLeuAsnLeuSerPheAsnLleAsnThrGlnValPheAsnGlyThrGlu 516
 QY 1311 -----GCCCTACCAAGCTCAGCTATAGATCTTGTAGTAAGTACCTGAGCTTTAGT 1364
 Db 517 PheSerSerMetProHleLleLysTyrLeuSerLeuThrAsnAsnArgLeuAspPheAsp 536
 QY 1365 GGTCGCTGTTCTTATCTGATTTGGGAAACAAAGCTGAGACACTTACCTGAGCTTC 1424
 Db 537 AspAsnAsnAlaPheSerAspLeu-----HisAspLeuGlnValLeuAspLeuSerHis 554
 QY 1425 AATGTCGCATCATTAATGAGTCCAAAT-----TTGATGGCTTA 1463
 Db 555 AsnAlaHisTyrPheSerLleAlaGlyValThrHisArgLeuGlyPheLleGlnAsnLeu 574
 QY 1464 GAAGAGCTGACGACCTGGATTTTTCAGACCTCACTTAAAAAGGTCACAGAA----- 1518
 Db 575 IleAsnLeuArgValLeuAsnLeuSer-HisAsnGlyLleTyrThrLeuThrGlnGluSe 594
 QY 1518 ----- 1518
 Db 594 RGLLeuLysSerLleSerLeuLysGlnLeuValPheSerGlyAsnArgLeuAspHisLe 614
 QY 1519 -----TTCTACGCTTCTTATCCCTGAAAGCTACTTTA 1553
 Db 614 UTTPAsnAlaAsnAspGlyLysTyrTrpSerLlePheLysSerLeuGlnAsnLleLeu 634
 QY 1554 CTTGATGATCTCTTATCTACTAACAACAAATGACTTGAGTGTATTTCTTGCTTG-- 1611
 Db 634 GLeuAspLeuSerTyrAsnAsnLeuGlnGlnLleProAsnGlyAlaPheLeuAsnLeuPr 654
 QY 1612 -ACCAAGCTCAACACTTAAATAATGCTGCAATCT-----TTCAAGACACACACCT 1664
 Db 654 ogInSerLeuGlnGlnLeuLleSerGlyAsnLysLeuArgPheAsnThrPheLle 674
 QY 1665 TTCAAATGCTTTGCAAAACACAAACCTTGACATTCCTGATCCTTAAATGCTCAAT 1724
 Db 674 ULeuGlnTyrPhe-----ProHleLeuHleLeuSerLeuSerArgAsnGlnLe 691
 QY 1725 GGAACAAATATCTGGGGGGATTTTGACACCCCTCATAGACTTCAATTTAATATAGAG 1784
 Db 691 UTYrPheLeuProAsnCysLeuSerLysPheAlaHisSerLeuGlnThrLeuLeuSe 711
 QY 1785 TCACAAACATCTATTTTGTGATTCATCCATTAATGACAGCTGATTCCTCAGACAC 1844
 Db 711 rHisAsnHisPheSerHisLeuProSerGlyPheLeuSerGlnAlaArgAsnLeuValHis 731
 QY 1845 TCTTGATGACGTTTCAATGCGATAGAG--ACATCTAAAGAAATAGTCAACATTTTCC 1901
 Db 731 sleuAspLeuSerPheAsnThrLleLysMetLleAsnLysSerLeuGlnThrLysMe 751
 QY 1902 AAGG--AGCTTACCTTTTCAATCTTACTAACAATCTGTTGCTGTATATGTGACA 1958
 Db 751 tLysThrAsnLeuSerLleLeuGlnLeuHleGlyAsnTyrPheAspCysThrCysAspI 771
 QY 1959 TCAGAAATTCCTGAGGAGGTCAGAAAGAAAGACAGATTC-----TTGGTGA 2006
 Db 771 eSerAspPheArgSerTyrLeuAspGlnAsnLeuAsnLleThrLleProLysLeuValHis 791
 QY 2007 TGTGGAACAATGACATGTGCAACACCTGTAGAGTAATACCTCTTAGTGTGATTT 2066
 Db 791 nVal-----llecysSerAsnProGlyAspGlnLysSerLysSerLleMetSerLe 808

QY 2067 TAATAATTCTACCTGATATATGTAACAAGACATGATGATGTCAGTGCAGGTGAT 2126
 Db 808 uAspLeuThrThrCysValSerPheThrThrAlaAlaValLeuPheLeuThrPheLe 828
 QY 2127 TGTGTATCCACTGTA-----GCATTTCTGATATACAC----- 2160
 Db 828 UThrThrSerMetValMetLeuAlaLeuValHisHleLeuPheTyrThrAspValTr 848
 QY 2161 -TTCTATTTTCACTG-----ATACTATTTGCTGCTGTAAAAAGTACAGCAGAGA 2213
 Db 848 PheLleTyrHisMetCysSerAlaLysLeuLysGlyTyrArgThrSerSerThrSerG 868
 QY 2214 AACGATCTATGATCATCTTATGATCTCTGAGTCCAGAAAT-----GAGGCTGGCT 2264
 Db 868 nThrPheTyrAspAlaTyrLleSerTyrAspThrLysAspAlaSerValThrAspTrpVa 888
 QY 2265 GAGAAATGAGCTGTGTAAGAATTTAGAAAGAGAGTCCCGC--TTTCACTGTGCT 2321
 Db 888 lIleAsnGlnLeuArgTyrHisLeuGlnGlnSerGlnAspLysSerValLeuLeuCysLe 908
 QY 2322 TCACTACAGACGTTTATTTCTGCTGTAGCCATTGCTGCCAATCATCCAGAAAGCTT 2381
 Db 908 UGlnGlnArgAspTrpAspProGlyLeuProLleIleAspAsnLeuMetGln--SerI 927
 QY 2382 CCAGAAAGCCGGAAGCTTATTTGTGAGTGTCTAGACACTTTATTCAGAGCCGTTGGTG 2441
 Db 927 eAsnGlnSerLysLysThrLlePheValLeuThrLysLysTyr----- 941
 QY 2442 TATCTTGAATATGAGATTCCTCAACATGACAGTTCCTGAGC----- 2484
 Db 942 -----AlaLysSerTrpAsnPheLysThrAlaPheTyrLeuAlaLe 955
 QY 2485 -----ACCGCTCTGCATCATCTTCAATGCTCTTGAAGAGTTGA 2525
 Db 955 UGlnArgLeuMetAspGlnAsnMetAspValLleLlePheLleLeuLeuGlnProValLe 975
 QY 2526 GAAGTCCCTGCTGACGAGCAGGAGGAAATTGTATCGCTTCTTACGAAACACTTACCT 2585
 Db 975 UGln-----TyrSerGlnTyrLeuArgLeuArgLysLysSerSerLleLe 993
 QY 2586 GGAATGGAGACAAATCTCTGGGAGGACATCTTGTGAGAGACTTAAAAATGCGCT 2645
 Db 993 UGlnTrpProAsnAsnProLysAlaGlnAsnLeuPheTrpGlnSerLeuLysAsnValVa 1013
 QY 2646 ATTG 2649 :|||
 Db 1013 lLeu 1014

RESULT 11
 US-10-272-502A-31
 ; Sequence 31, Application US/10272502A
 ; Publication No. US20030139364A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Krieg, Arthur M.
 ; APPLICANT: Schetter, Christian
 ; APPLICANT: Bratzler, Robert L.
 ; APPLICANT: Volmer, Jorg
 ; APPLICANT: Bauer, Stefan
 ; APPLICANT: Jurk, Marion
 ; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
 ; FILE REFERENCE: C01039.70065.US
 ; CURRENT APPLICATION NUMBER: US/10/272.502A
 ; PRIOR APPLICATION NUMBER: 2002-10-15
 ; PRIOR FILING DATE: 2001-10-12
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 31
 ; LENGTH: 1032
 ; TYPE: PR
 ; ORGANISM: Mus musculus

us-10-272-502a-31

Alignment Scores:

Pred. No.:	1,996-46	Length:	1032
Score:	559.00	Matches:	253
Percent Similarity:	38.61%	Conservative:	157
Best Local Similarity:	23.82%	Mismatches:	353
Query Match:	10.80%	Indels:	300
DB:	14	Gaps:	42

US-09-396-985b-46 (1-2951) x US-10-272-502a-31 (1-1032)

```
QY 211 ATGCTCC-----TGCTCTGCTAGACCTGATCATG-----GCA 249
  |||||
Db 4 MetProGlnSerTrpIleuThrCysPheCysLeuSerSerGlyThrSerAla 23
QY 250 CTGTTCTTCTCTGCTGACACCAAGAACTTGAATCCCTGCATAGAGTAATTCAT 309
  |||||
Db 24 IlePheHisValAsnIleArgSerGlyr---ProCysAspGluIleArgHisAsn 42
QY 310 -----ATTACCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 363
  |||||
Db 43 SerLeuValIleAlaGluCysAsnHisArgGlnLeuHisGluValProGlnThrIleGly 62
QY 364 TCTTCAACCAAGACATGATCTGAGCTTCAACCCCTTGAAGATTTAAAGCTATAGC 423
  |||||
Db 63 LysIleValThrAsnIleAspLeuSerAspAsnAlaIleThrHisIleThrIleGluSer 82
QY 424 TTTCTCAATTTTCAAGACTTCAAGTGGCTGATTTATTCAGGTGGAATTGAA----- 477
  |||||
Db 83 PheGlnIleAspLeuGlnAsnLeuThrIleValIleAspLeuHisHisAlaValGlnGlnHis 102
QY 478 -----ACAATTGACCAAGCATGATGATGATGATGATGATGATGATGATGATGAT 513
  |||||
Db 103 ProAsnGlnAsnIleValAsnGlyMetAsnIleThrGlnGluAlaLeuSerIleAspGln 122
QY 514 CTCTCAACTTGTATGATGACAGAAACCTTATCCAGATTTTCC-----CCAGA 564
  |||||
Db 123 LeuThrValIleLeuLeuGlnAspAsnGlnLeuThrIleProAlaGlyLeuProGlu 142
QY 565 AGTTTCTCTGACCTAACAAGTTTACACATCTGCTGCTGACAGACAAA----- 615
  |||||
Db 143 SerLeuIleGlnLeuSerIleGlnAsnAsnIlePheGlnValThrIleAsnAsnThr 162
QY 616 -----TTGGCTCTCTAGAAAGCTCCCTATTTGA----- 645
  |||||
Db 163 PheGlyLeuAspLeuGlnIleGluArgLeuThrIleGlnIleProAsnCysIlePheIleCysAsn 182
QY 646 -----CAGCTTATACCTTAAAGAACTCAAT 672
  |||||
Db 183 GlnThrPheIleValGluAspGlyAlaIlePheIleValAsnLeuIleHisIleLeuValLeuSer 202
QY 673 GTGGCTCACAAAT-----TTTATACATTTCTGTAAAGTTTAACTTGA----- 711
  |||||
Db 203 LeuSerPheAsnAsnLeuPheThrValProProIleuLeuProSerSerLeuArgIleLeu 222
QY 711 ----- 711
  |||||
Db 223 PheLeuSerAsnAlaIleValIleMetAsnIleThrGlnIleAspPheIleValGluLeuAsn 242
QY 711 ----- 711
  |||||
Db 243 LeuThrIleuLeuAspLeuSerGlyAsnCysProArgCysIleAsnAlaProPheProCys 262
QY 711 ----- 711
  |||||
Db 263 ThrProCysIleGluAsnSerIleHisIleHisProLeuAlaPheGlnSerLeuThr 282
QY 712 -----TATTTT 717
  |||||
Db 283 GlnLeuLeuIleThrLeuAsnLeuSerSerThrSerLeuArgThrIleProSerThrThrPhe 302
QY 718 TCCAACTGACGAACCTAGTACATGTGATCTTTCTTAACTAT---ATTCAAACTATT 774
```

```
Db 303 GluAsnLeuSerAsnLeuIleValGlnLeuHisIleLeuGlnIlePheAsnIleThrValGlnGluIle 322
  |||||
QY 775 ACTGTACAACACTTACAGTTTTCACGGAATAATCCAAAGTCAATGCTCTGTTAGACATG 834
  |||||
Db 323 AlaSerGly-----AlaPheIleThrIleLeuLeuProSerLeuIle---LeuAspLeu 339
QY 835 TCTTGAACCCCAATGATGATCTTCAAGAACCAAGCTTTCAGGGAATTAAGTCCATGAA 894
  |||||
Db 340 SerPheAsn-----PheGlnIleThrIleGluIleThrIleGlnIleHisIle----- 354
QY 895 CTGACTCTAAGAGTAATTTAATAGCTCAATATATATGAATAAGAACTTCCAAACCTG 954
  |||||
Db 355 -----SerSerAsnPheSerIleS---LeuArgSerLeu 364
QY 955 GCTGGTTTACACGTCATCGCTGATGCTTTCGAGAAATTTAAGATGAAGAAATTCGAA 1014
  |||||
Db 365 LysIleValLeuHisIleValArgGlyIleValPheArgIleuLeuIleValHis----- 381
QY 1015 ATTTTGAACCCCTATCATGAGAAAGCATGTGATGTGACCATGATGATGATGATGATGAT 1074
  |||||
Db 382 ---PheGlnHis-----LeuGlnSerLeuProAsnLeuAlaThrIleAsnLeuGlyIle 398
QY 1075 ACATATACAAATGATTTTCAATGATATGTTAAGTTCCATTTGCGGAAATGTTTCT 1134
  |||||
Db 399 AsnPheIleGluIleSile-----AspPheIleValAlaPheGlnAsnPheSerIleValAsp 416
QY 1135 GCATGCTCTGCGACAGGTGTATGATTAATATCTAAGAAAGATGTCTTAACATTTGAAA 1194
  |||||
Db 417 ValIleIleThrLeuSerGlyAsnArgIleAlaSerValLeuAspGlyThrAspIleYrSerSer 436
QY 1195 TGGCAATCCTT-----ATC 1208
  |||||
Db 437 TrpArgAsnArgLeuArgIleProLeuSerThrAspAspAspGluPheAspProHisVal 456
QY 1209 AATCATTAAGATGTCACACTTAAACAGTTT-----CCAAC 1241
  |||||
Db 457 AsnPheThrHisSerThrIleYsProLeuIleIleProGlnCysThrAlaIleIleValAla 476
QY 1242 CTGATCTACCTTT----- 1256
  |||||
Db 477 LeuAspLeuSerLeuAsnAsnIlePheIleIleGlyIleSerGlnPheGlnIle 496
QY 1257 ---CTTAAAGTTTGAATTAACATGACAAAGGCTTATCAATTTTAAAGATG--- 1310
  |||||
Db 497 AspIleAlaCysLeuAsnLeuSerPheAsnAlaAsnThrGlnValPheAsnGlyThrGlu 516
QY 1311 -----GCCCTACCAAGCTCAGCTATCTAGATCTTATGTAAGAAATGCACTGACCTTACT 1364
  |||||
Db 517 PheSerSerMetProHisIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 536
QY 1365 GGTGGCTGTTCTTATTTGATTTTGGGAACAAACAGCTGAGACCTTAAAGCTTACGCTTC 1424
  |||||
Db 537 AspAsnAsnAlaPheSerIlePhe---HisAspLeuGlnValLeuAspLeuSerHis 554
QY 1425 AATGTGCACTCATTAAGTGCCAAT-----TTCATGAGCTCTA 1463
  |||||
Db 555 AsnAlaHisIleThrPheSerIleAlaGlyValThrHisArgLeuGluPheIleGlnAsnLeu 574
QY 1464 GAAGAGCTGACAGCACTGATTTTTCAGCACTTATTAAGAAAGGTCACAGAA----- 1518
  |||||
Db 575 IleAsnLeuArgValLeuAsnLeuSer-HisAsnGlyIleThrThrIleThrGlnGluIle 594
QY 1518 ----- 1518
  |||||
Db 594 GluLeuLeuSerIleSerLeuIleValPheSerGlyAsnArgLeuAspHisIle 614
QY 1519 -----TTTCAGCGCTTATATCCCTTGAAGAAAGCTATTTA 1553
  |||||
Db 614 uTPAsnAlaAsnAspGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 634
QY 1554 CTTGACATCTTATTAACACCAAAATGCACTTGAATGATATTTCTTGAGCTTG-- 1611
  |||||
```

```

Db      634 glenAspLeuSerTyrAsnIleuGlnIleProAsnGlyAlaPheLeuAsnLeuPr 654
Qy      1612 -ACGAGCTCAACAATTAAATGGCTGGCAATCTCT-----TTCAAGACACACCCCT 1664
Db      654 ogLSerLeuIleuGlnLeuLeuIleSerGlyAsnLeuArgPheLeuAsnThrPhe 674
Qy      1665 TTCAATATGCTCTTGCACACACACACACACCTTGCATCTCTTGCATTAATGTCAT 1724
Db      674 uLeuGlnTyrPhe-----ProHISLeuHISLeuLeuAsnLeuSerArgAsnGlyLe 691
Qy      1725 GGAACAATATCTTGGGGGGATTTGACACCCCTCCATAGACTTCATATTATTAATGAG 1784
Db      691 uTyPheLeuProAsnGlySerLeuSerTyrPheAlaHISerLeuGlnThrLeuLeuSe 711
Qy      1785 TCACACAACTATATGTTTGGATTCATCCCATTAATACACAGCTGATTCCTCCACAGAC 1844
Db      711 rHISAsnHISerSerHISerLeuProSerGlyPheLeuSerIleuAlaArgAsnLeuAla 731
Qy      1845 TCTTGAATGACATTTCAATCCGATAGAG--ACATCTAAGAAATACTGACAAATTTTCC 1901
Db      731 sLeuAspLeuSerPheAsnThrIleuGlyMetIleAsnLeuSerLeuGlnThrIleGly 751
Qy      1902 AAAG--AGTCTACCTCTTCAATCTTCAATCTTCAATCTTCTGCTGTATATGTAACA 1958
Db      751 tTySerHISAsnLeuSerIleuGlnLeuHISGlyAsnTyrPheAspCysThrCysAspI 771
Qy      1959 TCAGAAATTCCTGACAGGCTGCACAGAACACAGACAGCTC-----TTGGTCA 2006
Db      771 eSerAspPheArgSerTyrPheAspArgLeuAsnLeuAsnIleThrIleProGlyLeuAla 791
Qy      2007 TGTTCACAAATGACATGTCACACACCTGTAGACATGATGATCTCTTGAATGTTGATTT 2066
Db      791 nVal-----IleCysSerAsnProGlyAspGlnLeuSerLeuMetSerLe 808
Qy      2067 TAATTAATTCACCTGTTATATGTAACAGACATCATCTGTGACAGTGTGACGTGAT 2126
Db      808 uAspLeuThrThrCysValSerAspThrThrAlaValLeuPheLeuThrPheLe 828
Qy      2127 TGTGTATCCACGTGA-----GCATTTCTGATATACAC----- 2160
Db      828 uThrThrSerMetValMetLeuAlaValLeuAlaHISerLeuPheTyrThrAspValTr 848
Qy      2161 -TTCTATTTTCACTG-----ATACTTATGCTGCTGCTGTAATAAATGACACAGAGAGA 2213
Db      848 pPheIleTyrHISerMetCysSerAlaIleLeuLeuGlyTyrArgThrSerSerThr 868
Qy      2214 AAGCATCTATGATCATTTGATCTACTCTGATCAGAAAT-----GAGACGTGGGT 2264
Db      868 nThrPheTyrAspAlaTyrIleSerTyrAspThrTyrAspAlaSerValThrAspTrp 888
Qy      2265 GAGAAATGAGCTGTAAGAATTTTGAAGAAGAGAGTCCCGC-----TTTCACTCTGCT 2321
Db      888 ILeAsnGlnLeuArgTyrHISerLeuGlnLeuSerGlnAspTyrSerValLeuLeuCys 908
Qy      2322 TCATACAGAGACATTTATCTGCTGTAGACCTGACACATCATCCAGAGAGGCTT 2381
Db      908 uGlnGlnArgAspTrpAspProGlyLeuProIleIleAspAsnLeuMetGln---Ser 927
Qy      2382 CCACAGAGCCGAGAGGTTATGTTGATGCTGTAGACATCTTATTCAGAGCCGTGGTG 2441
Db      927 eAsnGlnSerTyrSerThrIlePheValLeuThrIleTyrSer----- 941
Qy      2442 TATCTTGAATATAGATTCCTCAACATGTCAGCTTTCTGAGC----- 2484
Db      942 -----AlaTyrSerTyrPAsnPheTyrThrAlaPheTyrLeuAlaLe 955
Qy      2485 -----AGCCGCTCTGACATCATCTTCAATCTCTGAGAGGTTGA 2525
Db      955 uGlnArgLeuMetAspGlnAsnMetAspValIleIlePheIleLeuLeuGlnProVal 975
Qy      2526 GAATCCCTCTGCTGAGCAGCAGGTGAAATTTATCGCTTTCAGACAAACACCTACT 2585
Db      975 uGln-----TyrSerGlnTyrLeuArgLeuArgGlnArgIleCysTyrSerSerLe 993

```

```

Qy      2586 GGAATGAGAGACATCTCTGGGAGACACATCTTCTGAGAGACTTAAATGACCT 2645
Db      993 uGlnThrProAsnAsnProGlyAlaGlnAsnLeuPheThrPheIleuSerLeuYAsnVal 1013
Qy      2646 ATTG 2649
Db      1013 lleu 1014

RESULT 12
US-10-407-952-32
; Sequence 32, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides
; FILE REFERENCE: C01041,70037,US
; CURRENT APPLICATION NUMBER: US/10/407,952
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-407-952-32

Alignment Scores:
Pred. No.: 1,99e-46 Length: 1032
Score: 559.00 Matches: 253
Percent Similarity: 38.61% Conserved: 157
Best Local Similarity: 23.82% Mismatches: 353
Query Match: 15.80% Indels: 300
DB: Gaps: 42

US-09-396-985b-46 (1-2951) x US-10-407-952-32 (1-1032)
Qy      211 ATGCGTCCC-----TGAGCTCTGCTGCTAGACCTGTGATCATG-----GCA 249
Db      4 MetProProGlnSerTrpIleLeuThrCysPheCysLeuLeuSerSerGlyThrSerAla 23
Qy      250 CTGTTCTTCTCTGCTGCTGACACACAGAGCTTGAATCCCTGCATAGAGTATTCAT 309
Db      24 IlePheHISerLeuAlaAsnTyrSerArgSerTyr---ProCysAspGlnIleArgHISAsn 42
Qy      310 -----ATTACCTACCAATGATGATGATGATGATGATGATGATGATGATGATGAT 363
Db      43 SerLeuValIleAlaGlnCysAsnHISerArgGlnLeuHISerGlnValProGlnThrIleGly 62
Qy      364 TCTTCACACAAAGACATAGATCTGAGCTTCAACCCCTTGAAGAATCTTAAAGCTATAGC 423
Db      63 LysTyrValThrAsnIleAspLeuSerAspAsnAlaIleHISerIleThrIleGlnSer 82
Qy      424 TTCTCAATTTTTCAGAACTTCAAGTGGCTGATTTATCCAGAGTGAATGAA----- 477
Db      83 PheGlnLeuSerGlnAsnLeuThrTyrIleAspPheAsnHISerAsnAlaTyrGlnGlnHIS 102
Qy      478 -----ACAATTGAAGACAAAGCCTAGATGATGATGATGATGATGATGATGATGAT 513
Db      103 ProAsnGlnAsnLeuYAsnGlyMetAsnIleThrGlnIleValLeuLeuSerLeuArgAsn 122
Qy      514 CTCTCAACTTGTACTGACAGAGAAACCTATCCAGAGATTTTCC-----CCAGAG 564
Db      123 LeuThrValLeuLeuLeuGlnAspAsnGlnLeuTyrThrIleProAlaGlyLeuProGln 142
Qy      565 AGTTTCTGTGACTAACAAGTTTGAACATCTGAGTGGCTGTGAGACAA----- 615
Db      143 SerLeuYSerGlnLeuSerLeuIleGlnAsnAsnIlePheGlnValThrTyrAsnAsnThr 162

```

QY 616 -----TTGGCGCTCTAGAAAGCTTCCATTGGA----- 645
 DB 163 PheGlyLeuArgAnLeuGluArgLeuTyrLeuGlyTyrPheCysTyrPheLeuCysAsn 182
 QY 646 -----CAGCTTATTAACCTTAAAGAACTCAAT 672
 DB 183 GluThrPheValGluArgGlyAlaPheLeuAsnLeuLeuLeuValLeuSer 202
 QY 673 GTGGCTCACAAT-----TTTATACATTCCCTGAAGTTACTGCA----- 711
 DB 203 LeuSerPheAsnAnLeuPheTyrValProPheLeuProSerSerLeuArgGlyLeu 222
 QY 711 ----- 711
 DB 223 PheLeuSerAnAlaValIleMetAsnIleThrGlnGluAspPheGlyLeuGluAsn 242
 QY 711 ----- 711
 DB 243 LeuThrLeuAspLeuSerGlyAsnCysProArgCysTyrAnAlaProPheProCys 262
 QY 711 ----- 711
 DB 263 ThrProCysGlyGluAsnSerSerIleHisIleHisProLeuAlaPheGlnSerLeuThr 282
 QY 712 -----TATTTT 717
 DB 283 GluLeuLeuTyrLeuAsnLeuSerSerThrSerLeuArgThrIleProSerThrTyrPhe 302
 QY 718 TCCAACTGACGAAGCTAGTACATGAGATCTTCTTATACATAT--ATTCAAACTATT 774
 DB 303 GluAsnLeuSerAnLeuGlyGluLeuHisLeuGlnPheAsnTyrLeuValGlnGluIle 322
 QY 775 ACTGTCAACGACTTACAGTTTCTACGTGAAGAAATCCAAAGTCATCTCTTTGACATG 834
 DB 323 AlaSerGly-----AlaPheLeuThrLeuProSerLeuGlnIle--LeuAspLeu 339
 QY 835 TCTTTGAACCAATGACTTCATTCACAGAACCAAGCTTTGAGGAATTAAGCTCATGAA 894
 DB 340 SerPheAsn-----PheGlnTyrLeuGluTyrLeuGlnPheIleAsnIle----- 354
 QY 895 CTGACTCTAAGAGTAATTTTAATAGCTCAAAATTAATGAAGAACTTGCTCAAACTCG 954
 DB 355 -----SerSerAnPheSerLeuS-----LeuArgSerLeu 364
 QY 955 GCTGTTTACACGTCATCGTGTATCTGTGGAGAAATTTAAAGATGAAGAAATCTGGAA 1014
 DB 365 LysLeuLeuHisLeuArgGlyTyrValPheArgGluLeuGlyLysHis----- 381
 QY 1015 ATTTTGAACCTCTATCATGAGAGACTATGTAGTGAACCATTTGATGAGTTCAGGTTA 1074
 DB 382 ---PheGluHis-----LeuGlnSerLeuProAsnLeuAlaThrIleAsnLeuGlyIle 398
 QY 1075 ACATATACAAATGATTTTTCAGATGATATTTGATTAAGTTCCATTTGGCGAATGTTTCT 1134
 DB 399 AsnPheIleGluLysIle-----AspPheLysAlaPheGlnAsnPheSerLeuAsp 416
 QY 1135 GCAATGTCTCTGGCAGGTGTATCTATAAATATCTAGAAGATGTTCTTAACATTTCAA 1194
 DB 417 ValIleTyrLeuSerGlyAsnArgIleAlaSerValLeuAspGlyThrAspTyrSerSer 436
 QY 1195 TGGCAATTCCT-----ATC 1208
 DB 437 TrpArgAsnArgLeuArgGlyLeuProLeuSerThrAspAspArgGluPheAspProHisVal 456
 QY 1209 AATCATTAAGATGTCAACTAAGCAGTTT-----CCAACCT 1241
 DB 457 AsnPheTyrHisSerThrLeuProLeuLeuLysProGlnCysThrAlaTyrGlyLysAla 476
 QY 1242 CTGACTCAACCTTT----- 1256
 DB 477 LeuAspLeuSerLeuAsnAsnIlePheIleIleGlyLysSerGlnPheGlnGlyPheGln 496

QY 1257 ---CTTAAAGTTTGAAGCTTTAACTATGAACAAAGGCTATACAGTTTAAAGAGTG--- 1310
 DB 497 AspIleAlaLeuGlyLeuAsnLeuSerPheAsnAlaAsnThrGlnValPheAsnGlyThrGlu 516
 QY 1311 -----GCCCTTACCAAGTCTACAGTTATCTAGATCTTATAGTAAGAAATGACATGACTTTAGT 1364
 DB 517 PheSerSerMetProHisIleLysTyrLeuAspLeuThrAsnAsnArgLeuAspPheAsp 536
 QY 1365 GTGGCGCTTCTATTCATTCGATTTTGGGAACAAAGCTGTGACACATTTAGCTCAGCTTC 1424
 DB 537 AspAsnAsnAlaPheSerAspLeu-----HisAspLeuGlnValLeuAspLeuSerHis 554
 QY 1425 AATGTGCGCATCATTAATGAGTCCAAAT-----TTCATGGGCTTA 1463
 DB 555 AsnAlaHisTyrThrPheSerIleAlaGlyValThrHisArgLeuGlyPheIleGlnAsnLeu 574
 QY 1464 GAAGAGCTGCAGACCTGCAATTTTTCAGACCTCTACTTTAAAGGCTCACAGA----- 1518
 DB 575 IleAsnLeuArgValLeuAsnLeuSer-HisAsnGlyIleTyrThrLeuThrGluGluSe 594
 QY 1518 ----- 1518
 DB 594 GlnLeuLysSerIleSerLeuGlyGluLeuValPheSerGlyAsnArgLeuAspHisIle 614
 QY 1519 -----TTCTCAGCGTTCTTATCCCTTGAAGAAAGCTACTTTA 1553
 DB 614 uTPraAsnAlaAsnAspGlyLysTyrTrpSerIlePheLeuSerSerLeuGlnAsnLeuIleArg 634
 QY 1554 CTTTGACATCTCTTATTAACACCAAAATTTGACTTCGATGTATATTTCTTGAGCTTG-- 1611
 DB 634 GluAspLeuSerTyrLysAsnLeuGlnGlnIleProAsnGlyAlaPheLeuAsnLeuPyr 654
 QY 1612 -ACCAGCTCAACACATTAANAATGGCTGCAATTC-----TTCAAGAACCAACCT 1664
 DB 654 OGlnSerLeuGlnGluLeuLeuIleSerGlyAsnLysLeuArgPheAsnThrPheIle 674
 QY 1665 TTCAAATGTCTTTGCAACACCAACAACTTGACATTCCTGATCCTTAAATGTCAATT 1724
 DB 674 uLeuGlnTyrPhe-----ProHisLeuHisLeuLeuAspLeuSerArgAsnGluLe 691
 QY 1725 GGAACAAATATCTTGGGGGTATTTTGACACCCCTCATACCTTCATTAATTAATAGAG 1784
 DB 691 uTyrPheLeuProAsnCysLeuSerSerLysPheAlaHisSerLeuGlnThrLeuLeuSe 711
 QY 1785 TCACAAATCTATTTGTTTGTGATCATCCATTAATTAACAGCTGATTCCTCAGACAC 1844
 DB 711 ThrAsnHisPheSerHisLeuProSerGlyPheLeuSerGlnAlaArgAsnLeuValHis 731
 QY 1845 TCTTGATTTGAGTTTCAATGACATAGAG--ACATCTAAAGAAATCTGCAACATTTTCC 1901
 DB 731 GluAspLeuSerPheAsnThrIleLysMetIleAsnLysSerSerLeuGlnThrLysMet 751
 QY 1902 AAAG--AGTCTACCTTTCTTCAATCTTAACTTAACAATCTGTGCTTGATATGTGAACA 1958
 DB 751 ClysThrAsnLeuSerIleLeuGlnLeuHisGlyAsnTyrPheAspCysThrCysAspIle 771
 QY 1959 TCAGAAATTCCTGAGTGGGTCAAGAACAGAGCAAGTTC-----TTGCTGAA 2006
 DB 771 eSerAspPheArgSerTyrPheAspArgGluAsnLeuAsnIleThrIleProLysLeuValAs 791
 QY 2007 TGTTTGAACAAATGACATGTGCAACACCTGTAGAGATGAATACCTCTTATGTTGGATT 2066
 DB 791 nVal-----IleCysSerAsnProGlyAspGlnLysSerIleMetSerIle 808
 QY 2067 TAATTAATCTAAGCTGTATATATGTAACAAGACAAATCATGATGTCTACGTGCTGAT 2126
 DB 808 uAspLeuThrThrCysValSerAspThrThrAlaAlaValLeuPhePheLeuThrPheLe 828
 QY 2127 TGTGATTCACAGTGA-----GCATTTCTGATATACAC----- 2160
 DB 828 uThrThrSerMetValMetLeuValAlaLeuValHisIleuPheTyrTrpAspValTr 848
 QY 2161 -TTCTATTTTACAGCTG-----ATACTTATTTGCTGCTGTAAAGATGACAGAGAGAGA 2213

```

Db      848 pHeilleTyRHismetCySerAlaLyLeuLyseGlyTyRArgThrSerSerThrSergI 868
Qy      2214 AAGCATCATGATGATTTGGATGATCTACTGAGTACAGAT-----GAGAGCTGGCT 2264
Db      868 nThPherYrAspAlaTyRILeserTYrAspThrYrAspAlaSerValThrAspTrpVa 888
Qy      2265 GAGAAATGAGCTGGTAAAGAAATTTAGAAAGAGAGTGGCCCGC---TTTCACTCTGGCT 2321
Db      888 lIlaSngluLeuArgTyRHIsleGluGluSerGluAspLySerValLeuLeuCySe 908
Qy      2222 TCACACTAGAGACTTATTTCTGCTGTAGACATTCCTGCTCCCAATCATTCAGAGCGTT 2381
Db      908 uGlUgluArgAspTrpAspProGlyLeuProIleIleAspEnLeuMetGln---SerI 927
Qy      2382 CCAGAGCGCGGAGAGGTTATTTGCTAGTGTCTAGACATTTATTCAGAGCGTTG 2441
Db      927 eAsnGlnSerYrAspThrIlePheValLeuThrYrAspTyR----- 941
Qy      2442 TATCTTGATATGATGATTTGCTCAACATGACAGTTTCTGAGC----- 2484
Db      942 -----AlaYrSerTrpAspPheYrThrAlaPheTyRLeuAlaLe 955
Qy      2485 -----AGCCGCTCTGGCATCATCTTCATTTGCTCTTGGAGAGTTGA 2525
Db      955 uGlnArgLeuMetAspGluAsnMetAspValIleIlePheIleLeuGluProValLe 975
Qy      2526 GAATCCTCTGCTGAGCGACGAGTGGATTTGATTCGCTTTAGCAGAAACACTTACT 2585
Db      975 uGln-----TyRserGlnTyRLeuArgLeuArgGlnArgIleCyLySerSerIleLe 993
Qy      2586 GAATGGAGAGACATCTCTGGGAGGACATCTTGGAGAGACTTAATAATGCGCT 2645
Db      993 uGlnTrpAsnAsnProLySAlaGluAsnLeuPheTrpGlnSerLeuLyAsnValVa 1013
Qy      2646 ATTG 2649
Db      1013 lIeu 1014

RESULT 13
US-09-954-987B-187
; Sequence 187, Application US/09954987B
; Publication No. US20030104523A1
; GENERAL INFORMATION:
; APPLICANT: Stefan Bauer
; APPLICANT: Grayson B. Lipford
; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
; FILE REFERENCE: C1041/7016 (AMS)
; CURRENT APPLICATION NUMBER: US/09/954, 987B
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/233, 035
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/263, 657
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: US 60/291, 726
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/300, 210
; NUMBER OF SEQ ID NOS: 230
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 1059
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-954-987B-187

Alignment Scores:
Pred. No.: 4,11e-45 Length: 1059
Score: 546.00 Matches: 264
Percent Similarity: 39.32% Conservative: 165
Best Local Similarity: 24.20% Mismatches: 359

```

```

Query Match: 10.55% Indels: 304
DB: 10 Gaps: 45
US-09-396-985B-46 (1-2951) x US-09-954-987B-187 (1-1059)
Qy      162 TCGTCAATGTTCTCATGAGCGCTCCACTGGTTGAGAAATGCCAGATGATGCTCCCTG 221
Db      9 SerSerCySerLeuGlyLySgluThr-LysLyGluAsn-----Me 22
Qy      222 GCTCTGCTGAGACTGCTGATCATGACATGTTCTTC-----TCTGCTTAC 269
Db      22 tPheLeuGlnSerSerMetLeuThrCyRlePheLeuLeuIleSerGlySerCySgluLe 42
Qy      270 ACCAGAGACTTGAAT-----CCCTGATAGAGGTAGTCTTAAT----- 309
Db      42 uCyAlaGluGluAsnPheSerAspGlyTyRProCyAspGluLySgluAsnAspSe 62
Qy      310 -ATTACCTACCATGATGATGATGAGAAATCCAGGAAATGCCGTGATGACATTCCTTTC 368
Db      62 rValIleAlaGluCySerSerAsnArgLeuGlnGluValProGlnThrValGlyTy 82
Qy      369 AACCAAGACATGATGATGATGATCAACCCCTGAAGATCTTAAGACTTACCTTTC 428
Db      82 rValThrGluLeuAspLeuSerAspAsnPheIleThrHisIleThrAsnGluSerPheG 102
Qy      429 CAATTTTACAGAACTTCAGTGGCTGATTTATTC----- 462
Db      102 nGlyLeuGlnAsnLeuThrYrSileAsnLeuAsnHisAsnProAsnValGlnHisGlnAs 122
Qy      463 -----AGGTGTGAATTTGAAACAAATTGAGACAGAGCATGAGCTT 506
Db      122 nGlyAsnProGlyYrIleGlnSerAsnGlyLeuAsnIleThrAspGlyAlaPheLeuAsnLe 142
Qy      507 ACACCACTCTCAAACTTGAATGATGATGACAGGAAACCTTATCCAGAGTTTCCCGAGAG 566
Db      142 uLyAsnLeuArgGluLeuLeuLeuGluAspAsnGlnLeu-----ProGlnI 158
Qy      567 TTTCTGTGACTA---ACAAGTTTACCAATCTGCTGGCTGGTGGAGACAAATTTGGCGCTC 623
Db      158 eProSerGlyLeuProGluSerLeuThrGluLeuSerLeuIleGlnAsnIleTyRAs 178
Qy      624 TTAGAAGCTTCCTCATTTGAGACAGCTTATTAACCTTAAGAACTCAATGCTGCTCAAA 683
Db      178 nIleThrLySgluGlyIleSerArgLeuIleAsnLeuLyAsnLeuTyRLeuIleAtPAs 198
Qy      684 T-----TTTATACATTCCTGTAAGTTA-----CTGCAATTTTTCAAATCT 725
Db      198 nCyTyRPhAsnLySValCySgluTyRAsnIleGluAspGlyValPheGluThrLe 218
Qy      726 GAGGAACCTGATCATGTGATGATCTTTGATTAATATTAATCAAACTTACTGTCAGAGA 785
Db      218 uThAsnLeuGluLeuLeuSerLeuSerPheAsnSerLeuSerHisValSerProLySle 238
Qy      786 CTACAGATTTCTACGTGAATAATCCACAAGTCAATCTCTTTAGACATGTCTTGAAGCC 845
Db      238 uProSerSerLeuArgYs-----LeuPheLeuSerAsnThrG 251
Qy      846 AATTGACTTATTCAGACCAAGCCTTTCAGGGA---ATTAAAGCTCATGAAGTACTCT 902
Db      251 nIleTyRlyRleSerGluGluAspPheLySgluLeuIleAsnLeuThrLeuLeuAspLe 271
Qy      903 AAGAGTAAAT-----TTTAAT----- 918
Db      271 uSerGlyAsnCySerProArgCySAspAsnAlaProPheProCyValProCyAspGlyG 291
Qy      919 -----AGCTCAATATATATGAATACTGCTCAAAACCTGCTGTTTACAC----- 966
Db      291 yAlaSerIleAsnIleAspArgPheAlaPheGlnAsnLeuThrGlnLeuArgTyRLeuAs 311
Qy      967 -----GTCCATGCGTTGATCTTGGGAGAAATTTAAAGATGAAGAAATCT 1010
Db      311 nLeuSerSerThrSerLeuArgLySleAsnAlaAlaTrpPheLySAsnMetProHisLe 331

```

QY	1011	GGAAATTTTTGA	-----CCCTTATCATGGAAG	-----	1041
Db	331	uLyvAlLeuAspLeuGluPheAsnTyrLeuValGlyGluLeuAlaSerGlyAlaPheLe			351
QY	1042	-----CTATGATGTGACCATGATGAGTTACGATTAACATA			1079
Db	351	uThrMetLeuProArgLeuGluLeuAspLeuSerPheAsnTyrLeuGlySerTyr			371
QY	1080	T-----ACAAATGATTTTCA			1095
Db	371	rProGlnHisLeuAsnLeuSerArgAsnPheSerTyrAspProLeuSerLeuArgAlaLeuHis			391
QY	1096	-----GATGATATGTGTAAGTTCCATTGCT			1121
Db	391	sLeuArgGlyTyrValPheGlnGluLeuArgGlyAsnAspPheGlnProLeuMetGlnLe			411
QY	1122	GGCGAAATTTTCTGCATGTCTCTGGCAGGTGTATCTTAATAATCTACAAAGATGTTC			1181
Db	411	uProAsnLeuSerThrTrieAsnLeuGlyTrieAsnPheIleLeuGlnIleAsp			428
QY	1182	TAAACATTTCAA	-----TGGCAATCTCTTATCAATCAT		1215
Db	429	-----PheuysLeuPheGlnAsnPheSerAsnLeuGluIleTyrLeuSerGluAs			446
QY	1216	-----AGATGTCACTAAGCATTTTCCA			1238
Db	446	nArgLieserProLeuValysAspThrArgGlnSerTyrAlaAsnSerSerPheGln			466
QY	1239	ACTCGAGATC	-----TA		1250
Db	466	nArgHisIleArgGlyAspArgSerThrAspPheGluPheAspProHisAspAsnPheTyr			486
QY	1251	CCCTTTCTT	-----AAAAGTTGACTTT		1273
Db	486	rHisPheThrArgProLeuIleLysProGlnCysAlaIaLeuTyrGlyLysAlaLeuAspLe			506
QY	1274	AACTATGGAACAA	-----GGCTATATCAGTTTAAAAAGTC		1310
Db	506	uSerLeuAsnSerIlePhePheIleGlyProAsnGlnPheGlnLeuLeuProAspIleAl			526
QY	1311	-----GC			1312
Db	526	aCysLeuAsnLeuSerAlaAsnSerAsnAlaGlnValLeuSerGlyThrGluPheSerAl			546
QY	1313	CTTACCAAGTCTCAGACTGTCTAGATCTAGTGAATGACATGACGTTTATGCTGAGCTG			1372
Db	546	aIleProHisValLysTyrLeuAspLeuThrAsnAsnArgLeuAspPheAsnAlaSer			566
QY	1373	TTCTTATTTCTGATTTGGGAACAACAGCTGTGACACTTAACCTCAGCTTCATGCTGC			1432
Db	566	rAlaLeuThrGluLeu-----SerAspLeuGlnValLeuAspLeuSerTyrLeuSerHis			584
QY	1433	CATCATTTATGAGTGC	-----AATTTCATGCGTCT		1462
Db	604	sTyrPheArgIleAlaGlyValThrHisIleLeuGluPheIleGlnAsnPheThrAsnLe			624
QY	1463	AGAA-----GAGCTGACAGACTGATTTTTCAGACCTTATTAATAAGGCTCAG			1516
Db	624	uLysValLeuAsnLeuSerHisAsnAsnIleTyrThrIleu-ThrAspLysTyrAsnLeuG			642
QY	1517	AATTCTCAGCGTTTATTATCCCTTGAATAAGCTATTCAC	-----CTTGACATCT		1566
Db	642	uSerLys-----SerLeuValGlnLeuValPheSerGlyAsnArgLeuAspIleL			641
QY	1565	CTTATATCTAACACCAAAATGTACTTCGATGTATATTTCTTGCGCTTGACAGCTCTGACA			1622
Db	641	eutTyrAsnAspAspAsnArgTyrTrieSerTriePheLysGlyLeuLysAsnLeuThrA			661
QY	1625	CATTAAATATGGCTGGCAATCTTTCTTAAGAACAACACCTTGACATGCTTTGCAAC			1683
Db	661	rgLeuAspLeuSerLeuAsnArgLeuLys--HisIleProAsnGlnAlaPheLeuAsnL			680
QY	1684	--ACAACAACCTTGACATTTCTCGATGCTCTTCTTAATGTCAATTTGACAACAAATATCTTGGG			1741

Db	680	euproAlaSerLeuThrGluLeuHis11LeuAsnAspAsnMetLeuLysPhePheAsnTrpT	700
Qy	1742	GGGTAATTGGACACCCCTGCATCTTCATTTAAATTAATGATGACACAAATCTATGTT	1801
Db	700	hrLeuLeuGlnGlnPheProArgLeuGluLeuLeuAspLeuArgGlyAsnLysLeuLeuP	720
Qy	1802	TTTTGGATTCATCCCATTAATAACAGAGCTGATTCCTGCAGACCTCTTGATTCAGCTTCA	1861
Db	720	heLeuThrAspSerLeuSerAspPheThrSerSerLeuArgThrLeuLeuLeuSerHisA	740
Qy	1862	ATCCGATA-----G	1870
Db	740	snArgLysSerHisLeuProSerGlyPheLeuSerGluValSerSerLeuLysHisLeuA	760
Qy	1871	AGACATCTAAAGAAATCTGCACATTTTCCAAAGAT-----	1908
Db	760	spleuSerSerAsnLeuLeuLysThr11LeuAsnLysSerAlaLeuGluThrLysThrTrt	780
Qy	1909	-----CTAGCCCTTTCATCTTACTTAACAATTCGTGTGCTTGATATGACATCAGA	1963
Db	780	hrLysLeuSerMetLeuGluLeuHis16GluAsnProPheGluCysThrCysAsp11LeuGlyA	800
Qy	1964	AATTCTCGACATGGGTCAAGAAACAAGACAGTCTTGAGAAAGTTGAA-----	2013
Db	800	sppPheArgArgTrpMetAspGluHis-----LeuAsnValLys11LeuProArgL	816
Qy	2014	-----CAATACATCTGACCAACACCTGAGATGAATACCTCCTTGATGTGATTTTA	2068
Db	816	euvAlaAspVal11LeuCysAlaSerProGluAspGlnArgGlyLysSer11LeuAlaSerLeuG	836
Qy	2069	ATAATTCTACCTGTTATATGTACAAGACATCATCAGTGTCTCAGTGTCACTGTGATTG	2128
Db	836	1uLeuThrThrCysValSerAspValThrAlaVal11LeuPhePhePheThrPhePhe1	856
Qy	2129	TGGTATCCACTGTA-----GCATTCTGATATACACTTCTATTTTCAC-----	2172
Db	856	1eThrThrMetValMetLeuAla11LeuAlaHis15LeuPheLysThrAspVal1Trp	876
Qy	2173	-----CTGATCTTATTTGCTGCTGTAATAAAGTACAGCAGAGAGAAA	2215
Db	876	heLeuTrpAsnValCysLeuAlaLysLeuLysGlyTrpArgSerLeuSerThrSerGlnT	896
Qy	2216	GCATCTATGATGCAATTTGTGATCTACTCGATCGACAAAT-----GAGCAGCTGGGTGA	2266
Db	896	hrPheTrpAspAlaLysTrp11SerTrpAspThrLysAspAlaSerValThrAspTrpVal1	916
Qy	2267	GAATAGACTGTGTAAGAAATTTAAGAAGAGAGGCCCGC---TTTCACCTCTGCCTTC	2323
Db	916	1eAsnGluLeuArgTrp11LeuGlnGluSerArgAspLysAsnValLeuLeuLysLeuG	936
Qy	2324	ACTACAGAGACTTATATTCCTGCTGAGACATTTGCTGCCAATCATCTCAGAGAAAGCTTCC	2383
Db	936	1uGluArgAspTrpAspProGluLeuAla11LeuPheAsnLeuMetGln---Ser11LeuA	955
Qy	2384	ACAAGAGCCGAGAGATTATTTGTGTAGTGTCTGACACTTATTTACAAGCCGTTGGTGTA	2443
Db	955	asnGlnSerLysLysThrValPheValLeuThrLysLysTy-----	968
Qy	2444	TCTTTGAATAGCAATTGCTCAAAACATGGCACTTTCGAGC-----	2484
Db	969	-----AlaLysSerTrpAsnPheLysThrAlaPheTrpLeuAlaLeuG	983
Qy	2485	-----AGCCGCTCTGGCAACATCTTCATCTGATGCTTGAGAAAGGTGAGA	2527
Db	983	1uArgLeuMetAspGluAsnMetCaspVal11Leu11Phe11LeuLeuGluProValLeuG	1003
Qy	2528	AGTCCCTGCTGACGACGACGATGGAATTTGATCCCTTCTTGAGAGAAACACTACCTGG	2587
Db	1003	1uHis-----SerGlnTrpLeuArgLeuArgGlnArg11CysLysSerSer11LeuLeuG	1021
Qy	2588	AAATGGAGACAAATCTCTGGGAGGACCATCTTCTGGAGAAAGCTTAAAAATGCCCTAT	2647


```

Db      1021 IntPrOaSPaSPnProLySaLaGlUglYLeuPheTrGlnThrLeuAraGnaValL 1041
Qy      2648 TG-----GATGGAAGAGCTTCGAAT 2667
Db      1041 eutHrGlUaSPnSPSerArGTYrAenAen 1050

RESULT 14
US-10-407-952-30
; Sequence 30, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides
; FILE REFERENCE: C01041.70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent version 3.1
; SEQ ID NO 30
; LENGTH: 1059
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-407-952-30

Alignment Scores:
Pred. No.:      4,11e-45      Length:      1059
Score:          546.00      Matches:      264
Percent Similarity: 39.32%      Conservative: 165
Best Local Similarity: 24.20%      Mismatches: 359
Query Match:    10.55%      Indels:      304
DB:             15          Gaps:          45

US-09-396-985B-46 (1-2951) x US-10-407-952-30 (1-1059)
Qy      162 TCGTCAGTGTCTCTCATGCGCTCCACCTGTCGACGAAATGCCAGATGATGCCCTCC 221
Db      9 SerSerCysSerLeuGluYrGluThr-LysLysGluAaSn-----Me 22
Qy      222 GCTCTGAGCTGAGCTGATGATGACGACGTGCTTC-----TCCTGCTGAC 269
Db      22 tPhLeuGlnSerSerMetLeuThrCysIlePheLeuLeuIleSerGlySerCysGluLe 42
Qy      270 ACCAGAGAGCTTGAAT-----CCCTGATAGAGGTAGTTCTTAAT----- 309
Db      42 uCyAlaGluGluAaSPnSPSerArGserTYrProCyAaSPgluLysLysGlnAaSPse 62
Qy      310 -ATTACTACCAATGATGATGATGACGAAACTGACGAAAGTCCCTGATGACATTCCTTCTTC 368
Db      62 rValIleAlaGluLysSerAaSPnArGArGLeuGlnGluValProGlnThrValGlySerY 82
Qy      369 AACCAAGAACATAGATGAGCTTCAACCCCTGAGATCTTAAAGATCTTAAGCTTACCTTC 428
Db      82 rValThrGluLeuAaSPnSPSerArGpHeIleThrHisIleThrAaSPgluSerPheG 102
Qy      429 CAATTTTTCAGAACTTCAAGTGGCTGATTTATCC----- 462
Db      102 nGlyLeuGlnAaSPnSPSerArGLeuAaSPnSPSerArGLeuAaSPnSPSerArGLeuAaSPn 122
Qy      463 -----AGGTGTGAATTTGAACAAATTTGAACAGACAGGATGGCATGGCTT 506
Db      122 nGlyAaSPnProGlyLleGlnSerAaSPnGlyLeuAaSPnIleThrAaSPgluAaSPnLeuAaSPn 142
Qy      507 ACACACCTCTCAATCTGATGATGATGACGAGAAACCTATCCAGAGTTTTCGCCAGAG 566
Db      142 uLysAaSPnLeuAaSPnGluLeuLeuAaSPnAaSPnGlnLeu-----ProGlnI 158
Qy      567 TTTCCTGAGTA---ACAAGTTTGAACAATCTGCTGCTGAGACAAATTTGGCCTC 623

```

```

Db      158 eProSerGlyLeuProGlnSerLeuThrGlnLeuLeuSerLeuIleGlnAaSPnIleTYrAs 178
Qy      624 TCTGAAGAGCTTCCCTATTGACAGCTTATTAACCTTAAGAACTGATGAGCTACAA 683
Db      178 nIleThrLysGluGlyLleSerArGLeuIleAaSPnLysAaSPnLeuTYrLeuAaSPnAs 198
Qy      684 T-----TTTATACATTCCTGTAAGTTA-----CCTGCAATATTTTCCAAATCT 725
Db      198 nCyTYrPheAaSPnLysValCysGlyLysThrAaSPnIleGlnAaSPnGlyValPheGlnThrLe 218
Qy      726 GACGACCTTACATGATGATGATCTTTCTTATTAATTAATTAATTAATTAATTAATTAATTA 785
Db      218 uThrAaSPnLeuLysLeuSerLeuSerPheAaSPnSerLeuSerHisValSerProLYsLe 238
Qy      786 CTTACAGTTTCTAGTGAAATCCACAAGTCAATCTCTTTAACAATGCTTTGAACCC 845
Db      238 uProSerSerLeuAaSPnLys-----LeuPheLeuSerAaSPnThrG 251
Qy      846 AATTGACTTCATTAACACCAAGCTTTCAAGGA---ATTAAAGCTCAATGAAGTACTCT 902
Db      251 nIleLYrTYrLleSerGluGlnAaSPnPhelySGlyLeuIleAaSPnLeuThrLeuAaSPnLe 271
Qy      903 AAGAGTAAAT-----TTTAAT----- 918
Db      271 uSerGlyAaSPnCySPnProArGysPheAaSPnAlaProPheProCyValProCyAaSPnGly 291
Qy      919 ----AGCTCAATTAATTAAGAAACTTGCCTTCAAAACTGGCTGCTTACAC----- 966
Db      291 yAlaSerIleAaSPnIleAaSPnArGpHeAlaPheGlnAaSPnLeuThrGlnLeuAaSPnTYrLeuAaSPn 311
Qy      967 -----GTCCATCGTGTGATCTTGGAGAAATTTAAAGAGAAAGAAATCT 1010
Db      311 nLeuSerSerThrSerLeuAaSPnGlyIleAaSPnAlaAlaITrPheLysAaSPnMetProHisLe 331
Qy      1011 GGAATTTTGAAT-----CCCTTATCATGGAAGGA----- 1041
Db      331 uLysValLeuAaSPnLeuGluPheAaSPnTYrLeuValGlyGlnLeaSerGlyAlaPheLe 351
Qy      1042 -----CTATGTGATGTGACCATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1079
Db      351 uThrMetLeuProArGLeuGlnLleLeuAaSPnLeuSerPheAaSPnTYrLleYsGlySerTY 371
Qy      1080 T-----ACAAATGATTTTCA----- 1095
Db      371 rProGlnHisIleAaSPnIleSerArGpHeIlePheSerLeuTYrProLeuSerLeuAaSPnIle 391
Qy      1096 -----GATGATATTTGTAAGTTCCATTCCTT 1121
Db      391 sLeuAaSPnGlyTYrValPheGlnGluLeuAaSPnGluAaSPnAaSPnPheGlnProLeuMetGlnLe 411
Qy      1122 GCGCAATGTTTCTGCAATGTCCTGCGAGGTGATCTATTAATAATATCTAAGAGATGTTCC 1181
Db      411 uProAaSPnLeuSerThrIleAaSPnGlyIleAaSPnPhelyLysGlnIleAaSPn----- 428
Qy      1182 TAAACATTTCAAA-----TGCAATCCTTATCAATCAT----- 1215
Db      429 -----PheYLeuPheGlnAaSPnSPSerArGLeuGlnIleLeuTYrLeuSerGlyAaSPn 446
Qy      1216 -----AGATGTCACTTAAGCAATTTCA 1238
Db      446 nArGlyLeuSerProLeuValLysAaSPnThrArGlnSerTYrAlaAaSPnSerSerPheG 466
Qy      1239 ACTCTGATC-----TA 1250
Db      466 nArGlnHisIleArGlyArGArGserThrAaSPnPhelyPheAaSPnProHisSerAaSPnPhety 486
Qy      1251 CCTTCTT-----AAAATTGACTTT 1273
Db      486 rHisPheThrArGProLeuIleLysProGlnCYsAlaAlaTYrGlyLysAlaLeuAaSPnLe 506
Qy      1274 AACTATGAACAA-----GGGTCTATCAGTTTAAAGAGT----- 1310
Db      506 uSerLeuAaSPnSerIlePhePheIleGlyProAaSPnGlnPheGlnAaSPnLeuProAaSPnIleAl 526

```

QY 1311 -----GC 1312
Db 526 aCysleuAsnleuSerAlaAsnSerSerAlaGlnValleuSerGlyThrGluPheSerAl 546
QY 1313 CCGTAAAGCTGCTGAGTATCTAGATCTTAAGTAAGATGCACTGAGCTTGAAGTGGCTG 1372
Db 546 alleProHieValleyrleuSerleuThrAsnAsnArgleuSerPheAsnAlaSe 566
QY 1373 TTTCTATTCTGGGAAACAAAGCTGAGACCTTGAAGCTTCAAGCTTCAAGTGGTGC 1432
Db 566 rAlaIeuThrGluIeu-----SerAspLeuGlnValleuAspLeuSerGlyrAsnSerAl 584
QY 1433 CATCATATGAGTGC-----AATTTCATGGGTCT 1462
Db 584 sTyrrPheArgIleAlaGlyValThrHisleuGluPheIleGlnAsnPheThrAsnle 604
QY 1463 AGA-----GAGCTGAGACAGCTGATTTTTCAGACCTTACTTAAAGGCTGACAG 1516
Db 604 ulysValleuAsnleuSerHisAsnAsnIleTyrrThrleu-ThrAspIleTyrrAsnleuG 624
QY 1517 AATTCTGAGCGTTTATTCCTTGAAGAGCTACTTAC-----CTTGAACATCT 1564
Db 624 luserIys-----SerleuValGluIeuValPheSerGlyAsnArgleuAspIlel 641
QY 1565 CTATATCTAACACCAAAATGACTGATGATATTTCTTGGCTTGACAGCTGACAG 1624
Db 641 eutrAsnAspAspAspAsnArgTyrrIleSerIlePheIleGlyleuIleuAsnleuThra 661
QY 1625 CATTAATAATGGCTGGCAATCTTTCAAAGACAACACCTTTCAAATGCTTTCGAAAC- 1683
Db 661 rgleuAspLeuSerleuAsnArgleuIys---HisIleProAsnGlnAlaPheleuAsnI 680
QY 1684 --ACAAACAACCTTGAACATCTCGATCGCTTAAATGTCATTCGAAACAATATCTGGG 1741
Db 680 eufProAlaSerleuThrGluIeuHisIleAsnAspAsnMetleuIysPhePheAsnTrpT 700
QY 1742 GGGTATTTGACACCTGCATGATCATTAATTAATGATGACACAAATCATTTATGT 1801
Db 700 hrlleuLeuGlnGlnPheProArgleuGluIleuLeuAspLeuArgGlyAsnIleuLeuP 720
QY 1802 TTTTGAATTCATCCCATTAATTAACAGCTGATTCCTGACAGCTTGTGATGACATTTCA 1861
Db 720 heIeuThrAspSerleuSerAspPheThrIleSerleuArgThrleuIeuIeuSerHisA 740
QY 1862 ATCGCATR-----G 1870
Db 740 snArgIleSerHisleuProSerGlyPheIeuSerGluValSerSerleuIysHisIeuA 760
QY 1871 AGACATCTAAAGAAATCTGCAACATTTCCAAAGAGT----- 1908
Db 760 sPleuSerSerAsnleuIeuIysThrIleAsnIysSerAlaIeuGluThrIysThrT 780
QY 1909 -----CTAGCCTTCTTCACTTACTTAACAATTCCTGTGTGATATGTAAGATCAGA 1963
Db 780 hrlleuIeuSerMetleuGluIeuHisIleGlyAsnProPheGlnCytThrCysAspIleGlyA 800
QY 1964 AATTCTGCACTGGCTCAAGAAACAAGACAGTTCTTGTAATGTTGAA----- 2013
Db 800 sPheAspArgTyrrMetAspGlnHis-----leuAsnValIysIleProArgL 816
QY 2014 -----CAATGACATGTGCAACCTGTAAGATGAATACCTCTTATGTTGATTTTA 2068
Db 816 euvAlaPheValIleIeuValaSerProGlyAspGlnArgGlyIysSerIleValSerleuG 836
QY 2069 ATAATCTACCTGTATATGTACAAGAACATCATCATGTGTGCAAGTGTGATGATTTG 2128
Db 836 luleuThrThrCysValSerAspValThrAlaValIleIeuPhePhePheThrPhePheI 856
QY 2129 TGGTATCCACGTGA-----GCATTTCTGATATACACCTTCAATTTTTCAC----- 2172
Db 856 lethrThrMetValMetleuAlaAlaIeuAlaHisIleuPheTyrrTrpAspValTrpP 876

QY 2173 -----CTGATCTATTGCTGCTGTATAAAGTACAGCAGAGAGAAA 2215
Db 876 heIleTyrrAsnValCysleuAlaIysIleIleGlyTyrrArgSerleuSerThrSerGlnT 896
QY 2216 GCATCTATGATGCAATTTGATGATCTTACTCGAGTCAAAAT-----GAGGATGGGTGA 2266
Db 896 hrPheTyrrAspAlaTyrrIleSerTyrrAspThrIysAspAlaSerValThrAspTrpValI 916
QY 2267 GAAATGAGCTGGTAAGAAATTTAGAAAGAGAGAGTGGCCGCC-----TTTCACTCTGCTTC 2323
Db 916 lAsnGluIeuArgTyrrHisleuGluIeuSerArgAspIysAsnValleuIeuCysleuG 936
QY 2324 ACTACAGAGACTTAAATTCCTGTGTGAGCCATTCCTGCAACATCATTCAGAGAGCTTCC 2383
Db 936 lueGlnArgAspTrpAspProGlyIleuAlaIleIleAsnAsnMetGln---SerIleA 955
QY 2384 ACAAGAGCCGGAAGTTATTTGCTGATGCTTACAGACCTTATTCAGAGCCGTTGGTGA 2443
Db 955 snGlnSerIysIysThrValPheValleuThrIysIysTyrr----- 968
QY 2444 TCTTGAATATGAGATTCCTCAAAACATGCGAGTTCTGAGC----- 2484
Db 969 -----AlaIysSerTrpAsnPheIysThrAlaPheTyrrleuAlaIeuG 983
QY 2485 -----AGCCGCTGCGCATCATCTTCAATTCCTTGAAGAGTTGAGA 2527
Db 983 lnsArgleuMetAspArgIleuAsnMetAspValIleIlePheIleIeuGluPheValleuG 1003
QY 2528 AGTCCCTGCTGAGGACAGCAGCTGAATTTGATGCTTTCAGAGAAACACTTACCTGG 2587
Db 1003 lHis-----SerGlnTyrrleuArgleuArgGlnArgIleCysIysSerSerIleleuG 1021
QY 2588 AATGGAGAGCAGATTCCTGCGGAGAGCAGACATCTTTCGAGAGAACTTAATAAGCCCTAT 2647
Db 1021 lntPrProAspAsnProIysAlaGluGlyIeuPheTrpGlnThrIeuArgAsnValVal 1041
QY 2648 TG-----GATGAGAAAGCCTCGAAT 2667
Db 1041 eutrHrgIleuAsnAspSerArgTyrrAsnAsn 1050

RESULT 15
US-10-753-267-30
Sequence 30, Application US/10753267
Publication No. US20050037946A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceutical, Inc.
APPLICANT: Scagliano, Nancy E.
APPLICANT: Healy, Aileen
APPLICANT: Acton, Susan L.
APPLICANT: Galvin, Katherine M.
APPLICANT: Donoghue, Mary A.
APPLICANT: Rodriguez-Way, Amelie
APPLICANT: Tomlinson, James E.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,
10653, 9255, 21668, 17794, 2210, 6169, 10102, 21061, 17662,
1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,
3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,
9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,
44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,
32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,
TITLE OF INVENTION: 42028, 110291, 13886, 13942, 1673, 54946 OR 2419
FILE REFERENCE: MP103-003P1NOMNIM
CURRENT APPLICATION NUMBER: US/10/753, 267
PRIOR APPLICATION NUMBER: 2004-01-08
PRIOR FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: US 60/445, 216
PRIOR FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US 60/448, 036
PRIOR FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: US 60/454, 189
PRIOR FILING DATE: 2003-03-12

```

PRIOR APPLICATION NUMBER: US 60/457,541
PRIOR FILING DATE: 2003-03-25
PRIOR APPLICATION NUMBER: US 60/466,411
PRIOR FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US 60/469,041
PRIOR FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/477,414
PRIOR FILING DATE: 2003-06-10
PRIOR APPLICATION NUMBER: US 60/478,560
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/489,772
PRIOR FILING DATE: 2003-07-24
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 1059
TYPE: PR1
ORGANISM: Homo Sapiens
US-10-753-267-30

Alignment Scores:
Pred. No.: 4,11e-45 Length: 1059
Score: 546.00 Matches: 264
Percent Similarity: 39.32% Conservative: 165
Best Local Similarity: 24.20% Mismatches: 359
Query Match: 10.55% Indels: 304
DB: 17 Gaps: 45

US-09-396-985b-46 (1-2951) x US-10-753-267-30 (1-1059)
QY 162 TCGCATGTCCTCATGCGCTCCATGCGTTCAGAAATGCGAGATGATGCTCCCTG 221
DB 9 SererCyserLeuGlyLysGlnThr-LysLysGlnAsn-----Me 22
QY 222 GCTCGCTGAGTCACTGATCATGCGCTGCTTC-----TCCTGCTGAC 269
DB 22 tPhleuclnserSerMetLeuThrCysilePheleuclnleSerGlyserCysGluLe 42
QY 270 ACCGAGAACTTGAT-----CCCTGCTAGAGTGAAGTTCCTTAAT----- 309
DB 42 uCysalaglulnAsnPheserArGserTyPrOCysaspGluLysGlnAsnAspSe 62
QY 310 -ATTACCTACCAATGCATGCATGCAAGAACTGCAAGAACTGCTATGATTCCTTC 368
DB 62 rValilleaglucySerAsnArgArgLeuGlnGlnValProGlnThrValGlyLysTy 82
QY 369 AACCAAGAACATAGATCTGAGCTTCAACCCCTGGAAGATCTTAAAGACTATGCTTC 428
DB 82 rValThrGluLeuAspLeuSerAsnArgPheileThrileThrAsnGlnSerPheG 102
QY 429 CAATTTTTCAGACTTCAGTGGCTGATTAATCC----- 462
DB 102 nGlyLeuGlnAsnLeuThrLysileAsnLeuAsnHisAsnProAsnValGlnHisGlnAs 122
QY 463 -----AGGTGTGAATTTGAACAATTGAACAATTGAACAAGCATGCGCTT 506
DB 122 nGlyAsnProGlylleGlnSerAsnGlyLeuAsnMleThrAspGlyAlaPheLeuAsnLe 142
QY 507 AACACCCTCTCAACTGATGATGACAGAAACCTTACAGAGTTTTCCTCCAGAGAG 566
DB 142 uLysAsnLeuArgGluLeuLeuLeuGlnAsnGlnLeu-----ProGlnI 158
QY 567 TTTCTCTGAGACTA--ACAAATTAGACAATCTGCTGCTGCTGAGACAAATTTGGCTC 623
DB 158 eProSerGlyLeuProGlnSerLeuThrGlnLeuSerLeuThrAsnAsnIleTyAs 178
QY 624 TCTGAAGAAGCTCCCTTATGACAGCTTATTAACCTTAAAGAACTCAATGCTGCTACA 683
DB 178 nIleThrLysGlnGlylleSerArgLeuIleAsnLeuLysAsnLeuTyLeuAlaTyPAs 198
QY 684 T-----TTTATACATTCCTGTAAGTTA-----CCTGCATATTTTCCAAATCT 725
DB 684 T-----TTTATACATTCCTGTAAGTTA-----CCTGCATATTTTCCAAATCT 725

```

```

DB 198 nCyserTyPheAsnLysValCysGluLysThrAsnIleGluAspGlyValPheGluThrLe 218
QY 726 GACCACTCTATCATGATGATCTTTCTTATTAATCATTAATCAACTATTAATGCAACA 785
DB 218 uThrAsnLeuGluLeuLeuSerLeuSerPheAsnSerLeuSerHisValSerProLysLe 238
QY 786 CTTCAGATTCTTACGTGAATAATCCACAAGTCAATCTCTTTCATGACATGCTTTGAACCC 845
DB 238 uProSerSerLeuLys-----LeuHeLeuSerAsnThrG 251
QY 846 AATTGACTTCATTCAGACCAAGCTTTCAAGGA--ATTAAAGTCCATGAACTGACTCT 902
DB 251 nIleLysTyrlleSerGlnGlnAspPheLysGlyLeuIleAsnLeuThrLeuAspLe 271
QY 903 AAGAGTAAAT-----TTTAAT----- 918
DB 271 uSerGlyAsnCyserProArgCysPheAsnAlaProPheProCysValProCysAspGlyG 291
QY 919 -----AGCTCAATATTAATGAATAATCTGCTCAAAACCTGGCTGTTTACAC----- 966
DB 291 yAlaSerIleAsnIleAspArgPheAlaPheGlnAsnLeuThrGlnLeuArgTyrlleAs 311
QY 967 -----GTCCATCGTTGATCTTGGAGAAATTAAAGATGAAGAAATCT 1010
DB 311 nLeuSerSerThrSerLeuArgLysIleAsnAlaAlaTrpPheLysAsnMetProHisLe 331
QY 1011 GGAATTTTGA-----CCCTTATTCATGAAAGA----- 1041
DB 331 uLysValLeuAspLeuGlnPheAsnTyrlleuValGlyLysIleAlaSerGlyAlaPheLe 351
QY 1042 -----CTATGATGATGACCATTAATGATGATTCAGTTCAATTAACATA 1079
DB 351 uThrMetLeuProArgLeuGlnIleLeuAspLeuSerPheAsnTyrlleLysGlySerTy 371
QY 1080 T-----ACAAATGATTTTCA----- 1095
DB 371 rProGlnHisIleAsnIleSerArgAsnPheserTyrlleLeuSerLeuArgAlaLeuHis 391
QY 1096 -----GATGATATTTGTTAAGTTCCATGCTT 1121
DB 391 sLeuArgGlyTyrlleValPheGlnGlnLeuArgLysAspAspPheGlnProLeuMetGlnLe 411
QY 1122 GCGCAATGTTCTCATGATGCTGCGCAGGATGATATTAATAATATCATGAGATGTTCC 1181
DB 411 uProAsnLeuSerThrIleAsnLeuGlylleAsnPhelleLysGlnIleAsp----- 428
QY 1182 TAAACATTTTCAA-----TGCAATCCCTTATCAATCATT----- 1215
DB 429 -----PheLysLeuPheGlnAsnPheserAsnLeuGlnIleIleTyrlleuSerGluAs 446
QY 1216 -----AGATGTCACTAAGCAGTTTCCA 1238
DB 446 nArgIleSerProLeuValLysAspThrArgGlnSerTyrlleAsnSerSerPheG 466
QY 1239 ACTGTGATC-----TA 1250
DB 466 nArgHisIleLeuArgLysArgArgSerThrAspPheGlnPheAspProHisSerAsnPhety 486
QY 1251 CCCCTTCTT-----AAAGTTTGACTTT 1273
DB 486 rHisPheThrArgProLeuIleLysProGlnCysAlaAlaTyrlleGlyLysAlaLeuAspLe 506
QY 1274 AACTATGAACAA-----GGGTCTATCAGTTTAAAGATG----- 1310
DB 506 uSerLeuAsnSerIlePhePheIleGlyProAsnGlnPheGlnAsnLeuProAspIleAl 526
QY 1311 -----GC 1312
DB 526 aCyLeuAsnLeuSerAlaAsnSerAsnAlaGlnValLeuSerGlyThrGlnPheSerAl 546
QY 1313 CTTACCAAGTCTCAGCTATGATCTTATGATGAATAATGCACTGAGTTAGTGTGCTG 1372
DB 546 alleProHisValLysTyrlleuAspLeuThrAsnAsnArgLeuAspPheAspAsnAlaLe 566

```

```

Qy 1373 TTCTATTCGATTTGGGAACAAAGCCTGAGACATTAGACCTTCAATGGTGC 1432
Db 566 rAlLeuThrGluLeu-----SerAspLeuGluValLeuAspLeuSerTyrAsnSerHi 584
Qy 1433 CATCATTAATGAGTGC-----AATTTCAATGGTCT 1462
Db 584 sTyPheArgTrIleAlaGluValThrHiSerHiLeuGluPheTrIleGlnAsnPheThrAsnLe 604
Qy 1463 AGAA-----GAGCTGCAGACCTCGATTTTTCAGACACTTACTTAAAGGCTCAG 1516
Db 604 uLyValLeuAsnLeuSerHiAsnAsnTrIleTyrThrLeu-ThrAspLeuTyrAsnLeuG 624
Qy 1517 AATTCGAGCCTTCTATTCCTTGAAGAACTTATTC-----CTTGACATCT 1564
Db 624 luseTyr-----SerLeuValGluLeuValPheSerGlyAsnArgLeuAspIleL 641
Qy 1565 CTTAATACACACCAAAATTTGACTTCGATGGTATATTTCTTGCTTGACAGTCTCAACA 1624
Db 641 eUTrPAsnAspAspAspAsnArgTyrTrIleSerTrIlePheGlyLeuLysAsnLeuThra 661
Qy 1625 CATTAATAATGGCTGGCAATCTTTCAAGAACAACCCCTTCAATGTCTTTGCAAC- 1683
Db 661 rGLeuAspLeuSerLeuAsnArgLeuLys--HisIleProAsnGluAlaPheLeuAsnL 680
Qy 1684 --ACAACAACCTTGACATTCCTTGATCCTTAAATGCAATTTGGAACAATATCTTGGG 1741
Db 680 euProAlaSerLeuThrGluLeuHisIleAsnAspAsnMetLeuLysPhePheAsnTrpT 700
Qy 1742 GGGTATTTGACACCCCTCATAGACTCTCAATATTAAATATAGTACACAACATCTATTGT 1801
Db 700 hrLeuLeuGlnGlnPheProArgLeuGluLeuLeuAspLeuArgGlyAsnLysLeuLep 720
Qy 1802 TTTTGAATCATCCCATTAATAACAGCTGTATTCCTTACAGACCTTATGACGTTTCA 1861
Db 720 heLeuThrAspSerLeuSerAspPheThrSerSerLeuArgThrLeuLeuLeuSerHiSa 740
Qy 1862 ATCGCATTA-----G 1870
Db 740 snAlGllLeSerHiSleuProSerGlyPheLeuSerGluValSerSerLeuLysHISleuA 760
Qy 1871 AGACATCTAAAGAAATCTGCAACATTTTCCAAAGAGT----- 1908
Db 760 sPLeuSerSerAsnLeuLeuLysThrIleAsnLysSerAlaLeuGluThrLysThrThrt 780
Qy 1909 -----CTAGCCTTCTTCAATCTTACTAACAATCTGTGCTTGATATGTAACATCAGA 1963
Db 780 hrLysLeuSerMetLeuGluLeuHisGlyAsnProPheGluCysThrCysAspIleGlyA 800
Qy 1964 AATTCCTGAGTGGGTCAAGGAACAAGACAGATTCTTGTAATGTGTA----- 2013
Db 800 spPheArgArgTrIleMetAspGluHis-----LeuAsnValLysIleProArgL 816
Qy 2014 -----CAATGACATGTGCCAACACTGTAGAGATGAAATACCTCTTAGTGTGATTTTA 2068
Db 816 euValAspValIleCysAlaSerProGlyAspGlnArgGlyLysSerTrIleValSerLeuG 836
Qy 2069 ATAATTCACCTGTATATGTACAAGACATCATCAGTGTGACGTGCTGATGTG 2128
Db 836 luleuThrThrCysValSerAspValThrAlaValIleLeuPhePheThrPhePheI 856
Qy 2129 TGGTATCCACTGTA-----GCATTTCTGATATACCACTTCAATTTTCA----- 2172
Db 856 leThrThrMetValMetLeuAlaAlaLeuAlaHisHisLeuPheTyrTrPAspValTrp 876
Qy 2173 -----CTGATCTTAATGTGCTGTGCTGTAAGAAAGTACAGACAGAGAAA 2215
Db 876 heIleTyrAsnValCysLeuAlaLysTrIleLysGlyTyrArgSerLeuSerThrSerGlnT 896
Qy 2216 GCATCTATGATGCAATTTGTGATCTTCTGAGTCAGAAAT-----GAGACTGGGTGA 2266
Db 896 hrPheTyrAspAlaLysTrIleSerTyrAspThrLysAspAlaSerValThrAspTrValI 916

```

```

Qy 2267 GAATGAGCTGTGTAAGAAATTTAGAGAAGAGTCCCCC-----TTTCACTGTGCTTC 2323
Db 916 leAsnGluLeuAlaGlyTyrHisLeuGluLysSerTrArgAspLysAsnValLeuLeuCysLeuG 936
Qy 2324 ACTACAGACATTTATTTCTGTGTAGCCCAATGTGTCGCAACATCATCATCAGAGAGCTTCC 2383
Db 936 lueGluArgAspTrAspProGlyLeuAlaIleIleAspAsnLeuMetGln---SerIleA 955
Qy 2384 ACAAGACCGGAAGTATTTGTGTAGTGTGTCAGACCTTATTCAGAGCGCTTGCTGA 2443
Db 955 enGlnSerLysLysThrValPheValLeuThrLysLysTyr----- 968
Qy 2444 TCTTTGAATATGAGATTGCTCAACATGACAGATTCTGAGC----- 2484
Db 969 -----AlaLysSerThrAsnPheLysThrAlaPheTyrLeuAlaLeuG 983
Qy 2485 -----AGCCGCTTGCAATCATCTTCAATTTGTCCTTGAAGAGTTGAGA 2527
Db 983 lnrGLeuMetAspGluAsnMetAspValIleIlePheIleLeuLeuGluProValLeuG 1003
Qy 2528 AGTCCCTGCTGAGGACAGAGTGGAAATTGTATGCGCTTTAGCAGAAACACTTACCTGG 2587
Db 1003 lnrHis-----SerGlnTyrLeuArgLeuArgGlnArgIleCysLysSerSerIleLeuG 1021
Qy 2588 AATGGAGACAATCTCTCTGGGAGGACACATCTTCTGAGAGAAGATTAAATGCCCCAT 2647
Db 1021 lnrTrProAspAsnProLysAlaGluGlyLeuPheTrpGlnThrLysArgAsnValVal 1041
Qy 2648 TG-----GATGAAAAGCTTCGAAAT 2667
Db 1041 eutThrGluAsnAspSerArgTyrAsnAsn 1050

```

Search completed: March 30, 2005, 04:43:24
 Job time : 193.022 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 30, 2005, 03:00:48 ; Search time 628 Seconds
(without alignments)
20023.170 Million cell updates/sec

Title: US-09-396-985B-47
Perfect score: 33065
Sequence: 1 tccctactctcttccacat.....catgaabdcabdcabdc 18989

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1407402 seqs, 331100923 residues
Total number of hits satisfying chosen parameters: 2814804

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ n2p model -DEV=xlh
-O=/cgn2_1/USPRO_pool/US09396985/runat_28032005.155745_21245/app_query.fasta_1.85098
-DB=Published Applications_AA -OFW=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPEL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09396985@cgn 1.1 3955 @runat_28032005.155745_21245
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSELOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result

Query

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	3903.5	11.8	799	10	US-09-950-041-8	Sequence 8, Appli
2	3903.5	11.8	799	14	US-10-128-166-7	Sequence 7, Appli
3	3903.5	11.8	799	16	US-10-732-563-8	Sequence 8, Appli
4	3903.5	11.8	799	16	US-10-732-796A-8	Sequence 8, Appli
5	3903.5	11.8	837	15	US-09-950-041-26	Sequence 26, Appli
6	563.5	1.7	661	15	US-10-038-854-135	Sequence 135, App
7	563.5	1.7	661	15	US-10-037-417-107	Sequence 107, App
8	561.5	1.7	784	10	US-09-950-041-4	Sequence 4, Appli
9	561.5	1.7	784	15	US-10-456-947-46	Sequence 46, Appli
10	560.5	1.7	784	14	US-10-095-627-12	Sequence 12, Appli
11	560.5	1.7	784	16	US-10-732-563-4	Sequence 4, Appli
12	560.5	1.7	784	16	US-10-732-796A-4	Sequence 4, Appli
13	560.5	1.7	784	17	US-10-741-600-1390	Sequence 1390, Ap
14	560.5	1.7	784	17	US-10-741-600-1391	Sequence 1391, Ap
15	557.5	1.7	784	13	US-10-145-014-23	Sequence 23, Appli
16	543.5	1.6	1032	10	US-09-954-887B-192	Sequence 192, App
17	543.5	1.6	1032	14	US-10-272-502A-31	Sequence 31, Appli
18	543.5	1.6	1032	15	US-10-407-952-32	Sequence 32, Appli
19	536	1.6	1050	10	US-09-954-887B-175	Sequence 175, App
20	536	1.6	1050	14	US-10-272-502A-22	Sequence 22, Appli
21	536	1.6	1050	15	US-10-407-952-26	Sequence 26, Appli
22	529	1.6	661	13	US-10-114-893-10	Sequence 10, Appli
23	529	1.6	661	15	US-10-038-854-134	Sequence 134, Appli
24	519	1.6	1032	9	US-09-950-041-37	Sequence 37, Appli
25	519	1.6	1040	9	US-09-864-761-18325	Sequence 38325, A
26	519	1.6	1041	10	US-09-954-887B-184	Sequence 184, App
27	519	1.6	1041	10	US-09-954-887B-186	Sequence 186, App
28	519	1.6	1041	14	US-10-272-502A-26	Sequence 26, Appli
29	519	1.6	1041	15	US-10-407-952-28	Sequence 28, Appli
30	519	1.6	1041	16	US-10-732-563-16	Sequence 16, Appli
31	519	1.6	1041	16	US-10-732-796A-16	Sequence 16, Appli
32	518	1.6	1041	9	US-09-168-978-3	Sequence 3, Appli
33	518	1.6	1041	9	US-09-978-285A-498	Sequence 498, App
34	518	1.6	1041	9	US-09-978-697-198	Sequence 498, App
35	518	1.6	1041	9	US-09-978-192A-498	Sequence 498, App
36	518	1.6	1041	9	US-09-999-832A-498	Sequence 498, App
37	518	1.6	1041	9	US-09-978-189-498	Sequence 498, App
38	518	1.6	1041	10	US-09-978-608A-498	Sequence 498, App
39	518	1.6	1041	10	US-09-978-585A-498	Sequence 498, App
40	518	1.6	1041	10	US-09-978-191A-498	Sequence 498, App
41	518	1.6	1041	10	US-09-978-403A-498	Sequence 498, App
42	518	1.6	1041	10	US-09-978-564A-498	Sequence 498, App
43	518	1.6	1041	10	US-09-999-813A-498	Sequence 498, App
44	518	1.6	1041	10	US-09-981-915A-498	Sequence 498, App
45	518	1.6	1041	10	US-09-978-824-498	Sequence 498, App

ALIGNMENTS

RESULT 1
US-09-950-041-8
; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
GENERAL INFORMATION:
APPLICANT: Hardman, Gerard T.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Ho, Stephen W.K.
TITLE OR INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
FILE REFERENCE: DX0724XK1
CURRENT APPLICATION NUMBER: US/09/950, 041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293

```
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-8

Alignment Scores:
Pred. No.: 0 Length: 799
Score: 3903.50 Matches: 757
Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Indels: 9
DB: 10 Gaps: 1

US-09-396-985b-47 (1-18989) x US-09-950-041-8 (1-799)
QY 12216 TCAATGCTTTTATTC-----TGTAGGTGTAATC 12248
Db 31 SerTySerPheSerPheProGluLeuGlnValLeuAspLeuSerArgCysGluIle 50
QY 12249 CAGCAATTGAAGTGGGCGCATTCAGAGCCTTAAGCCCTCTCTCACTTAATTTGACA 12308
Db 51 GlnThrIleGluIleGluIleGluIleGluIleGluIleGluIleGluIleGluIle 70
QY 12309 GGAACCCCATCGAGGTTTACCGCTGGAGCCTTTCTGTGACATTCAGATTACAGAA 12368
Db 71 GlyAsnProIleGlnSerIleValIleGluIleValIlePheSerGlyLeuSerSerIleGlnIlys 90
QY 12369 CTGGGCTGTGAGACAAATCTAGCATCTGTAGAACTTCCCATTTGACATCTCAA 12428
Db 91 LeuValAlaValAlaGluThrAsnLeuAlaSerLeuGluIleAsnProIleGlyIleLeuIys 110
QY 12429 ACTTGAAGAACTTAATGTGGCTCAACAATCTTAATCCAACTTTCAATTCCTGAGAT 12488
Db 111 ThrLeuIysGluIleAsnValAlaIleAsnLeuIleGlnSerPheIysLeuProGluIyr 130
QY 12489 TTTTCTATCTGACCAATCTAGAGCATTTGAGACCTTTCAGCAACAGATTCAAGTATT 12548
Db 131 PheSerAsnLeuThrAsnLeuGluIleIleAsnProIleGlnSerSerAsnIysIleGlnSerIle 150
QY 12549 TATTGACAGACTTGCAGGCTTCTACATCAAAATGCCCTACTCAATCTCTTTAGACCTG 12608
Db 151 TyrCysThrAspLeuArgValLeuIleGlnMetProLeuLeuAsnLeuSerLeuAspLeu 170
QY 12609 TCCCTGAACCTTAAGAACTTTATCCACAGGCTGATTAAGAAATTAAGGCTTCATAG 12668
Db 171 SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheIysGluIleArgLeuIleIlys 190
QY 12669 CTGACTTAAGAAATTAATTTGATAGTTAATGAATGAAGAACTTGATCAAGGCTG 12728
Db 191 LeuThrLeuAsnGluAsnAsnPheAsnSerLeuAsnValIleCysIleGlnIleGlu 210
QY 12729 GCTGGTTTGAAGTCCATCGTTGGTTCTGGAGAAATTTAGAAATGAAGAACTTGGA 12788
Db 211 AlaGlyLeuGluValAlaIleArgLeuValLeuGlyGluPheArgAsnGluGlyAsnLeuIu 230
QY 12789 AAGTTTGAACAATCGCTCTAGAGGCGCTGTGCAATTTGACATTTGAAGAAATTCGAGATTA 12848
Db 231 LysPheAspIysSerAlaLeuGluIleGluCysAsnLeuThrIleGluGluPheArgLeu 250
QY 12849 GCATCTAGAGTACTACTCGATGATATATTATTTAGTATTGTTTGAACAATGTT 12908
Db 251 AlaTyrLeuAspIyrTyrLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnVal 270
QY 12909 TCTTCAATTTCCCTGGTGAAGTGTGACTATTGAAGGTTAAAGACTTTTCTTATTAATTC 12968
```

```
Db 271 SerSerPheSerLeuValSerValThrIleGluArgValIysAspPheSerTyrAsnPhe 290
QY 12969 GAGTGGCAACTTTAGATTAAGTAACTGAATTTGACAGATTCCCACTTGAACATC 13028
Db 291 GlyTyrGlnIleIleGluIleValIleAsnCysIysPheGlyGlnPheProThrLeuIysLeu 310
QY 13029 AAATCTCTCAAAAGGCTTACTTTCACTTCCCAACAAAGTGGGAATGCTTTTCAGAAATT 13088
Db 311 LysSerLeuIysArgLeuThrPheThrSerAsnIysGlyGlyAsnAlaPheSerGluVal 330
QY 13089 GATCTACCAAGCCTTGATTTCTAGATCTCAGTAGAAATGCTTGATTTCAAAAGTTTC 13148
Db 331 AspLeuProSerLeuGluIlePheLeuAspLeuSerArgAsnIleIysLeuSerPheIysGlyCys 350
QY 13149 TGTTCCTCAAGATTTTGGGACCAACAGCCTTAAAGTATTAGATCGACCTCAATGCT 13208
Db 351 CysSerIleSerAspPheGlyIyrThrSerLeuIysTyrLeuAspLeuSerPheAsnGly 370
QY 13209 GTTATTACCATGAGTTCAAACTTCTGGGCTTAGAACCACTAGAACATCTGATTTCCAG 13268
Db 371 ValIleThrMetSerSerAsnPheLeuGlyLeuGluGlnIleGluIleIleLeuAspPheGln 390
QY 13269 CATTCCAATTTGAACAAATGAGTGAATTTCAATTCCTATCTCATCAGAAACCTCAT 13328
Db 391 HisSerAsnLeuIysGlnMetSerGluPheSerValPheLeuSerLeuArgAsnLeuIle 410
QY 13329 TACCTTGACATTTCTCATCTACACAGAGTTGCTTCAATGGCAATCTTCAATGGCTTG 13388
Db 411 TyrLeuAspIleSerIleSerIleSerIleSerIleSerIleSerIleSerIleSerIle 430
QY 13389 TCCAGTCCGAGTCTTGAATAATGCTGGAGCAATTTCTTCCAGAGAAACTTCTCCAGAT 13448
Db 431 SerSerLeuIleValLeuIysMetAlaGlyAsnSerPheGlnIleAsnProIleAsp 450
QY 13449 ATCTTCAAGAGCTGAGAACTTGACCTTCTGACCTCTCTCACTGATCACTGAGACAG 13508
Db 451 IlePheThrGluIleArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGluGln 470
QY 13509 TTGCTCCACAGACTTAACTCACTCCAGTCTTCAAGTAAATAGGACCAAC 13568
Db 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
QY 13569 AACTTCTTTCATTTGATGATGATGTTTCTTATTAAGTGTGAACTCCCTCAGGTTCTTGAT 13628
Db 491 AsnPhePheSerLeuAspThrPheProTyrIleCysIleAsnSerLeuGlnValLeuAsp 510
QY 13629 TACAGTCTCATCATCATATGACTTCCAAAAAACGGAATCTACAGCATTTTCCAAGTAT 13688
Db 511 TyrSerLeuAsnHisIleMetThrSerIysGlnIleGluGlnIleAsnProSerSer 530
QY 13689 CTAGCTTTCTTAAATCTTACTCAGAAATGACTTTGCTTGTGAACCCAGAGTTTC 13748
Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGluIleGlnSerPhe 550
QY 13749 CTGCAATGATCAAGACGACGAGGAGCTTGGTGGAGTTGGAACGAATGGAATGTGCA 13808
Db 551 LeuGlnThrIleIysAspGlnArgGlnLeuLeuValGluValGluArgMetGluCysAla 570
QY 13809 ACACCTTCAGATTAAGCAGGCGATGCTGTGCTGATGATTGAATATCACCTGTCAATGAT 13868
Db 571 ThrProSerAspIysGlnIlyMetProValLeuSerLeuAsnIleThrCysGlnMetAsn 590
QY 13869 AAGACCATCAATGGTGTGGGTCTCAGTGTGCTGTAGATATCTGTAGACGTTCTG 13928
Db 591 LysThrIleIleGlyValSerValLeuSerValLeuValValSerValAlaAlaValLeu 610
QY 13929 GTCTATAGTATTCTATTTTCACTGATGCTTCTGCTGGCTGCAATTAAGTATGATGAGGT 13988
Db 611 ValTyrIysPheTyrPheIleIleMetLeuLeuAlaCysIleIleTyrGlyArgGly 630
QY 13989 GAAACATCTATGATGCTTGTGTTATCTCAAGCCAGATGAGACTGGGTAAAGAAAT 14048
Db 631 GluAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGluAspTyrValArgAsn 650
```

```

QY 14049 GAGCTAGTAAGATTTAGAAAGAGGGTGCCTCCATTTCAGTCTGCGCTTCACTACAGCA 14108
|
|
|
Db 651 GluLeuValIysAsnLeuGluGluGlyValProProhPheGlnLeuCybLeuHisTyrArg 670
|
|
|
QY 14109 GACTTTATTCCTCCGGGTGTGGCCATTGCTGCCAATCATCATGAAAGTTTCCATPAAGC 14168
|
|
|
Db 671 AspheIleProGlyValAlaIleAlaAlaAsnIleIleHisGluGlyPheHisIleYser 690
|
|
|
QY 14169 CGAAGGAGATTTGTGTGTGTGTCCAGACATTCATCCAGAGCCCTGGTGTATCTTTGAA 14228
|
|
|
Db 691 ArgIysValIleValIleValIleSerGlnHisPheIleGlnSerArgTyrCybIlePheGlu 710
|
|
|
QY 14229 TATGAGATTTGCTAGACCTTGAGCAGTGTCTGAGCAGTGTGTGTGTATCTTCATGTC 14288
|
|
|
Db 711 TyrIleuIleAlaGlnIleHisTyrPheGlnPheLeuSerSerArgIleIleIlePheIleVal 730
|
|
|
QY 14289 CTGCAAGAGTGTGAGAAAGACCTGTCTCAGGAGCAGAGTGTGAGCTGTATCCGCTTCTCAGC 14348
|
|
|
Db 731 LeuGlnIysValIleGluYsThrLeuLeuArgGlnGlnIleValIleuYsArgLeuLeuSer 750
|
|
|
QY 14349 AGGAACACTTATCCCTGAGCTGTGAGAGACAGTGTCTCTGGGGCGGCACATCTTCTGAGACGA 14408
|
|
|
Db 751 ArgAsnThrTyrLeuGluTyrPheGluAspSerValLeuGlyArgHisIlePheTyrArgArg 770
|
|
|
QY 14409 CTCGAAAGAGCCCTGCTGATGTATAATCATGGAATCCAGAAAGACAGTGGGTACAGGA 14468
|
|
|
Db 771 LeuArgIysAlaLeuLeuAspGlyIlySerTyrPheAsnProGluGlyThrValIleGlyThrGly 790
|
|
|
QY 14469 TGCATTTGGCAGAGACCAATCTATC 14495
|
|
|
Db 791 CysAsnTyrPheGlnIleuAlaThrSerIle 799
|
|
|
RESULT 2
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US20030077279A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAJAVASHISTH, TRIPATHI
; APPLICANT: SHAH, PREMIDAN K.
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; FILE REFERENCE: 81476-0255398
; CURRENT APPLICATION NUMBER: US/10/128,166
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 799
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-128-166-7

Alignment Scores:
Pred. No.: 0 Length: 799
Score: 3903.50 Matches: 757
Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Indels: 9
DB: 14 Gaps: 1

US-09-396-985b-47 (1-18989) x US-10-128-166-7 (1-799)
QY 12216 TCAATGCTTTTATTTC-----TGTAGGTGTAATC 12248
|
|
|
Db 31 SerTyrSerPhePheSerPheProGluLeuGlnValIleuAspLeuSerArgCybGluIle 50
|
|
|
QY 12249 CAGCAATTGAAGATGGGAGCATATCAGAGCTTAAGCACTCTTACTTAATTTGACA 12308
|
|
|
Db 51 GlnThrIleGluAspGlyAlaTyrGlnIleSerLeuSerHisLeuSerThrLeuIleLeuThr 70
|
|
|
QY 12309 GGAACCCCATCCAGAGTTTATGCTGTGGAGCTTTTCTGAGTATCAAGTTTACAGAG 12368
|
|
|

```

```

Db 71 GlnAsnProIleGlnSerLeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIys 90
|
|
|
QY 12369 CTGTGGCTGTGGAGACAAATCTAGCATCTCTTAAGAACTTCCCATTTGACATCTCAA 12428
|
|
|
Db 91 LeuValAlaValGluThrAsnLeuAlaSerLeuGlnAsnProIleGlyHisLeuIys 110
|
|
|
QY 12429 ACTTGAAGAAGCTTAATGTGGCTCACAACTTCAATCTTCAATCTTCAATCTGAGTAT 12488
|
|
|
Db 111 ThrLeuYsGluLeuAsnValAlaHisAsnLeuIleGlnSerPheIysLeuProGluTyr 130
|
|
|
QY 12489 TTTTCTAATCTGACCAATCTAGACACTTGGACCTTTCCAGCAACAAGATTCAAGTAT 12548
|
|
|
Db 131 PheSerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnIysIleGlnSerIle 150
|
|
|
QY 12549 TATTGCACAGACTGGGGGTCTTACATCAAAATGCCCTACTCAATCTCTCTTGAAGCTG 12608
|
|
|
Db 151 TyrCybThrAspLeuAspValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 170
|
|
|
QY 12609 TCCCTGAACCTTATGAATTTATGCAACAGTGTCAATTTAAGAAATTAAGGCTTCATPAG 12668
|
|
|
Db 171 SerLeuAsnProMetAsnPheIleGlnProGlyAlaPheIysGluIleArgLeuHisIys 190
|
|
|
QY 12669 CTGACTTTAAGAAATTAATTTGATATGTTAAATGTAAATGAATCTGTATTCAGAGTCTG 12728
|
|
|
Db 191 LeuThrLeuArgAsnAsnPheAspSerLeuAsnValMetIysThrCybIleGlnGlyLeu 210
|
|
|
QY 12729 GCTGCTTTAAGATGTCATCGTTTGTCTGTGGAGAAATTTAGAAATGAAGAACTTGAA 12788
|
|
|
Db 211 AlaGlyLeuGlnValHisArgLeuValLeuGlyGluPheArgAsnGluIysAsnLeuGln 230
|
|
|
QY 12789 AAGTTTGAACAATGCTGTCTAGAGAGGCTGTGCAATTTGACATTTGAAGAATTCGATTA 12848
|
|
|
Db 231 LysPheAspIysSerAlaLeuGluGlyLeuCybAsnLeuThrIleGluGluPheArgLeu 250
|
|
|
QY 12849 GCATACTTGAAGTACTTACCTCGATGATATTAATGACTTAATTTAATGTTTGAACAATGTT 12908
|
|
|
Db 251 AlaTyrLeuAspTyrTyrLeuAspAspIleIleAspLeuPheAsnCybLeuThrAsnVal 270
|
|
|
QY 12909 TCTTCATTTTCCCTGTGAGTGTGACTATTTGAAGAGTAAAGACTTTTCTTAATATTC 12968
|
|
|
Db 271 SerSerPheSerLeuValSerValThrIleGluIysValIysAspPheSerTyrAsnPhe 290
|
|
|
QY 12969 GGAATGCAACATTTAAGATTAAGTTAACTGAATTTGACAGGTTCCCAACTTGAATCTC 13028
|
|
|
Db 291 GlyTyrGlnHisLeuGluLeuValAsnCybLysPheGlyGlnPheProHisLeuIysLeu 310
|
|
|
QY 13029 AAATCTCTCAAAAGGCTTACTTTCATCTTCACTCAACAAAGTGGGAATGCTTTTTCAGAAATT 13088
|
|
|
Db 311 LysSerLeuIysArgLeuThrPheThrSerAsnIysGlyGlyAsnAlaPheSerGluVal 330
|
|
|
QY 13089 GATCTCAACAAAGCTTGAGTTTCTAGATCTCAGTGAAGAAATGGCTTGAAGTTTCAAGTTTC 13148
|
|
|
Db 331 AspLeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheIysGlyCys 350
|
|
|
QY 13149 TGTTCGAAGTATTTTGGGACACACAGGCTAAAGTATTTAGATCGAGGTTCAATGGT 13208
|
|
|
Db 351 CysSerGlnSerAspPheGlyThrThrSerLeuIysTyrLeuAspLeuSerPheAsnGly 370
|
|
|
QY 13209 GTTATTACATGAGTCAAACTTCTGGGCTTGAACAACTAGAACTGATTTTCAG 13268
|
|
|
Db 371 ValIleThrMetSerSerAsnPheLeuGlyLeuGlnGlnIleuGlnHisLeuAspPheGln 390
|
|
|
QY 13269 CATTCGAATTTGAACAATAGAGTATTCAGTATTCCTATCATCTCAAGAACTCAATT 13328
|
|
|
Db 391 HisSerAsnLeuIysGlnMetSerGluPheSerValPheLeuSerLeuArgAsnLeuIle 410
|
|
|
QY 13329 TACTTGACATTTCTCATCTACACACAGAGTGTTCATAGGCACTTCATAGGCTTG 13388
|
|
|
Db 411 TyrLeuAspIleSerHisThrHisThrArgValAlaPheAsnGlyIlePheAsnGlyLeu 430
|
|
|
QY 13389 TCCAGTCTCCAGAGCTTTGAATATGGCTGTGCAATTTCTTCCAGAAAACTTCCTTCAGAT 13448
|
|
|

```

Db 431 SerSerLeuGluValLeuLysMetAlaGlyAsnSerPheGlnGluAsnPheProAsp 450
QY 13449 ATCTTCACAGAGCTGAGAACTTGAACCTTCTGAGACCTCTCTAGTTCTCACTGGAGACAG 13508
Db 451 IlePheThrGluLeuAsnLeuThrPheLeuAspLeuSerGlnGlnLeuGln 470
QY 13509 TTGTCTCCACAGACATTAATCACTCTCCAGTCTTCAAGTACTTAATTAATGAGCACAC 13568
Db 471 LeuSerProThrAlaPheAsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsn 490
QY 13569 AACTCTTTTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 13628
Db 491 AsnPheSerSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValLeuAsp 510
QY 13629 TACAGTCTCATATCAATATGATCTTCAAAAACAGAACTATGACGATTTTCCAGAGT 13688
Db 511 TyrSerLeuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPheProSerSer 530
QY 13689 CTAGCTTTCTTAAATCTTAACTCAGAAATGATGATGATGATGATGATGATGATGATGAT 13748
Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPhe 550
QY 13749 CTGCAATGATGATCAAGACAGAGGAGCTCTTGAGTGAAGTTGAACGAATGGAATGTGA 13808
Db 551 LeuGlnThrPheLysAspGlnAspGlnLeuValGlnValGlnAspMetGlnCysAla 570
QY 13809 AACCTTCAATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 13868
Db 571 ThrProSerAspLysGlnGlnLysMetProValLeuSerLeuAsnHisIleThrCysGlnMetAsn 590
QY 13869 AAGACATCATGAGTGTGAGGAGCTCTCAGTGTGCTTGAATGATGATGATGATGATGATGAT 13928
Db 591 LysThrIleIleGlnValSerValLeuSerValLeuValValSerValAlaValLeu 610
QY 13929 GTCTAATAGTTCTAATTTTCACTGATGCTTCTTGCTGCTGATAAAGTATGATGAGT 13988
Db 611 ValTyrLysPheTyrPheHisIleMetLeuLeuAlaGlyCysIleLysTyrGlnLysArg 630
QY 13989 GAAACATCTATGATGCTTTTGTATTTATCTCAAGCCAGATGAGACTGGGTAAAGAAAT 14048
Db 631 GluAsnHisLysAspAlaPheValIleTyrSerSerGlnAspGlnAspThrValAlaAsn 650
QY 14049 GAGCTAATAAAGATTTAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 14108
Db 651 GluLeuValLysAsnLeuGlnGlnValProProPheGlnLeuCysLeuHisTyrArg 670
QY 14109 GACTTATTCCTCCGGTGTGGCCATGTGTGCCAATCATTCATGAAAGTTTCCATAAAGC 14168
Db 671 AspPheIleProGlnValAlaIleAlaAlaAsnIleIleHisGlnGlnPheHisLysSer 690
QY 14169 CGAAGGTGATGT 14228
Db 691 ArgLysValIleValValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGln 710
QY 14229 TATGAGATTTGCTGAGCTGAGCAATTTCTGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 14288
Db 711 TyrGlnIleAlaGlnHisThrPheGlnPheLeuSerSerArgAlaGlyIleIlePheHisLys 730
QY 14289 CTGCAAGAGTGAAGAAAGCCCTGTCTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 14348
Db 731 LeuGlnLysValGlnLysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSer 750
QY 14349 AGGAACACTTACCTGAGAGTGGGAGAGAGAGTCTCTGGGGCCGGACATTTTGGAGACGA 14408
Db 751 ArgAsnHisTyrLeuGlnTyrPheGlnAspSerValLeuGlnArgHisIlePheThrPheArg 770
QY 14409 CTCGAAAAGCCCTGCGAGATGTAATCATGAAATCAGAAAGGAAAGAGGAGGAGGAGGAGGAG 14468
Db 771 LeuArgLysAlaLeuLeuAspGlnLysSerThrAsnProGlnGlnHisValGlnLysThrGly 790
QY 14469 TGCATTTGCGAGAGAGCAATCTATC 14495
Db 791 CysAsnThrPheGlnGlnAlaThrSerIle 799

RESULT 3
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Pink, Jason R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 58183W003
; CURRENT APPLICATION NUMBER: US/10/732,563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-732-563-8
Alignment Scores:
Pred. No.: 0 Length: 799
Score: 3903.50 Matches: 757
Percent Similarity: 98.57% Conservative: 1
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 11.81% Indels: 9
DB: 16 Gaps: 1
US-09-396-985b-47 (1-18989) x US-10-732-563-8 (1-799)
QY 12216 TCAATGCTTTTATTTATCC-----TGTAGGTGGAATC 12248
Db 31 SerTyrSerPhePheSerPheProGlnLeuGlnValLeuAspLeuSerArgCysGlnIle 50
QY 12249 CAGACATTTAGAGATGGGAGATATCAGAGCTTAAGCCACTCTTCACTTAATATTTGACA 12308
Db 51 GlnThrIleGlnAspGlnAlaTyrGlnSerLeuSerHisIleuSerThrLeuIleLeuThr 70
QY 12309 GAAACCCCATCCAGAGTTTGAAGCCCTGGAGGCTTTTCTGTGACTATTAAGTTTACAGAG 12368
Db 71 GlyAsnProIleGlnSerLeuAlaLeuGlnAlaPheSerGlyLeuSerSerLeuGlnLys 90
QY 12369 CTGTGGCTGTGGAGCAAACTTAGACATCTTAGAGAACTTCCCATTTGAGACATTCGAA 12428
Db 91 LeuValAlaValGlnThrAsnLeuAlaSerLeuGlnAsnPheProIleGlnHisLeuLys 110
QY 12429 ACTTTGAAGAACTTAATGTGGCTCACAATCTTAATCCAACTTTTCAATTAACCTGAGTAT 12488
Db 111 ThrLeuLysGlnLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGlnTyr 130
QY 12489 TTTTCTAATGTAGCAATCTTAGAGCACTTGGACCTTCCAGCAAAAGATTTCAAGATTT 12548
Db 131 PheSerAsnLeuThrAsnLeuGlnHisIleAspLeuSerSerAsnLysIleGlnSerIle 150
QY 12549 TATTGACAGACTTGGGGGTTTACATCAATGCAATGCCCTACTCAATCTCTTTAGACCTG 12608
Db 151 TyrCysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeu 170
QY 12609 TCCCTGAACCTTGAACCTTATATCAACAGGTGATTTAAAGAAATTAAGCTTCAATAG 12668
Db 171 SerLeuAsnProMetAsnPheIleGlnProGlnAlaPheLysGlnIleArgLeuHisLys 190
QY 12669 CTGACTTAAAGAAATAATTTTGAATGATTAATGTAATGAATACTTGATTTCAAAGTGTG 12728
Db 191 LeuThrLeuArgAsnAsnPheAspSerLeuAsnValMetCysThrCysIleGlnGlnLeu 210
QY 12729 GCTGGTTTAAAGTCAATCGTTTGTCTTGGGAGAAATTTGAATGAAGAAATCTTGAA 12788
Db 211 AlaGlyLeuGlnValHisArgLeuValLeuGlnGlnPheArgAsnGlnLysAsnLeuGln 230
QY 12789 AAGTTTGACAAACTGCTCTAGAGGAGCTGTGCAATTTGACATTTGAAGATTTCCGATTA 12848

Db	231	lyshpheasbpysserlaleuengllyleucybasnleuthrlleglunlupheargleu	250
Qy	12849	GCATACCTTAAGACTACCTGACGATGATATATTGACTTATTTAATGTTTGACAAATGTT	12908
Db	251	AlatyrlleuasbpyrlyrlyrleuAspApelelleaspeupheasncysleuthraenVal	270
Qy	12909	TCCTCATTTTCCCGGAGTGAGTCATATTGAAAGGGTAAAGACTTTTCTTATAATTTC	12968
Db	271	SerSerheSerleuValSerValThrleglarVallyAspPheSerlyraenPhe	290
Qy	12969	GGATGGCAACATTTAGAAATTAAGTTAACTGTAAATTTGGACAGATTTCCCACTGAAACAC	13028
Db	291	GLyThrpglnhlsleuGluleuValAsnCylybPhegllyglinhPheProthrleuysleu	310
Qy	13029	AAATCTCTCAAAAGGCTTACTTTCACTTCCACAAAGTGGAAGTCTTTTCAGAAAT	13088
Db	311	LySerleuysargleuthrPheThrSerAsnlygllycylyAsnAlaPheSergluVal	330
Qy	13089	GATTCACCAAGCCCTTGAGTTTCTAGATCTGAGTAAAGAAATGGCTTGAGTTTCCAAAGTTGC	13148
Db	331	AspLeuProSerleuGlupheLeuAspLeuSerArgsnllyleuSerPheylsglyCys	350
Qy	13149	TGTTCTCAAAAGTGATTTTGGGACACACAGGCTTAAAGATTTTAAGTCTGAGCTTCAATGGAT	13208
Db	351	CysSerelInserAspPhegllyThrThrSerleuyleryrleuAspLeuSerPheAsngly	370
Qy	13209	GTTATTAACATGATTCAAACTTCTTGAGGCTTGAACAACTAGAACATCTGATTTCCAG	13268
Db	371	ValIleThrMetSerSerAsnPhelengllyleuGlunleuUnhlsleuAspPheglIn	390
Qy	13269	CATTCCAAATTTGAAACCAATAGAGTGAATTTTCAGTATCTCATCACTCGAAACCTCATT	13328
Db	391	HisSerAsnleuysglInMetSerGlupheSerValPheleuSerleuArgsnleuIle	410
Qy	13329	TACCTTGAACATTTCTCATCTACACACAGAGTTGCTTCAATGGACCTTCAATGGCTTG	13388
Db	411	TyrleuAspIleSerhlsrlnhlsrlnhAsgValAlaPheAsnlyllePheAsnglyleu	430
Qy	13389	TCCAGTCTCGAAGTCTTGAAGAAATGGCTGGCAATTTCTTCCAGGAAACCTTCTCCAGAT	13448
Db	431	SerSerleuenglValleuysMetAlaglYAsnSerPheglInlunsnheleuProAsp	450
Qy	13449	ATCTTTCACAGAGCTGAGAAACTTGACTTCTTGAGACTCTCTCAGTGTCACTGAGACAG	13508
Db	451	IlePheThrGluleuArgsnleuthrPheleuAspLeuSerGlncysGlInleuGlunIn	470
Qy	13509	TTTGCTCCACAGAGATTTAACCTCACTCTCCAGTCTCAGGTACTTAATTAATGAGCCACAC	13568
Db	471	LeuSerProthrAlaPheAsnSerleuSerleuGlInAlaLeuAsnMetSerhlsAsn	490
Qy	13569	AACCTCTTTTCATTTGATGACGTTTCCCTTAATAGTGTCTGAACCTCCACAGGTTCTTGAT	13628
Db	491	AsnPhheSerleuAspThrPheProYrlylyCybLeuAsnSerleuGlInAlaLeuAsp	510
Qy	13629	TACAGTCTCATCATCATTAATGACTTCCAAAAACAGAACTACAGCAATTTTCCAAAGTACT	13688
Db	511	TyrSerleuAsnhsrlsleMetThrSerlylyglIngluleuGlInhlsPheProSerSer	530
Qy	13689	CTAGCTTCTTAAATCTTACTCAGAAAGACTTTTGACTTGTAACCTGTGAACACAGAGTTTC	13748
Db	531	LeuAlaPheleuAsnleuthrGlInAsnAspPheAlaCythrCysglunhlsglInSerPhe	550
Qy	13749	CTCGAATGATTAAGACACAGAGGAGCTTTGGTGAAGTTGAAAGAAATGATGCA	13808
Db	551	LeuGlInThrPllylelyAspGlInAsnglInleuLeuValGlulValGlnArgMetGlucysAla	570
Qy	13809	ACACCTTCAGATTAAGACAGGGGCATGCTGTGCTGATGATTGAATATCACTGTCAAGATGAAT	13868
Db	571	ThrProSerAspysglIngllyMetProValleuSerleuAsnIleThrCysglInMetAsn	590
Qy	13869	AAGACCATCAATGGGTGTGTGGCTTCCAGAGTGGCTGTGATACCTGTTACAGATTCG	13928
Db	591	LyThrIlellelegllyValSerValleuSerValleuValSerValValAlaValleu	610

[illegible]

Dh 31 SerTySerPhePheSerPheProGluLeuGlnValIleuAspLeuSerArgCysGluIle 50
Qy 12249 CAGCAATTGAAAGTGGGCGATATCAGAGCCCTTAAGCCACTCTTACCTTAATATTGACA 12308
Db 51 GlnThrIleGluAspGlyAlaTygIleSerIleuSerHsiIleuSerThrIleuIleLeuThr 70
Qy 12309 GAAAGCCCAATCCAGAGTTTAGCCCTGGAGACCTTTTCTGGACATATGAAAGTTTACAGA 12368
Db 71 GlyAsnProIleGlnSerIleuAlaIleuGlnAlaPheSerGlyLeuSerSerIleuGlnIly 90
Qy 12369 CTGGGCTGTGGAGACAATCTAGACATCTCTAGAGAACTTCCCATTTGACATCTCAAA 12428
Db 91 LeuValAlaValIleGluThrAsnLeuAlaSerIleuGlnAsnProIleGlnHsiIleuIly 110
Qy 12429 ACTTTGAAAGAACTTAATGTGGCTCACAATCTTATCCAACTTTTCAAAATTAACCTGAGTAT 12488
Db 111 ThrIleuysGluIleuAsnValAlaHsiAsnLeuIleGlnSerPheIlyLeuProGluTy 130
Qy 12489 TTTTCTATCTGACCAATCTAGAGCACTTGGACCTTTCCAGACAACAAGATTCAAAATATT 12548
Db 131 PheSerAsnLeuThrAsnLeuGlnHsiIleuAspLeuSerSerAsnIlyIleGlnSerIle 150
Qy 12549 TATTGACAAGACTTGGGGTTCTACATCAAAATGCCCTTACTCAATCTCTCTTTAGACCTG 12608
Db 151 TyCysThrAspLeuArgValIleuHsiIleGlnMetProIleuLeuAsnLeuSerIleuAspLeu 170
Qy 12609 TCCCTGAACCTTAAGAACTTTATCCAAACAGGTGCACTTTAAAGAAATTAAGCTTCATAG 12668
Db 171 SerIleuAsnProMetAsnPheIleGlnProGlyAlaPheIlyGlnIleArgLeuHsiIly 190
Qy 12669 CTGACTTTAAGAAATTAATTTTGTAGATTAAATGAAATAAAGCTTGAATCAAGTCTG 12728
Db 191 LeuThrIleuAspAsnAsnPheAspSerIleuAsnValIleCysIleGlnGlyIleu 210
Qy 12729 GCTGGTTTGAAGATCCATCGTTTGCTGTGGAGAAATTTAGAAATGAAGAACTTGAA 12788
Db 211 AlaGlyIleuGlnValHsiArgLeuValIleuGlyIlePheArgAsnGlnIlyAsnLeuGln 230
Qy 12789 AAGTTTGACAAATCTGCTCTAGAGGGCTGTGCAATTTGACCAATTTGAAAGATTCGATTA 12848
Db 231 LysPheAspIlySerAlaIleuGlnGlyIleuCysAsnLeuThrIleGlnGluPheArgLeu 250
Qy 12849 GCATCTAGACTAGACTACCTCGATGATATTAATGACTATTTAAATTTGTTGACAAATGTT 12908
Db 251 AlaTyIleuAspTyTyIleuAspAspIleIleAspLeuPheAsnCyIleuThrAsnVal 270
Qy 12909 TCTTCATTTTCCGTGGTGAAGTGAATTAATGAAGGTAAGAAGCTTTCTTATTAATTC 12968
Db 271 SerSerPheSerIleuValSerValThrIleGlnArgValIlyAspPheSerTyAsnPhe 290
Qy 12969 GGATGGCAACATTTTGAATTTGATTAACGTAAATTTTGGACAGTTTCCACATTTGAAATCTC 13028
Db 291 GlyTyPginHsiIleuGlnLeuValAsnCyIlySylusPheGlyIlePheProThrIleuIlySyl 310
Qy 13029 AAATCTCTCAAAAGGCTTACTTTCACTTCAACAAGGTGGGAAATGCTTTTTCAGAAAT 13088
Db 311 LysSerIleuIlyAspGluThrPheThrSerAsnIlySylIlyAsnAlaPheSerGlnVal 330
Qy 13089 GATTCACCAAGCTTGAAGTTTCTAGATCTCAGTAGAAATGGCTTGAAGTTTCAAAAGTTGC 13148
Db 331 AspLeuProSerIleuGlnPheLeuAspLeuSerArgAsnGlyLeuSerPheIlySylCys 350
Qy 13149 TGTTCCTCAAGTGAATTTTGGGACAAACAGCCCTAAAGTATTTAGATCTGAGCTTCAATGCT 13208
Db 351 CysSerGlnSerAspPheGlyThrThrSerIleuIlySylIlyAspLeuSerPheAsnIly 370
Qy 13209 GTTATTACATGAGTTCAAACTTTTGGGCTTGAACAACATGACATCTGATTTCCAG 13268
Db 371 ValIleThrMetSerSerAsnPheLeuGlyIleuGlnIleuGlnHsiIleuAspPheIln 390
Qy 13269 CATTCCAATTTGAAACAATGAGTGAAGTTTTCAGTATTCATATCTCAGAAACCTCAT 13328
Db 391 HisSerAsnLeuIlyGlnMetSerGlnPheSerValPheLeuSerIleuAspAsnLeuIle 410

Qy 13329 TACCTTGACATTTCTCATACTCACACAGAGTTGCTTCAATGGCACTTCAATGGCTT 13388
Db 411 TyIleuAspIleSerHsiIleThrHsiIleArgValAlaPheAsnIlyIlePheAsnGlyIleu 430
Qy 13389 TCCAGTCTCGAAGCTTGAATAATGGCTGGCAATCTTTCCAGGAAACATTCCTTCAGAT 13448
Db 431 SerSerIleuGlnValIleuIlySylIleuIlyAsnSerPheGlnIleuAsnProAsp 450
Qy 13449 ATCTTCACAGAGCTGAGAAATTTGACCTTCTGGACCTCTCTCAAGTGTCAACTGGAGCAG 13508
Db 451 IlePheThrGluIleuIlyAsnLeuThrPheIleuAspLeuSerGlnCysGlnIleuGln 470
Qy 13509 TTGCTTCACACAGATTTAATCTCACTCCAGCTTCCAGGTATCAATATAGACCCAAAC 13568
Db 471 LeuSerProThrAlaPheAsnSerIleuSerSerIleuGlnValIleuAsnMetSerHsiAsn 490
Qy 13569 AACTTCTTTTCAATGGATAGATTCCTTATAGTGTCTGAAGTCCCTCCAGGTTCTTGAT 13628
Db 491 AsnPheSerSerIleuAspThrPheProTyIlyCysIleuAsnSerIleuGlnValIleuAsp 510
Qy 13629 TACAGTCTCAATCAATATGACTTCCAAAAACAGGAATACAGCACTTTTCCAAAGTACT 13688
Db 511 TySerIleuAsnHsiIleMetThrSerTyIlySylGlnIleuGlnHsiIlePheProSerSer 530
Qy 13689 CTAGCTTTCTTAATCTTACTCAGAAATGACTTTGGCTTGTGTAACACACAGAGTTTC 13748
Db 531 LeuAlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHsiIleGlnSerPhe 550
Qy 13749 CTGCAATGATCAAGACACAGAGCAGCTTGTGGTGAAGTGAACCAATGGAATGTGCA 13808
Db 551 LeuGlnThrIleIlyAspGlnArgGlnIleuLeuValGlnIlyArgMetGlyCysAla 570
Qy 13809 ACACCTTCATATAGACGGGCAATGCCCTGCTGAGTTTGAATATCACTTCAGATGAAT 13868
Db 571 ThrProSerAspIlySylGlnIlyMetProValIleuSerIleuAsnIleThrCysGlnMetAsn 590
Qy 13869 AAGACATCAATGGTGTGGTGGCTCCAGTGTGCTTGAATATCTGTTGAGACGTTCTG 13928
Db 591 LysThrIleIleGlyIlyAlaSerValIleuSerValIleuValIlyAlaSerValIlyAlaValIleu 610
Qy 13929 GTCTATAGTCTTAATTTTCACTGATGCTTCTTGCTGGCTGCAATTAAGTATGTAAGT 13988
Db 611 ValTyIlySerPheTyIlyPheHsiIleuMetIleuAlaGlyCysIleTyIlyArgGly 630
Qy 13989 GAAACATCTATGATGCTTTGTTATTAATTAACCAAGCAGATGAGACCTGGTGAAGGAAT 14048
Db 631 GlyAsnIleTyIlyAspAlaPheValIleTySerSerGlnAspGlnAspTyIlyAlaArgAsn 650
Qy 14049 GAGCTTAAGAATTTAAGAAGAGGGGTGCTTCATTTCAAGCTGCTTCATACAGAA 14108
Db 651 GlyIleuValIlyAsnIleuGlnGlyIlyAlaProProPheGlnIleuCyIleuHsiIlyArg 670
Qy 14109 GACTTAATTCCTGGTGTGGCAATTTGCTGCAACATCATCAATGAAGTTTCCATTAAGC 14168
Db 671 AspPheIleProGlyValAlaIleAlaIleAlaAsnIleIleHsiGlnIlyPheHsiIlySer 690
Qy 14169 GAAAGGTGATTTGTGTGTGTGCCACACTTATCATCCAGACCGCTGTGAATTTGAA 14228
Db 691 ArgIlyValIleValIlyAlaIlyAlaIlySerGlnHsiPheIleGlnSerArgTyIlyPheGln 710
Qy 14229 TATGAGATGCTCAGACTGAGCTGAGTTCTGAGCAGTGTGCTGGTATCATCTTCAATGTC 14288
Db 711 TyIleGlnIleAlaGlnIleThrPginPheIleuSerSerArgAlaGlyIleIlePheIleVal 730
Qy 14289 CTGCAGAAAGGTGAGAAACCTGCTCAGGACGACGAGGTGAAGCTGACCGCTTCTCAGC 14348
Db 731 LeuGlnIlyValIleGlnIlySerIleuIlyArgGlnIlyAlaGlyIleuTyIlyArgLeuIleSer 750
Qy 14349 AGGAACCTTACCTGAGAGTGGAGAGACAGTGTCTGGGGCGGACATCTTCTGAGAGACA 14408
Db 751 ArgAsnThrTyIleuGlnIlyPginIlyAspSerValIleuGlyIlyArgHsiIlePheIlyArgArg 770


```
Db 529 AasnpheSerleuAapThrPheProTyrIleCysIleuAenSerleuGlnValIleuAasp 548
Qy 13629 TACAGTCTCATCATCAATTAATGACTTCCAAAATAAGAGAACTACAGCATTTTCCAAAGT 13688
Db 549 TySerleuAanHsIleMeTThSerIySgInIleuGlnHsPheProSerSer 568
Qy 13689 CTACCTTTCTTAATCTTACTCAGAAATGACTTCTTGATCTTGATCTTGAAACACAGAGTTTC 13748
Db 569 LeuAlaPheLeuAanLeuThrGlnAanAspPheAlaCysThrCysGlnHsGlnSerPhe 588
Qy 13749 CTGCAATGATCAAGAACAGAGGACGCTTGTGATGAAAGTTGAACGAATGGAATGTGCA 13808
Db 589 LeuGlnTrpIleIySAspGlnArgGlnIleuIleuValGlnValGlnArgMeGlnCysAla 608
Qy 13809 ACACCTTCAGATTAAGAGAGGAGGAGCTGTGCTGATGATTAATCACTGCAATGAAT 13868
Db 609 ThrProSerAerIySgInIyMeCProValIleuSerleuAanIleThrCysGlnMeCAsn 628
Qy 13869 AAGACCATCATTTGGTGTGGCTCCTCAGTGTGCTTGATGATCTGTTGTAGCAGTTCTG 13928
Db 629 LysThrIleIleGlyValSerValIleuSerValIleuValIleuValIleuValIleu 648
Qy 13929 GTCTATAAGTCTATTTTACCTGATGCTGCTTGTGCTGCTGATTAAGTATGATGAGGT 13988
Db 649 ValTyrIySPhetYrPheHsIleuMeTleuIleuAglIyCysIleIySgIyArgGly 668
Qy 13989 GAAACATCTATGATGCTTGTGATTAATCACTCAAGCCAGATGAGAGCTGGTAAAGAAAT 14048
Db 669 GluAanIleYrAerPAlaPheValIleYrSerSerGlnAerGlnAerTrpValAArgAsn 688
Qy 14049 GAGCTAGTAAGAAATTTGAAGAAGGSGCTCCTCATTTGACCTGCTGCTGCTGCTGCTG 14108
Db 689 GluIleuValIySAsnIleuGlnIyValIleProPheGlnIleuCysIleHsIleYrArg 708
Qy 14109 GACTTTATTTCCCGGTGTGGCCATGTGCTGCAACATCATCATGAAGTTTCCATTAAGC 14168
Db 709 AspPheIleProGlnIyAlaIleIleAlaAanIleIleHsGlnIyPheHsIleYrSer 728
Qy 14169 CGAAAGTGATTTGTTGGTGTGCTCCAGACATTCATCCAGACCCCTGTGTATCTTTGAA 14228
Db 729 ArgIySValIleValIleValIleSerGlnHsPheIleGlnSerArgTrpCysIlePheGln 748
Qy 14229 TATGAGATTTGCTGACCTGAGCATGTTTCTGACAGTGTGCTGATCATCTTCATTTGTC 14288
Db 749 TyrGlnIleAlaGlnIleThrTrpGlnPheIleuSerSerArgAlaGlyIleIlePheIleVal 768
Qy 14289 CTGCAAGAGGTGAGAAAGACCTGTCTCAGGACGAGGAGTGTGAGCTGTACCGCTTCTCAGC 14348
Db 769 LeuGlnIySValIleGlnIyThrIleuIleuArgGlnIleValIleuIleYrArgIleuIleuSer 788
Qy 14349 AGGAACATCTTACCTGAGATGAGGAGACAGTGTCTGCGGGCGGACATTTCTGAGAGAGA 14408
Db 789 ArgAsnTrpIyTrpLeuGlnIyTrpGlnAerPheValIleuGlnIyArgHsIlePheTrpArgArg 808
Qy 14409 CTCGAAAAAGCCCTGCTGATGTTAATCATGGAATCCAGAAAGAGAGTGGGTTCAGAGA 14468
Db 809 LeuAlaGlySAlaIleuIleuAaspGlnIySAspTrpPheAsnProGlnIyThrValGlnIyThrIy 828
Qy 14469 TGCATTTGGCAGAGAGACATCTATTC 14495
Db 829 CysAanTrpGlnIleuAlaIleThrSerIle 837
```

```
RESULT 6
US-10-038-854-135
; Sequence 135, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eissen, Andrew J
```

```
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shinkets, Richard A
; APPLICANT: Tchermey, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Paturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangoli, Baba A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenda
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 661
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-038-854-135
```

```
Alignment Scores:
Pred. No.: 7.18e-45 Length: 661
Score: 563.50 Matches: 178
Percent Similarity: 44.91% Conservative: 109
Best Local Similarity: 27.86% Mismatches: 261
Query Match: 1.70% Indels: 91
DB: 15 Gaps: 18
```

```
US-09-396-985b-47 (1-18989) x US-10-038-854-135 (1-661)
```

```
Qy 12171 TTAATATTCTATTTTGTAGTCTTNA-----TTACGACGAAATATT 12209
Db 58 LeuAluPheSerPheAanValIleuProThrIleGlnAanThrThrPheSerArgIleuIle 77
Qy 12210 AGATTAATCAATGCTTTTATTC---TGTAAGTGTGAATCCAGACATGAAGAGGG 12266
Db 78 -----AanLeuThrPheLeuAerPheLeuThrArgCysGlnIleIyTrpIleHsGlnAer 95
```

```

Qy 12267 GCATATCAGACCTTAAGCCCTCTATCTTAATATTGACAGAAACCCATCCAGAGT 12326
Db 96 ThrPheGlnSerGlnHisArgLeuAspThrLeuValLeuThrAlaAsnProLeuIlePhe 115
Qy 12327 TTAAGCCCTGGAGACCTTTTCTGAGACTATCAAGATTACAGAAAGCTGGCTGGAGACA 12386
Db 116 MetAlaGlnThrAlaLeuSerGlyProLysAlaLeuLysHisIleLeuPhePheIleGlnThr 135
Qy 12387 AATCAGACCTCTAGAGAACTCCCATCTGAGCACTCCAAACCTTGAAGAACTTAAAT 12446
Db 136 GlyIleSerSerIleAspPheIleProLeuHisAsnGlnLysThrLeuGlnSerLeuLys 155
Qy 12447 GTGGCTCAACAATCTTATCCAACTTTCAAAATTAACCTGAGTATTTTCTAATCTGACCAAT 12506
Db 156 LeuGlySerAsnHisIleSerSerIleLysLeuProLysGlnPheProThr---GlnLys 174
Qy 12507 CTAAAGCACTTGACCTTTCCAGCAACAAGATTCAAAATATTATTTATGACAGACTTGGCG 12566
Db 175 LeuLysValIleuAspPheGlnAsnAsnAlaIleHisIleLysSerLysGlnAspMetSer 194
Qy 12567 GTTTCATCAATCAATGCCCTCACTCAATCTCTTATGACCTGGCCCTGACCCATATGAC 12626
Db 195 SerLeuGlnGln-----AlaThrAsnLeuSerLeuAsnLeuAsnGlnLysAsnAspIleAla 212
Qy 12627 TTATCCAAACGAGTGCATTTAAAGAAATTAGGCTTCAAGCTGACTTTAAGAAATAT 12686
Db 213 GlyIleGlnProGlnAlaPheAspSerAlaValPheGlnSerLeu-----Asn 228
Qy 12687 TTTGATAGTTTAAATGTRATGAAAATTGATTTCAAGCTGGCTGGCTTTGAAGTCCAT 12746
Db 229 PheGlyGlyThrGlnAsnLeuLeuValIlePheLysGlyLeuLysAsnSerThrIleGln 248
Qy 12747 CGTTGGTCTGGGAGAAATTGAAAGAACTGGAAGAAAGTTTGACAAATCTGCT 12806
Db 249 SerLeuThrLeuGlyThrPheGlnAspMetAspAsp---GlnAspIleSerProAlaVal 267
Qy 12807 CTAGAGGCGCTGTGCATTTGACCATTTGAGAAATTCGATTTAGCATTAAGTACTATC 12866
Db 268 PheGlnGlyLeuGlyGlnMetSerValGlnSerIleAsnLeu---GlnLysHisTyrPhe 286
Qy 12867 CTCGATGATATTATTTGACTTTTAAATTTGTTGACAAATGTTTCTTCAATTTCCCTGGTG 12926
Db 287 PheAsnIleSerSerAsnThrPheHisCysPheSer----- 298
Qy 12927 AGTGTGACTATTGAAGGTAAGAAAGCTTTCTATATATTGGATGGCAATTTAGAA 12986
Db 299 -----GlyLeuGlnGlnLeuAsp 304
Qy 12987 TTAGTTAACTGTAAATTTGACAGTTTCCACA-----TTGAAGCTCAATCTCTCAAA 13040
Db 305 LeuThrAlaThrHisIleuSerGlnLeuProSerGlyLeuValGlnSerThrLeuLys 324
Qy 13041 AGGCTTACTTTCACTTCCACAAAGAGTGGAGAT-----GCTTTTTCAGAAATTGATCTA 13094
Db 325 LysLeuValIleuSerAlaAsnLysPheGlnLysLeuGlnLysSerAlaSerAsnPhe 344
Qy 13095 CCAAGCCTTAGTT----- 13109
Db 345 ProSerLeuThrHisLeuSerIleLysGlyAsnThrLysArgLeuGlnLeuGlyThrGly 364
Qy 13110 -----CTAGATCTCAGTAGAAATGCGCTTAGTTTC 13139
Db 365 CysLeuGlnAsnLeuGlnAsnLeuArgLysLeuAspLeuSerHisAspAspIleGlnThr 384
Qy 13140 AAAGTTGCTGTTTCTCAAGTATTTGGGACAAACGAGCTTAAAGTATTTAGATCTGAGC 13199
Db 385 SerAspCysAsnLeuGlnLeuArgAsnLeuSerHisLeuGlnSerLeuAsnLeuSer 404
Qy 13200 TTCAATGGTGTATTATCAATGATGTTCAAA-----TTCTTGGGCTTGAAGAACTGAACAT 13256
Db 405 TyrAsnGlnProLeuSerLeuLysThrGlnAlaPheLysGlnLysProGlnLeuGlnLeu 424
Qy 13257 CTGGATTTCAGACATTCCAATTTGAAACAAATGAGTGAAGTTTTCAGTATTCCTATCATCTC 13316

```

```

Db 425 LeuSerLeuAlaPheThrArgLeuLysValLysAspAlaGlnSerProPheGlnAsnLeu 444
Qy 13317 AGAAACCTCATTTTACTTGACATTTCTGATCTATCTACACACAGAGTGGCTTTCAATGGCATC 13376
Db 445 HisLeuLysValIleAsnLeuSerHisIleSerLeuAspIleSerGlnGlnLeu 464
Qy 13377 TTCAATGGCTGTGTCAGTCTGAGTCTGAGTCAAAATGCGTGGCAATTTCTTCAGGAAAC 13436
Db 465 PheAspGlyLeuProAlaLeuGlnHisLysAsnLeuGlnGlnLysAsnHisPheProLysGly 484
Qy 13437 TTCCTT-----CCAGATCTTTCACAGAGCTGGAACAACTTGACCTTCTGGACCTCTCT 13490
Db 485 AsnIleGlnLysThrAsnSerLeuGlnThrLeuGlnLysArgLeuGlnIleLeuValLeuSer 504
Qy 13491 CAGTCTCACTGAGACGAGTGTCTCCACACAGCATTTTATCTCATCTCCAGTCTTCAGGTA 13550
Db 505 PheCysAspLeuSerSerIleAspGlnHisAlaPheThrSerLeuLysMetMetAsnHis 524
Qy 13551 CTAAATATGAGCCCAACAACCTTTCTTCAATGATGATAGTTTCTTAAAGTGTCTGAC 13610
Db 525 ValAspLeuSerHisAsnArg-----LeuThrSerSerSerIleGlnAlaLeuSer 541
Qy 13611 TCCCTCCAG-----GTTCTTGATTACAGTCTCAATGACATTAATGACTTCCAAAAACAG 13664
Db 542 HisLeuLysGlyIleTyrLeuAsnLeuAlaSerAsnHisIleSerIleIle----- 558
Qy 13665 GAACCTACAGATTTTCCAACTGATCTGACTTTCTTA-----AATCTT 13706
Db 559 -----LeuProSerLeuLeuProIleLeuSerGlnGlnArgThrIleAsnLeu 574
Qy 13707 ACTCAGATGACTTGTGCTTGACTTGTAACACACAGATTCTCCGAAATGGATCAAGAC 13766
Db 575 ArgGlnAsnProLeuAspCysThrCysSerAsnLysTyrPheLeuGlnTyrLysGln 594
Qy 13767 CAGAGGAGCTCTGTGTGAGAAAGTTGACGAATGGAATGTCACACCTTCAGATTAACAG 13826
Db 595 AsnMetGlnLysLeuGlnAspThrGlnAspThrLeuLysGlnAsnProProLeuLeuArg 614
Qy 13827 GGCATGCCCTGTGCTGAGTTTGAATATCACTGTGCAGATGAATAGACCATCATTTGGTGTG 13886
Db 615 GlyValArgLeuSerAspValThrLeuSerCysSerMetAlaAlaValGlyIlePhePhe 634
Qy 13887 TCCGCTCCTCAGTGGCTTGATATCGTGTGTGACAGTTCGGTCTAATGTTAT 13943
Db 635 LeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePheAlaValLysTyrPhe 653

RESULT 7
US-10-037-417-107
; Sequence 107, Application US/10037417
; Publication No. US20040052806A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Rameeh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patrudajan, Meera
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine B
; APPLICANT: Vermet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Eilerman, Karen
; APPLICANT: Malvanekar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G

```

```

APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eissen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIORITY APPLICATION NUMBER: 60/260,018
PRIORITY FILING DATE: 2001-01-05
PRIORITY APPLICATION NUMBER: 60/260,360
PRIORITY FILING DATE: 2001-01-08
PRIORITY APPLICATION NUMBER: 60/272,411
PRIORITY FILING DATE: 2001-02-28
PRIORITY APPLICATION NUMBER: 60/272,817
PRIORITY FILING DATE: 2001-03-02
PRIORITY APPLICATION NUMBER: 60/291,186
PRIORITY FILING DATE: 2001-05-15
PRIORITY APPLICATION NUMBER: 60/303,231
PRIORITY FILING DATE: 2001-07-05
PRIORITY APPLICATION NUMBER: 60/305,060
PRIORITY FILING DATE: 2001-07-12
PRIORITY APPLICATION NUMBER: 60/318,405
PRIORITY FILING DATE: 2001-09-10
PRIORITY APPLICATION NUMBER: 60/318,700
PRIORITY FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 107
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus
US-10-037-417-107

Alignment Scores:
Pred. No.: 7,18e-45 Length: 661
Score: 563.50 Matches: 178
Percent Similarity: 44.91% Conservative: 109
Best Local Similarity: 27.86% Mismatches: 261
Query Match: 1.70% Indels: 91
DB: Gaps: 18

US-09-396-985b-47 (1-18989) x US-10-037-417-107 (1-661)
QY 12171 TTATATTCATTAGGTTT-----TTCAGCAGAAATATT 12209
DB 58 LeuGluPheSerPheAsnValLeuProThrIleGlnAsnThrPheSerArgLeuIle 77
QY 12210 AGATPAATCATGTCTTTTATTC---TGATGCTGTAATCCAGACATGAAGATGG 12266
DB 78 -----AsnLeuThrPheLeuAspLeuThrArgCysGlnIleYrTrpIleHisGluAsp 95
QY 12267 GCATATCAAGCCCTAAGCCACTCTTAACCTTAATTGACAGAAACCCCATCAGAGT 12326
DB 96 ThrPheGlnSerGlnHisArgLeuAspThrIleValLeuThrIleAsnProLeuIlePhe 115
QY 12327 TTAAAGCCCTGGAGGCTTTCTGACATCAAGTTTACAGAGCTGGCTGTGAGACA 12386
DB 116 MetIleGluThrIleLeuSerGlyProIleValLeuValHisLeuPheIleGlnThr 135
QY 12387 AATATGATCTTCAAGAACTTCCCATGACATCCAAACCTTGAAGAACTTAAT 12446
DB 136 GlyIleSerSerIleAspPheIleProLeuHisAsnGlnIleThrLeuGlnSerLeuIle 155
QY 12447 GTGGCTCAACATCTTATTCATCTTTCAATTAACCTGAGTATTTTCAATCTGACCAAT 12506
DB 156 LeuGlySerAsnHisIleSerSerIleLeuSerProIleValLeuPheProThr---GluVal 174
QY 12507 CTAAAGCACTTGACCTTTCCAGCAACAAGTTCAAGATATTATTGACACAGACTTGGCG 12566
DB 175 LeuValValLeuAspPheGlnAsnValIleHisIleValSerIleValAspMetSer 194

```

```

QY 12567 GTTCTACATCAATATGCCCTACTCAATCTCTTTAGACCTGTCCGAAACCTATGAAAC 12626
DB 195 SerLeuGlnGln-----AlaThrPheLeuSerLeuAsnLeuAsnIleValIleAla 212
QY 12627 TTTATCCACACAGCTGCATTTAAAGAAATTAGGCTTCATAGGCTGACTTTAGAAATAT 12686
DB 213 GlyIleGluProGlyAlaPheAspSerAlaValPheGlnSerLeu-----Asn 228
QY 12687 TTTGATAGTTTAATGTAAGAAACTTGATATTCAAGGTGCTGCTTTGAGATGCAT 12746
DB 229 PheGlyGlyThrGlnAsnLeuValIlePheValGlyLeuValAsnSerThrIleGln 248
QY 12747 CGTTTGCTTGGAGAAATTAGAAATGAAAGAACTTGAAAAGTTTGACAAATGTGCT 12806
DB 249 SerLeuThrLeuGlyThrPheGluAspMetAspAsp---GluAspIleSerProIleVal 267
QY 12807 CTAGAGGCTGTGCAATTGACATTTGACATGAAGAAATTCGATTAACATTTAGACTACTAC 12866
DB 268 PheGluGlyLeuValSerGluMetSerValGluSerIleAsnLeu---GluValHisIleValPhe 286
QY 12867 CTGATGATATTTATGACTTATTTAATGTTTGACAAATGTTTCTTCATTTCCCTGCTG 12926
DB 287 PheAsnIleSerSerAsnThrPheHisCysPheSer----- 298
QY 12927 AGTGTACTATTGAAAGGGTAAAGACTTTTCTTAATATTCGATGCGAACATTTAGAA 12986
DB 299 -----GlyLeuGlnGluLeuAsp 304
QY 12987 TTAGTTAACTGTAAATTTGGACAGTTTCCACAC-----TTGAACATCAATCTTCAAA 13040
DB 305 LeuThrAlaThrHisIleSerSerGluLeuProSerGlyLeuValGlyLeuSerThrLeuVal 324
QY 13041 AGGCTTACTTTCACCTTCCAAACAAGGTGGGAT-----GCTTTTCAGAAATGTTGATCTA 13094
DB 325 LeuValValLeuSerAlaAsnValysPheGluAsnLeuValSerIleSerAlaSerAsnPhe 344
QY 13095 CCAAGCCTTGAGTTT----- 13109
DB 345 ProSerLeuThrHisIleSerSerIleValGlyAsnThrIleArgLeuGluLeuGlyThrGly 364
QY 13110 -----CTGATCTCAGTGAAGAAATGCTTGAGTTTC 13139
DB 365 CysLeuGluValAsnLeuGluAsnLeuValArgGluLeuAspLeuSerHisValAspArgIleGluThr 384
QY 13140 AAGGTTGCTGCTCTCAAGATGATTTTGGGACACAGAGCTTAAGTATTAGATCGAGC 13199
DB 385 SerAspCysCysAsnLeuGlnLeuValArgAsnLeuSerHisIleuGlnSerLeuAsnLeuSer 404
QY 13200 TTCAATGCTGTATTATTCATGAGTTCACAC---TTCCTGGCTTAGAACACTAGAACAT 13256
DB 405 TyrAsnGluProLeuSerIleValHisIleValAlaPheValGlyCysProGlnLeuGluLeu 424
QY 13257 CTGGATTTCCAGATTTCCAAATTTGAAACAATAGAGAGTTTCAATATTCATCTACATC 13316
DB 425 LeuAspLeuAlaPheThrArgLeuValValysAspAlaGlnIleSerProPheGlnAsnLeu 444
QY 13317 AGAAACCTTATACCTTCATGATTCATGACATCCACACAGAGTGGCTTCAATGCGCAT 13376
DB 445 HisLeuLeuValValLeuAsnLeuSerHisSerLeuLeuAspIleSerSerGluGlnLeu 464
QY 13377 TTCAATGCTGCTTGCAGATCTCGAAGTCTTGAAATGGCTGGCAATCTTTCCAGAAAAC 13436
DB 465 PheAspGlyLeuProAlaLeuGlnHisIleValAsnLeuGlnIleValHisIlePheProVal 484
QY 13437 TTCCTT-----CGAGTATCTTCAACAGCTGAGAAACTTGAACCTTCTGCAACCTGCT 13490
DB 485 AsnIleGlnIleThrAsnSerLeuGlnThrLeuGlyArgLeuGluIleLeuValLeuSer 504
QY 13491 CAGTGTCAATGAGACAGTGTCTCCACACAGCTTTAATCTCACTCTCCATCTTCAGGTA 13550
DB 505 PheValAspLeuSerSerIleAspGlnHisIleAlaPheHisIleValIleValMetMetAsnHis 524
QY 13551 CTAAATATGAGCCACAAACATCTCTTTTCATGATAGCTTTCTTAAAGTGTGTAAC 13610

```

```

Db      525 ValAspSerHisAsnArg-----LeuThrSerSerSerIleGluAlaLeuSer 541
Qy      13611 TCCCTTCAG-----GTTCTGATTAACAGTCTCATACATCAATAGACTTCCAAAAACAG 13664
Db      542 HisLeuYsgIyIeYrLeuAsnLeuAlaSerHisIleSerIleIle----- 558
Qy      13665 GAACATACAGCATTTTCCAGAGTCTAGCTTCTTA-----AATCTT 13706
Db      559 -----LeuProSerLeuLeuProIleLeuSerGlnIArgThrIleAsnLeu 574
Qy      13707 ACTGAGATGACTTGGCTTGTACTTGTGACACAGAGTTTCTGCAATGAGTCAAGAC 13766
Db      575 ArgGlnAsnProLeuAspCysThrCysSerAsnIleYrPheLeuGluTrpTyIyGln 594
Qy      13767 CAGAGGAGCTCTTGAGAGAGTTGAACGATGAAGTGAACACCTTCAGATTAACAG 13826
Db      595 AsnMetGlnYsLeuGluAspThrGlnAspThrLeuYsGlnAsnProLeuLeuArg 614
Qy      13827 GGCATGCTGTGCTGAGTTTGAATATGACCTGTGACATGAATAGACCATGATGCTG 13886
Db      615 GYValArgLeuSerAspValThrLeuSerCysSerMetAlaAlaValGlyIlePhePhe 634
Qy      13887 TCGGTCTCAGTGTCTTGTGATGATCTGTGTGACAGTCTGTCTTAATGTTCTAT 13943
Db      635 LeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePheAlaValIyPhe 653

```

RESULT 8

```

US-09-950-041-4
; Sequence 4, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DX0724XX1
; CURRENT APPLICATION NUMBER: US/09/950,041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-4

```

Alignment Scores:

```

Pred. No.:      1.24e-44      Length:      784
Score:          561.50      Matches:      220
Percent Similarity: 41.59%      Conservative: 121
Best Local Similarity: 26.83%      Mismatches: 260
Query Match:    1.70%      Indels:      219
DB:            10      Gaps:      38

```

US-09-396-985b-47 (1-18989) x US-09-950-041-4 (1-784)

Qy 12246 ATCCAGCAATTGAGATGGGCGCATATCAGAGCCTTAAGCACTCTCTACCTTAATATTG 12305

```

Db      88 IleAsnThrIleGluGluAspSerPheSerSerLeuGlySerLeuGluHisLeuAspLeu 107
Qy      12306 ACGGAAGACCCCATCCAGATTTAGACCTTGAGACCTTTCTTGACATATCAAGTTTACAG 12365
Db      108 SerTyraAsnYrLeuSerAsnLeuSerSerSerTrpPheYsProIleSerSerLeuThr 127
Qy      12366 AAGCTG-----GTGCTGTGAGACAAT 12389
Db      128 PheLeuAsnLeuLeuGluYsAsnProTyIyLeuThrLeuGluYrIleThrSerLeuPheSerHis 147
Qy      12390 CTAGCATCTGTAGAGAACTTCCCATGACATCTCAAACT----- 12431
Db      148 LeuThrYsLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrIyIleGlnArg 167
Qy      12432 -----TTCAAGAACTTAATGTGGTCAACATCTTAATCA 12467
Db      168 LysAspPheAlaGlyLeuThrPheLeuGluGluLeuGluIleAspAlaSerAspLeuGln 187
Qy      12468 TCTTTCAATTAACCTGAGTATTTTCTAATCTGACCAATCTAGACACTTGACCTTCC 12527
Db      188 SerTyrcIu---ProYsSerLeuYsSerIleGlnAsnValSerHisIleLeuHis 206
Qy      12528 AGCAACAAG-----ATTCAAGTATTATTATGC 12554
Db      207 MetYsGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerValGluCys 226
Qy      12555 ACAGACTGGGGGTTCTACATCAAAAGCCCTACTCATCTCTTTAGACCTTCCCTG 12614
Db      227 LeuGluLeuArg-----AspThrAspLeu 234
Qy      12615 AACCCATGAACCTT-----ATCCAAACAGTGCATTTAAGAAATTAAGGCTTCATAG 12668
Db      235 AspThrPheHisPheSerGluLeuSerThrGlyGluThrAsnSerLeu---IleYsYls 253
Qy      12669 CTGACTTTAAGAAAT-----AATTGATAGTTTA---AATGTAATGAAAACTGT 12716
Db      254 PheThrPheArgAsnValYsIleThrAspGluSerLeuPheGlnValMetYsLeuLeu 273
Qy      12717 -----ATTCAAGTCTGGCTGTTTGAAGTCCATGCTTTGGTTCG-----GGA 12761
Db      274 AsnGlnIleSerGlyLeuGluLeuGluPheAspAspCysThrLeuAsnGlyValGly 293
Qy      12762 GAATTAGAAATGAAAGAACTTGAAAGAGTTTGAACAATCTGCTAGAGGCGCTGTC 12821
Db      294 AsnPheArgAlaSerAspAsnAspArgValIleAspProGlyYsValGlu----- 310
Qy      12822 AATTGACATTTGAGAAATTCGATTAAGCA-----TACTTAAGACTACTCGATGAT 12875
Db      311 ThrLeuThrIleArgThrGluHisIleProArgPheTyIeLeuPheTyI-----Asp 327
Qy      12876 ATTAATGACTTATTAATTTCTTGAACAATGTTTCTTCAATTTCCCTGGTGAAGTGA 12935
Db      328 LeuSerThrLeuYrSerLeuThrGluArgValYs-----ArgIleThr 342
Qy      12936 ATTGAAGAGGTAAAGACTTTCTTAATTTGGATGGCAACATTTAGAATTGAATTAA 12995
Db      343 ValGluAsnSerYsValPhe-----LeuValPro 352
Qy      12996 TGTAAATTTGAGAGTTTCCACATGAAATCAAAATCTCAAAAAGGCTTACTTCACT 13055
Db      353 CysLeuLeuSerGln----- 357
Qy      13056 TCCAAACAAGGTGGAAAGTCTTTTTCAGAAAGTTGATCTACCAAGCTTGAGTTTCA 13115
Db      358 -----HisLeuYsSerLeuGluGluTyIyLeuAsp 366
Qy      13116 CTCAGTAGAAAT-----GGCTGAGTTTCAAGGTTGCTGTTCAAGT 13160
Db      367 LeuSerGluAsnLeuMetValGluGluTyIyLeuYsAsnSerAlaCys----- 382
Qy      13161 GATTTTGGAGCAACAGCCTTAAGTATTTAGATCTGAGCTTCAATGGTGTATTATTAACAG 13220

```



```

Db      383  GLuAspAla1trpProSerLeuGlnThrLeu1leuArgGlnAsn----- 397
Qy      13221 AGTTCAAACTTTGGGCTTAGAAACAATGAAACATGTGATTTCCAGCATTCGAATTTG 13280
Db      398  -----HisLeu-----AlaSerLeu 402
Qy      13281 AAACAAATGAGTGGTTTTCAGTATTCCTATCACTCAGAAAACCTCATTTTACCTTGACATT 13340
Db      403  GlnUlyeThrGlyGlu-----ThrLeuThrLeuUlyAsnLeuThrAsn1leuApr1le 420
Qy      13341 TTCATATCTCAACACACAGATTGCTTTCAATGGCATTTTCATATGGCTTTGCCAGTCTCGAA 13400
Db      421  SerUlyS----- 422
Qy      13401 GTGTGAAAATGGGTGGCAATTTCTTCCAGAAAACCTTCCTCCAGATATCTTCACAGAG 13460
Db      423  -----AsnSerPheHisSer-----MetProGlnUthrCysGlnTrp 434
Qy      13461 CTGAGAAACTTGAACCTTCCTGACACTCTCAAGTGTCAAGTGGAGAGAGTTGCT----- 13514
Db      435  ProGlnUlyeMetUlySerUlyLeuAsnLeuSerSerUthrArgLeuHisSerValThrGlyCys 454
Qy      13515 ---CCAAAGACATTTAACTCACTCTCCAGTCTTCAAGTACTTAATATGAGCCACAC-- 13568
Db      455  IlePro-----LysThrLeuGlnUlyLeuAspValSerAsnAsnAsn 468
Qy      13569 ---AACTCTTTTCATTGGAT----- 13586
Db      469  LeuAsnLeuPheSerLeuAsnLeuProGlnLeuUlyGlnUlyTrpIleSerArgAsnUlyS 488
Qy      13587 ---ACGTTTCTCT--TATTAAGTGTCTGAACCTCCCTCAGGTTTCTGATTAACAGTCTC 13637
Db      489  LeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValLeuUlySleSerArg 508
Qy      13638 AATCACTATAGACTTCCAAAAACAGAACTACAGCATTTTCCAACTAGTCTAGCTTTC 13697
Db      509  AsnAla1leThrThrPheSerUlyGlnGlnLeuAspSerPhe--HisThrLeuUlyThr 527
Qy      13698 TTTAATTTTACTGAGATGATGATTTGCTGTGATCTGTAACACACGAGTTTCTGCAATGG 13757
Db      528  LeuGlnUlaGlyGlnUlyAsnAsnPhe1leCysSerCysGlnUlyPheUlySerPheThrGln-- 546
Qy      13758 ATCAAGGACCAAGGACAGCTCTGTGTAAGTT-----GAACGAAATGAAA 13802
Db      547  -----GlnGlnGlnAlaLeuAlaValLeuValLeuUlyLeuAspTrpProAlaAsnTrpLeu 563
Qy      13803 TGTGCAACACCTTCAATTAAGCAGGAGCATGCTGTGCTGCTGATTTGAATATCAC-- 13856
Db      564  CysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSerValSer 583
Qy      13857 ---TGTCAATGATTAAGACATCATTTGGTGTGTGCGTCCATGTCGCTGTGATGATCT 13913
Db      584  GlnCysUlyHisArgThrAlaLeuValSerGlyMetCysCysAlaLeuPheLeuUlyLeu 603
Qy      13914 GTTGTACAGACTTGTGTCTATTAAGTTCTAT-----TTTCACTGATGCTTCTGTGCTGCG 13967
Db      604  LeuThrUlyValLeuUlyCysHisArgPheHisGlyLeuTrpUlyMetUlySmetMetTrpAla 623
Qy      13968 TGCATTAAGTATGATA-----GGTGAACAACTC--TATGATGCC 14006
Db      624  TrpLeuGlnAlaUlyAspGlySProArgUlyAsnAlaProSerArgAsn1leCysUlyAspAla 643
Qy      14007 TTTGTATTCTATCAACCCAGATGAGAGATGGGTAAGAGATGAGATGAGTAAGTAATTTA 14066
Db      644  PheHisSerUlySerGlnUlyAspAlaUlyTrpTrpAlaGlnUlyAsnUlyMetValGlnGlnUly 663
Qy      14067 GAAGAAAGGAGTCCCATTTCAAGCTGTGCTTCACTACAGAGACTTATATCCCGGTGTG 14126
Db      664  GlnUlyAsnPheAsnProProPheUlyLeuUlyCysUlyHisUlyAspArgPhe1leProGlyUlyS 683
Qy      14127 GCCATTGCTGCCAATCATCATGAAAGTTTCCATTAAGCCGAAAGGTGATGTTGTG 14186
Db      684  Trp1le1leAspAsn1le1le--AspSer1leGlnUlySerHisUlySthrValPheVal 702

```

```

Qy      14187 GTGTCCAGACATTTCATCCAGACCCGCTGTGATCTTTGAATATGATGATGCTCAGACC 14246
Db      703  LeuSerGlnAsnPheValUlySserGlnUlyTrpCysUlyTrpGlnUlyAsnProPheSerHisPhe 722
Qy      14247 TGGCAGTTTCTGAGCAGCTGTGCTGTATCATCTTATGCTTCTGCAAGAGGTGAGAG 14306
Db      723  ArgLeuPheGlnUlyAsnAspAlaAla1leUlyLeuUlyLeuUlyPro1leGlyUlyS 742
Qy      14307 ACCCTGTACAGGACAG--GTGAGACTGTACCGGCTTCTGACAGAAACCTTACCTG 14363
Db      743  LysAla1leProGlnArgPheCysUlySLeuArgUlyS1leUlyAsnThrUlySthrUlyLeu 762
Qy      14364 GAGTGGAGAGCAGTGTCTGTGGGCGGACATTTTCTGAGACAGTCAAGAAAGCCCTG 14423
Db      763  GluTrpProMetAspArgUlyAlaGlnArgGlnUlyGlyPheTrpValAsnUlyArgAla1le 782

RESULT 9
US-10-456-947-46
; Sequence 46, Application US/10456947
; Publication No. US20040053841A1
; GENERAL INFORMATION:
; APPLICANT: Kevin J. Tracey
; APPLICANT: Huan Yang
; TITLE OF INVENTION: INHIBITORS OF THE INTERACTION BETWEEN
; TITLE OF INVENTION: HMGB POLYPEPTIDES AND TOLL-LIKE RECEPTOR 2 AS
; FILE REFERENCE: 3268.1001-007
; CURRENT APPLICATION NUMBER: US/10/456, 947
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 10/147, 447
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,034
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 784
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-10-456-947-46

Alignment Scores:
Pred. No.: 1,246-44 Length: 784
Score: 561.50 Matches: 220
Percent Similarity: 41.59% Conservative: 121
Best Local Similarity: 26.83% Mismatches: 260
Query Match: 1.70% Indels: 219
Gaps: 38

US-09-396-985b-47 (1-18989) x US-10-456-947-46 (1-784)
Qy      12246 ATCCAGACATTTAGAGATGGGCGCATATACAGGCTTAAGCCACTCTTACTTAATTTG 12305
Db      88  1leAsnThr1leGlnUlyAspSerPheSerSerUlySerLeuGlnUlySleUlyAspLeu 107
Qy      12306 ACGGAACCCCATCCAGATTAAGCCCTGGAGGCTTTCTGAGATCAATGAATTTTACAG 12365
Db      108  SerUlyAsnUlyTrpUlySerAsnLeuSerSerTrpPheUlyProUlySerSerLeuThr 127
Qy      12366 AACGTG-----GTGGCTGTGAGACAAAT 12389
Db      128  PheUlyAsnLeuUlyAsnProUlyTrpUlyThrLeuUlyGlnUlyThrSerLeuPheSerHis 147
Qy      12390 CTAGCATCTTGAAGAACTTCCCATTTGACATCTCAAACT----- 12431
Db      148  LeuThrUlySerUlyLeuUlyArgValGlyAsnMetAspThrPheThrUlyS1leGlnArg 167
Qy      12432 -----TTGAAGAACTTAATGGCTGACCAATCTTATCCAA 12467
Db      168  LysAspPheAlaGlyLeuThrPheLeuGlnUlyUlyUlyLeuUlyAspAlaSerAspLeuGln 187
Qy      12468 TCTTTCAATTAACCTGATTTTCTTAATCTGACCAATCTAAGACACTTGACCTTCC 12527

```



```

Db 188 SerYrgru---ProlySerLeuYserIleGlnValSerHisLeuIleHis 206
QY 12528 AGCAACAG-----ATTCAAAGATTATATTC 12554
Db 207 MetYsglnHisIleLeuLeuGlnIlePheValAspValIthrSerValGluCys 226
QY 12555 ACAGACTGGGGTTTTCATCATCAATGCCCTACTCATCTCTTTAGACTTCGCCG 12614
Db 227 LeuGluLeuArg-----AspThrAspLeu 234
QY 12615 AACCTATGACATT-----ATCCAAACAGTGCATTAAAGAAATTAGCTTCATAG 12668
Db 235 AspThrPheHisPheSerGluLeuSerThrGluIthrHisSerLeu---IleValCys 253
QY 12669 CTGACTTTAGAAAT-----AATTGATAGTTTA---AATGTAATAAACTTGT 12716
Db 254 PheThrPheArgAsnValIleThrAspGluSerLeuPheGlnValMetIleLeu 273
QY 12717 -----ATTCAAGGCTGGCTGGTTTAGAGTCCATGCTTGGTTG-----GGA 12761
Db 274 AsnGlnIleSerGlyLeuGlnLeuGlnIlePheAspAspCysThrLeuAsnGlyValGly 293
QY 12762 GAATTGAAATGAAGAACTTGAAGAAAGTTTGAACAATCTGCTTAGAGGCGCTGTC 12821
Db 294 AsnPheArgIleSerAspAsnAspArgValIleAspProGlyValGlu----- 310
QY 12822 AATTGACCATGGAAGATTCCGATTAGCA-----TACTTAGACTTACTCTGATGAT 12875
Db 311 ThrLeuThrIleAspArgLeuHisIleProArgPheYrLeuPheYr-----Asp 327
QY 12876 ATTATGACTATTTAATTATGTTTGAACAATGTTTCTTCATTTCCCTGGTAGTGACT 12935
Db 328 LeuSerThrLeuYrSerLeuThrGluArgValCys-----ArgIleThr 342
QY 12936 ATTGAAGGGGTAAAGACTTTTCTTAATTTGCGATGCGAACAATTAGAATTAGATTAC 12995
Db 343 ValGluAsnSerIleValPhe-----LeuValPro 352
QY 12996 TGTAAATTGGACAGTTTCCACATTTGAACCTCAAACTCTCAAAAGGCTTACTTCACT 13055
Db 353 CysLeuLeuSerGln----- 357
QY 13056 TCCAAACAAAGGTGGAAATGCTTTTCAGAGTTGATTCACCAAGCTTGAAGTTTCTAGAT 13115
Db 358 -----HisLeuYsSerLeuGluYrLeuAsp 366
QY 13116 CTCAGTAGAAT-----GGCTTGAGTTTCAAGGTTGCTGTTCTCAAGT 13160
Db 367 LeuSerGluAsnLeuMetValGluGluYrLeuYsAsnSerIleCys----- 382
QY 13161 GATTTTGGACACCAAGCTTAAGATTTAGATTTGAGCTTCAATGCTGTTATTACATG 13220
Db 383 GluAspIleArgProSerLeuGlnIleThrLeuIleLeuArgGlnAsn----- 397
QY 13221 AGTTCAAACTCTTGGGCTTAGACAACACTGAACATGATTTCAGCAATTCGCAATTTG 13280
Db 398 -----HisLeu-----AlaSerLeu 402
QY 13281 AAACAATGAGTAGTTTTCAGATTTCTATCTCATCTGAGAAACCTCATTTACTGACAT 13340
Db 403 GluIleThrGlu-----ThrLeuLeuThrLeuYsAsnLeuThrAsnIleAspIle 420
QY 13341 TCTCATCTACACCAAGTGTCTTCAATGGCATCTTCAATGGCTGTGTCAGTCTGAA 13400
Db 421 SerYs----- 422
QY 13401 GTCTTGAATAATGCTGGCAATTTCTTCAGAGAAATCTCTCGAGATCTTCACAGAG 13460
Db 423 -----AsnSerPheHisSer-----MetProGluIthrCysGlnTrp 434
QY 13461 CTGAGAACTTGACCTTCGAGACCTCTCATGTCAGTCAACTGAGAGCTGTCT----- 13514
::: :::::

```

```

Db 435 ProGluYsMetYsYrLeuAsnLeuSerSerThrArgIleHisSerValIthrGlyCys 454
QY 13515 -----CCACAGCATTTAATCACTCTCAGCTTCAGGTTACTTAATATGACCAAC----- 13568
Db 455 IlePro-----LysThrLeuGlnIleLeuAspValSerAsnAsnAsn 468
QY 13569 -----AATCTTTTTCATTGGAT----- 13586
Db 469 LeuAsnLeuPheSerLeuAsnLeuProGlnLeuYsGluLeuYrIleSerArgAsnIle 488
QY 13587 -----ACGTTTCT---TATAAGTCTGAATCTCTCCAGGTTCTTGATTACAGTCTC 13637
Db 489 LeuMetThrLeuProAspIleSerLeuLeuProMetLeuLeuValIleYsIleSerArg 508
QY 13638 AATCACTAATGACTTCCAAAACAGAACTACAGATTTTCCAAAGTACTGCTTTC 13697
Db 509 AsnIleIleThrThrPheSerIleYsGluGlnLeuAspSerPhe---HisThrLeuYsThr 527
QY 13698 TTAATCTTACTCAGATGACTTGTGCTTGTACTTGTGAACACAGAGTTTCTGCAATGG 13757
Db 528 LeuGlnIleArgIleAsnAsnPheIleCysSerCysGluIleLeuSerPheThrGln--- 546
QY 13758 ATCAAGGACCAAGGACGCTTGTGTGAAGTT-----GAACGAATGAA 13802
Db 547 -----GluGlnGlnIleLeuAlaIleValLeuIleAspTrpAlaAsnYrLeu 563
QY 13803 TGTGCAACACTTCAGATTAAGCAAGGACGCTGTGCTGTGATTTGAATATCAC----- 13856
Db 564 CysAspSerProSerHisValIleArgGlyGlnGlnIleAlaIleAspValIleLeuSerValSer 583
QY 13857 -----TGTCAAGTGAATAAGAACCATCATTTGCTGTGCTGCTGCTGCTGCTGATGATCT 13913
Db 584 GluCysHisArgThrIleAlaLeuValSerClyMetCysGlyAlaLeuPheLeuIleLeu 603
QY 13914 GTTGACAGCTTGTGCTTAATGTTCTAT-----TTCACTGATGCTTCTTGTGCGC 13967
Db 604 LeuThrGlyValLeuCysHisAspPheHisGlyLeuIthrYrMetIleYsMetMetTrpAla 623
QY 13968 TGCATTAAGTATGGTGA-----GTGAAAAATC---TATGATGCC 14006
Db 624 TrpLeuGlnIleAspValYsYrProArgIleValAspSerArgAsnIleCysYrAspAla 643
QY 14007 TTTGTTATCTACTCAAGCCAGATGAGAGCTGGGTAGAATGAGTAGTAAGAACTTTA 14066
Db 644 PheValSerYrSerGluAsnArgPheAlaYrTrpValGluAsnLeuMetValGlnGluLeu 663
QY 14067 GAAGAAAGGCTGCTTCATTTAGCTTGTGCTTCACTACAGAGACTTATTCGCGGTG 14126
Db 664 GluAsnPheAsnProProPheYsLeuCysLeuHisIleYsArgPheIleProGlyYs 683
QY 14127 GCCATTGCTGCCAAATCATTCATGAAGGTTTCCATTAAGCCGAAGGTTGTTGTG 14186
Db 684 TrpIleIleAspAsnIleIle---AspSerIleGluYsSerHisYsIthrValPheVal 702
QY 14187 GTGTCCAGCACTTCAACAGAGCGGCTGTATCTTTGAATATGATGATGCTCAGACC 14246
Db 703 LeuSerGluAsnPheValIleYsSerGluTrpCysIleYrGluLeuAspPheHisPhe 722
QY 14247 TGGCAGTTTCTGACAGCTGCTGTGTATCATTTCTATTCCTGCAAGAGGTGAGAG 14306
Db 723 ArgLeuPheGluGluAsnAsnAspAlaIleIleuIleLeuLeuGlnProIleGluYs 742
QY 14307 ACCCTGCTACGACAGAG---GTGAGCTGTACCGCTTCTCAGACGAACATTTACTG 14363
Db 743 LysAlaIleProGlnIthrPheCysYsLeuAlaArgYsIleMetAsnThrYsIthrYrLeu 762
QY 14364 GAGTGGAGAGACAGTGTCTGGGCGGACATCTTCTGAGAGAGACTCAAGAAAGCCCTG 14423
Db 763 GluIthrProMetAspGluAlaGlnArgGluGlyPheTrpValAsnLeuArgAlaIleIle 782

```

RESULT 10
 US-10-095-627-12
 ; Sequence 12, Application US/10095627

```

Publication No. US20030027260A1
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
Goddowski, Paul J.
Gurney, Austin
Mark, Melanie
Yang, Ruy-Bing
TITLE OF INVENTION: Human Toll Homologues
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/095,627
FILING DATE: 11-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/105,413A
FILING DATE: 26-Jun-1998
APPLICATION NUMBER: 60/083322
FILING DATE: 28-Apr-1998
APPLICATION NUMBER: 60/065311
FILING DATE: 13-Nov-1997
APPLICATION NUMBER: 60/062250
FILING DATE: 17-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marchang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1154-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 784 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-095-627-12
Alignment Scores:
Pred. No.: 1.55e-44 Length: 784
Score: 560.50 Matches: 220
Percent Similarity: 41.59% Conservative: 121
Best Local Similarity: 26.83% Mismatches: 260
Query Match: 1.70% Indels: 219
Gaps: 38
DB: 14
US-09-396-985b-47 (1-18989) x US-10-095-627-12 (1-784)
QY 12246 ATCCAGCAATTTGAAGATGGGGCATATCAGAGCCATCTCTACCTTAATATG 12305
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 88 IlenanhrilleglugluapserPheSerSerleuGluHisleuApsleu 107
QY 12306 ACAGAAACCCCATCCAGATTAGACCTTGAGACCTTTTCTGACTATCAAGTTTACAG 12365
::: ||| :::: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 108 SerTyranTyrlenSerAenleuSerSerSerTrpPheLysProleuSerSerleuThr 127
QY 12366 AAGCTG-----GTGGCTGTGGAACAAT 12389
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 128 PheleuAnleuGluYAsnProTyrlsThrleuGluGluThrSerleuPheSerHis 147
QY 12390 CTACATCTCTAGAGAACTTCCCATTTGACATCTCAAAACT----- 12431
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

```

Db 148 LeuThrTyLeuGluInIleleuArgValGlyAsnMetAspThrPheThrLysIleGlnArg 167
QY 12432 -----TTGAAGAAGCTTAAGTGGCTACAAATCTTAATCCAA 12467
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 168 LysAspPheAlaGlyLeuThrPheleuGluGluLeuGluInleuApsleuAserleuGln 187
QY 12468 TCTTCAAAATTACAGATATTTTCTAACTGACCAATCTAAGACACTTGACCTTGCC 12527
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 188 SerTyrlGlu---ProLysSerleuLysSerIleGlnAsnValSerHisleuIleuHis 206
QY 12528 AGCAACAAG-----ATTCAAGATTAATTGC 12554
::: |||
Db 207 MetLysGlnHisIleleuLeuGluIlePheValAspValThrSerSerValGluCys 226
QY 12555 ACAGACTGGGGTCTACATCAAAAGCCCTACATCTCTTGAACCTGCTCCCT 12614
::: |||||
Db 227 LeuGluLeuArg-----AspThrAspLeu 234
QY 12615 AACCCATATGAACTTT-----ATCCAAACGATGATTTAAAGAAATTAGCTTCATTAAG 12668
::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 235 AspThrPheHisPheSerGluLeuSerThrGlyGluThrAsnSerleu---IleLysLys 253
QY 12669 CTGACTTTAAGAAAT-----AATTGTATAGTTTA---AATGTATGAAGAACTTGT 12716
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 254 PheThrPheArgAsnValLysIleThrAspGluSerIlePheGlnValMetLysleuLeu 273
QY 12717 -----ATTCAAGCTGCTGGCTTTAGAAATCCATCGTTGGTCTG-----GGA 12761
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 274 AsnGlnIleSerGlyLeuGluGluPheAspAspCysThrleuGluGlyValGly 293
QY 12762 GAATTAGAAATGAGAAAGAACTTGAAAGAAATCTGCTAGAGGCGCTGTGC 12821
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 294 AsnPheArgAlaSerAspAsnAspArgValIleAspProGlyLysValGlu----- 310
QY 12822 AATTGACCATTAAGAATTCGATTAACA-----TACTTACATTAATCTGATGAT 12875
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 311 ThrleuThrIleArgArgleuHisIleProArgPheTyrlleuPheTyrl-----Asp 327
QY 12876 ATATTGACTTAATTATTTGTTGACAAATGTTTCTTCAATTTCCCTGGATGATGACT 12935
::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 328 LeuSerThrleuTyrlSerleuThrGluArgValLys-----ArgIleThr 342
QY 12936 ATTGAAGGGGTAAAGACTTTCTTATTAATTGCGATGCAATTTAGATTAGTTAAC 12995
::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 343 ValGluAsnSerLysValPhe-----LeuValPro 352
QY 12996 TGTAAATTGGACAGTTTCCACATTTGAAATCTCAAAATCTCAAAAGCTTACTTCACT 13055
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 353 CysleuLeuSerGln----- 357
QY 13056 TCCAAACAAGGTGGAGATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAGTTCTTAT 13115
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 358 -----HisleuLysSerleuGluTyrlLeuAsp 366
QY 13116 CTCAGTAGAAAT-----GGCTTGAGTTTCAAAAGGTGCTGTTCTCAAAAGT 13160
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 367 LeuSerGluAsnleuMetValGluGluTyrlleuLysAsnSerAlaCys----- 382
QY 13161 GATTTTGGACAACACAGCTTAAAGATTTAGATCTGAGCTTCAATGATGTTATTAATCCATG 13220
::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 383 GluAspAlaTrpProSerleuGlnThrleuIleleuArgGlnAsn----- 397
QY 13221 AGTTCAAACTTTTGGGCTTAAGAACACTAGAACATTTGATTTCCAGCATTCGAATTTG 13280
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 398 -----Hisleu-----AlaSerleu 402
QY 13281 AAACAATAGTAGATTTTCAATTCCTATCACTCGAAGAACTTATTACTTGACATT 13340
::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 403 GluLysThrGlyGlu-----ThrleuLeuThrleuLysAsnleuThrAsnIleAspIle 420
QY 13341 TCTCATCTACACACAGAGTTGCTTTCATGAGCATTTCAATGGCTTGTCAGCTTCGAA 13400
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 SerLys----- 422

```

```

QY 13401 GTCTTGAATAATGGCTGGCAATCTTTCAGAGAAATCTCTTCAGATATCTTCACAGAG 13460
Db 423 -----AsnSerPheHisSer-----MetProGluThrCysGlnTrp 434
QY 13461 CTGAGAAATCTGACCTTCCTGAGACCTCTTCAGAGTCACTGGAGCACTGTCT----- 13514
Db 435 ProGluMetCysTyrLeuAsnLeuSerThrArgGlnIleHisSerValThrGlyCys 454
QY 13515 ---CCAAAGAGATTTAACTCACTCCAGCTTCAGAGTCACTGAATATAGACCAAC--- 13568
Db 455 IlePro-----LysThrLeuGlnIleLeuAspValSerAsnAsn 468
QY 13569 ---AATCTTTTCATGGAT----- 13586
Db 469 LeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGlnLeuTyrIleSerArgAsnLys 488
QY 13587 -----ACGTTTCCT---TATAAGTGTCTGAATCCCTCCAGGTTCTTGATTAACAGTCTC 13637
Db 489 LeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValLeuLysIleSerArg 508
QY 13638 AATCACAATAAGATCTCCAAAAACAGAACTTACAGCACTTTCCAAAGTACGTACCTTTC 13697
Db 509 AsnAlaIleThrTrpPheSerLysGlnLeuAspSerPhe---HisThrLeuLysThr 527
QY 13698 TTTAATCTTACTCAGATGATCTTGCTGTGATCTTGTAACACAGAGTTTCCTGCAATGG 13757
Db 528 LeuGlnAlaGlyGlyAsnAsnPheIleCysSerCysGlnPheLeuSerPheThrGln--- 546
QY 13758 ATCAAGACAGAGGACGCTCTGTGTGAGTT-----GAAAGATGGA 13802
Db 547 -----GluGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsnTyrLeu 563
QY 13803 TGTGCAACACTTTCAGATAGACGGGCATGCCCTGCTGCAATTTGAATATACCC----- 13856
Db 564 CysAspSerProSerHisValArgGlyGlnGlnAlaGlnAspValArgLeuSerValSer 583
QY 13857 ---TGTGATGATGAATTAAGCAATCATGTGATGTCCTCAGTGCCTGTGATGATCT 13913
Db 584 GluLysHisArgThrAlaLeuValSerGlyMetCysValAlaLeuPheLeuIleLeu 603
QY 13914 GTTGTGAGATCTGTGCTGTATAGTTCTAT-----TTTCACTGATGCTCTTCTGTGGC 13967
Db 604 LeuThrGlyValLeuCysHisArgPheHisGlyLeuTrpTyrMetLysMetMetTrpAla 623
QY 13968 TGCATTAAGTATGGTGA-----GGTGAACATC---TATGATGCC 14006
Db 624 TrpLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTyrAspAla 643
QY 14007 TTTGTTATCTACTCAAGCCAGATAGAGACTGGGTAAGGAATGAGCTAGTAAGATTTA 14066
Db 644 PheValSerTyrSerGluArgAspAlaTyrTrpValGluAsnLeuMetValGlnGlnLeu 663
QY 14067 GAAGAAGGGGTGCTCCATTTCAAGCTCTGCTTCACATACAGAGACTTATATCCGGGTGG 14126
Db 664 GluAsnPheAsnProProPheLysLeuLysLeuHisLysArgAspPheIleProGlyLys 683
QY 14127 GCCATTGCTGCCAATATATCATGAAAGTTTCCATTAAGCCGAAAGGATTTGTTGG 14186
Db 684 TrpIleIleAspAsnIleIle---AspSerIleGluLysSerHisLysThrValPheVal 702
QY 14187 GTGTCACGACCTTCACAGCCGCGGTGATCTTTGAATTAAGATTCACAGACC 14246
Db 703 LeuSerGluAsnPheValLysSerGluTrpCysLysTyrGlnLeuAspPheSerHisPhe 722
QY 14247 TGGCAGTTTCTGACAGTCTGCTGTATCATCTTCATCTTCACAGAGGTGAGAG 14306
Db 723 ArgLeuPheAspGluAsnAsnAspAlaAlaIleLeuIleLeuGlnProIleGlnLys 742
QY 14307 ACCCTGCTCAGGACGAG---GTGAGCTGTACCGCTTTCAGACAGAACTTTACTCG 14363
Db 743 LysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThrTyrLeu 762

```

```

QY 14364 GAGTGGAGAGACAGTGTCTGGGGGCGACACTTCTTGAGACGACTCAGAAAAAGCCCTG 14423
Db 763 GluTrpProMetAspGluAlaGlnArgGlnGlyPheThrValAsnLeuArgAlaIle 782

RESULT 11
US-10-732-563-4
; Sequence 4, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 581830003
; CURRENT APPLICATION NUMBER: US/10/732,563
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-732-563-4

Alignment Scores:
Pred. No.: 1,55e-44 Length: 784
Score: 560.50 Matches: 220
Percent Similarity: 41.59% Conservative: 121
Best Local Similarity: 26.83% Mismatches: 260
Query Match: 1,70% Indels: 219
DB: Gaps: 38

US-09-396-985b-47 (1-18989) x US-10-732-563-4 (1-784)
QY 12246 ATCCAGCAATTAAGATGGGGCATATACAGCTTAAGCCACTCTCTAATTAATTTG 12305
Db 88 IleAsnThrIleGlnGluAspSerPheSerSerLeuGlySerLeuGlnIleAspLeu 107
QY 12306 ACAGAAACCCCAATCCAGATTAAGCCCTTTCTGAGTATCAAGTTTACAG 12365
Db 108 SerTyrAsnTyrLeuSerAsnLeuSerSerSerTrpPheLysProLeuSerSerLeuThr 127
QY 12366 AAGCTG-----GTGCTGTGAGACAAT 12389
Db 128 PheLeuAsnLeuLeuGlyAsnProTyrLysThrLeuGlyGlnThrSerLeuPheSerHis 147
QY 12390 CTAGCATCTGTAGAACTTCCCATTCGACATCTCAAACT----- 12431
Db 148 LeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIleGlnArg 167
QY 12432 -----TTGAAGAATTAATGTGGCTCAATCTTATGCCA 12467
Db 168 LysAspPheAlaGlyLeuThrPheLeuGlnGlnLeuGlnIleAspAlaSerAspLeuGln 187
QY 12468 TCTTTAAATTAATCTGTGATATTTTCTAATCTGACATCTAGAGCACTTGACCTTCC 12527
Db 188 SerTyrGln---ProLysSerLeuLysSerIleGlnAsnValSerHisLysIleLeuHis 206
QY 12528 AGCAACAG-----ATTCAAGTATTTATGTC 12554
Db 207 MetLysGlnHisIleLeuLeuLeuGlnIlePheValAspValThrSerSerValGluCys 226
QY 12555 ACAGACTTGGGGGTTCATCAATCAAAATCCCTACTCAATCTCTTTAGACCTGCTCC 12614
Db 227 LeuGlnLeuArg-----AspThrAspLeu 234
QY 12615 AACCTATGAAGTT-----ATCCAAACAGGTGATTTAAGAATTAAGGCTTCATTAAG 12668
Db 235 AspThrPheHisPheSerGluLeuSerThrGlyGlnThrAsnSerLeu---IleLysLys 253
QY 12669 CTGACTTAAGAAT-----AATTTGATAGTTTA---AATGTAATGAATAACTGT 12716
Db 254 PheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMetLysLeuLeu 273

```

```

Qy 12717 -----ATCAAGGCTGGCTGGTTTGAAGTCATGGTTGGTTG-----GGA 12761
Db 274 AsnGlnIleSerGlyLeuLeuGlnLeuGlnPheAspSerGlyThrLeuAsnGlyValGly 293
Qy 12762 GAATTGAAGAAATGAAGAAATGTTGAAAAGTTGACAAATGCTGTAGAGGGCTGTGC 12821
Db 294 AsnPheArgIleSerAspAsnAspArgValIleAspProGlyLeuValGln----- 310
Qy 12822 AATTGACATTAATGAAGATTCGCAATGCA-----TACTAGCTACTACCTGATGAT 12875
Db 311 ThrLeuThrIleAspArgLeuGlnIleProArgPheGlyLeuPheGly-----Asp 327
Qy 12876 ATTATGACTATTAATTAATGTTTGACAAATGTTTCTTCATTTCCCTGGTAGAGTGACT 12935
Db 328 LeuSerThrLeuGlyTrpSerLeuThrGlnArgValys-----ArgIleThr 342
Qy 12936 ATTGAAGGGTAAAGAACTTTCTTAATATTTCGATGGCAACATTGAATTAATTAAAC 12995
Db 343 ValGlnAsnSerGlyValPhe-----LeuValPro 352
Qy 12996 TGTTAAATTTGACACGTTTCCCACTGAAACTCAATCTCCAAAGGCTTACTTCACT 13055
Db 353 CysLeuLeuSerGln----- 357
Qy 13056 TCCAAACAAGGTGGGAATGTTTTCAGAAAGTTGATCTACCAAGCTTGAAGTTTCTGAT 13115
Db 358 -----HisLeuGlySerLeuGlnGlyLeuAsp 366
Qy 13116 CTCAGTGAAT-----GGCTGAGTTTCAAAGGTGCTGTCTTCAAAAGT 13160
Db 367 LeuSerGlnLeuMetValGlnGlyTrpLeuGlyAsnSerAlaCys----- 382
Qy 13161 GATTTGGGACAAACGCTTAAGTATTAATTAATGATGAGCTTCAATGGGTATTACCATG 13220
Db 383 GlnAspAlaTrpProSerLeuGlnThrLeuIleLeuArgGlnAsn----- 397
Qy 13221 AGTTCAAACTTCTGGGCTTGAACAACACTAGAACCTGATTTCCAGACTTCCAAATTTG 13280
Db 398 -----HisLeu-----AlaSerLeu 402
Qy 13281 AAACAAATGAGTGAATTTTCAGTATCTCTATCACTGACAAACCTCATTTACCTGACAT 13340
Db 403 GlnGlySerThrGlnGly-----ThrLeuLeuThrLeuAsnLeuThrAsnIleAspIle 420
Qy 13341 TCTCATCTACACACAGAGTTGCTTCAATGAGCATTTCAATGAGCTGTCTGCAAGTGGAA 13400
Db 421 SerIys----- 422
Qy 13401 GTCTTGAATAATGGCTGGCAATTTCTTCCAGAAAACTTCTCCAGATATCTTCACAGAG 13460
Db 423 -----AsnSerPheHisSer-----MetProGlnThrCysGlnTrp 434
Qy 13461 CTGAGAAACTTGACCTTCCTGGACCTCTCTCAAGTCACTGAGACAGAGTGTCT----- 13514
Db 435 ProGlnGlyMetGlyTrpLeuAsnLeuSerSerThrArgIleHisSerValThrGlyCys 454
Qy 13515 ---CCAACAGCATTAATCACTGCTCCAGTCTTCAGAGTCAATTAATGAGCACAAC--- 13568
Db 455 IlePro-----LysThrLeuGlnIleLeuAspValSerAsnAsnAsn 468
Qy 13569 ---AAGTCTTTTCATTTGAT----- 13586
Db 469 LeuAsnLeuPheSerLeuAsnLeuProGlnIleuGlyLeuGlyTrpIleSerArgAsnLys 488
Qy 13587 -----ACGTTTCTT---TATTAAGTCTGAACTCCCTCCAGGTTCTTGATTACAGTCTC 13637
Db 489 LeuMetThrLeuProAspAlaSerLeuLeuProMetLeuValLeuValIleSerArg 508
Qy 13638 AATCATATATGACTTCCAAAAACAGAACTACAGCATTTTCCAAAGTACTGACTTTC 13697
Db 509 AsnAlaIleThrThrPheSerGlyGlnIleuAspSerPhe---HisThrLeuGlyThr 527

```

```

Qy 13698 TTAAATCTTACTGAGATGACTTTGCTGTGTAATGTAACACAGAGTTTCTGCAATGG 13757
Db 528 LeuGlnAlaGlyLeuGlyAsnAsnPheIleCysSerCysGlnPheLeuSerPheThrGln--- 546
Qy 13758 ATGAGGACCAAGGCGACTTGTGTGGAAGTT-----GACGAAATGGAA 13802
Db 547 -----GlnGlnGlnIleAlaLeuAlaGlyValLeuIleAspTrpProAlaAsnGlyLeu 563
Qy 13803 TGTGCAACACCTTCAGATTAAGACAGGCAATGCTGTGCTGATGTTGAATATACAC----- 13856
Db 564 CysAspSerProSerGlnValArgGlyGlnGlnAlaGlnAspValArgLeuSerValSer 583
Qy 13857 ---TGTCAATGATTAAGACATCAATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 13913
Db 584 GlnCysHisArgThrAlaLeuValSerGlyMetCysCysValAlaLeuPheLeuIleLeu 603
Qy 13914 GTTGTACAGCTTGTGTGTATTAAGTTGTAT-----TTTCACTGATGCTTGTGTGTGTG 13967
Db 604 LeuThrGlyValIleuGlyCysHisArgPheHisGlyLeuThrTrpGlyMetGlyMetTrpAla 623
Qy 13968 TGCATAAGATGATGA-----GGTAAACATC---TATGATGCC 14006
Db 624 TrpLeuGlnAlaGlySerGlyValProArgGlyValAlaProSerArgAsnIleCysGlyAspAla 643
Qy 14007 TTTGTATCTACTCAAGCCAGATGAGCACTGGGTGAAGATGAGCTAGTAAAGAAATTTA 14066
Db 644 PheValSerGlySerGlnGlnAspAlaGlyTrpValGlnLeuMetValGlnGlnLeu 663
Qy 14067 GAAGAAAGGGTGTGCTGATTTCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 14126
Db 664 GlnAspPheAsnProGlyPheGlyLeuGlyCysValGlnIleValArgAspPheIleProGlyLys 683
Qy 14127 GCAATGTCTGCCAAATCATGCAATGAAGTTTCCATTAAGCCGAAAGGATGTTGTGTG 14186
Db 684 TrpIleIleAspAsnIleIle---AspSerIleGlySerSerIleGlyTrpValPheVal 702
Qy 14187 GTGTCCAGCACTTCAATCCAGACCCGCTGTGATCTTGTGAATATGATGATGTGTGCAAGC 14246
Db 703 LeuSerGlnAsnPheValGlySerGlnTrpCysGlySerGlyGlnLeuAspPheSerHisPhe 722
Qy 14247 TGGCACTTTCAGACAGCTGTGTGTGATCATCTTCAATGCTCTGCGAAGAGTGGAGAG 14306
Db 723 ArgLeuPheAspGlnAsnAsnAspAlaAlaIleLeuIleLeuLeuGlnProIleGlnLys 742
Qy 14307 ACCGTGCTACGAGCAGAG---GTGAGCTGTACCGCTTCTGACGAGAACTTACTGCTG 14363
Db 743 LysAlaIleProGlnArgPheCysGlyValLeuArgLysIleMetAsnThrLysThrTrpLeu 762
Qy 14364 GAGTGGAGAGACAGTGTCTGGGAGCGGACATCTTCTGAGACGACTCAGAAAAAGCCCTG 14423
Db 763 GlnTrpProMetAspGlnAlaGlnArgGlnGlyPheThrValAsnLeuArgAlaIleIle 782

RESULT 12
US-10-732-796A-4
; Sequence 4, Application US/10732796A
; Publication No. US20040197865A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tarun K.
; APPLICANT: Fink, Jason R.
; TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines
; FILE REFERENCE: 58182US004
; CURRENT APPLICATION NUMBER: US/10/732,796A
; CURRENT FILING DATE: 2003-12-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 784
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-10-732-796A-4
Alignment Scores:

```

Pred. No.:	1.55e-44	length:	784
Score:	560.50	Matches:	220
Percent Similarity:	41.59%	Conservative:	121
Best Local Similarity:	26.83%	Mismatches:	260
Query Match:	1.70%	Indels:	219
DB:	16	Gaps:	38

US-09-396-985B-47 (1-18989) X US-10-732-796A-4 (1-784)

QY	12246	ATTCAGACATTGAAATGGGGCATATACAGAGCTTAAGCAACCTCTCTACCTTAATATGG	12305
Db	88	IIleAnthrIIleGluuIleuAspSerPheSerSerGluGlySerIleuIhIleuAspLeu	107
QY	12306	ACAGAAACCCCATCCAGAGTTTAGCCCTGGAGACCTTTTCTGACATCAAGTTTACAG	12365
Db	108	SerTrpAnthrIleuSerIleuSerIleuSerSerSerTrpPheIleuProIleuSerIleuThr	127
QY	12366	AAAGCTG-----GTGGCTGTGGACAAAT	12389
Db	128	PheIleuAsnIleuGluIleAsnProTyrIleThrLeuGlyGlyIleuThrSerIleuPheSerHis	147
QY	12390	CTAGACATCTAGAGAACTCCCATTTGACATCTCAAACT-----	12431
Db	148	LeuThrIleuLeuGlnIleIleuArgValGlyAsnMetAspThrPheThrIleuIleGlnArg	167
QY	12432	-----TTGAAAGAACTAAATAGTGCTCACAATCTTAACCA	12467
Db	168	LysAspPheIleuGlyLeuThrPheIleuGlnGluIleuGlnIleAspAlaSerAspLeuGln	187
QY	12468	TCATTCAATTAAGCTGAGATTTTTCATCTGACCAATTCAGATGACAGACTTGACCTTTC	12527
Db	188	SerTyrGlu---ProIysSerIleuIysSerIleGlnAsnValSerHisIleuIleuHis	206
QY	12528	AGCAACAG-----ATTCAAGATTATATGSC	12554
Db	207	MetIysGlnIhIleIleuLeuLeuGlnIlePheValAspValIleuSerSerValGluCys	226
QY	12555	ACAGACTGTGGGGTTCTACATCAAAAGCCCTCAATCTCTTTAGACCTGTGCCGTG	12614
Db	227	LeuGluIleuArg-----AspIleuAspLeu	234
QY	12615	AACCCATGAACATT-----ATCCAAACAGTGCAATTAAAGAAATTAGGCTTCAAG	12668
Db	235	AspIleuPheHisPheSerGluIleuSerThrGlyIleuThrAsnSerLeu---IleuIysIys	253
QY	12669	CTGACTTAAGAAT-----AATTGTAATGTTTA---AATGTATGAAAATTGT	12716
Db	254	PheThrPheIleuArgAsnValIysIleThrAspGluSerIleuPheGlnValMetIysLeuLeu	273
QY	12717	-----ATTCAAGGTCTGCTGGGTTTAGAAGTCCATCGTTGGTTCTG-----GGA	12761
Db	274	AsnGlnIleSerGlyLeuLeuGlnIleuGlnPheAspAspCysThrIleuAsnGlyValGly	293
QY	12762	GAATTGAAATGAAAGAACTTGAAAAAGTTTGACAAATCTGCTCTAGAGGGCCTGTGC	12821
Db	294	AsnPheArgIleAserAspAsnAspArgValIleAspProGlyIleValGlu-----	310
QY	12822	AATTGGCCATTGAAGAATTCGACTTAGCA-----TACTTAGACATCTACTCCATGAT	12875
Db	311	ThrIleuThrIleuArgIleuHisIleProArgPheTyrIleuPheTyr-----Asp	327
QY	12876	ATTATTCACATTATTAATGTGGACAAATGTTTCTTCAATTTCCCTGTGATGATGACT	12935
Db	328	LeuSerThrIleuTyrSerIleuThrGlnArgValIys-----ArgIleThr	342
QY	12936	ATTGAAAAGGTAAAGACTTTTCTTATTAATTTTCGATGCAACATTAGATTAGTTAATC	12995
Db	343	ValGluAsnSerIysValPhe-----LeuValPro	352
QY	12996	TGTAAATTGAGACGTTTCCACATTTGAAACTCAAAATCTCTCAAAAAGCTTACTTCACT	13055
Db	353	CysIleuLeuSerGln-----	357

OY	13056	TCCAACAAAGGTGGAAATGCTTTTTCAGAAAGTTGATCTACCAAGCTTGAGTTCTTACAT	13111
Db	358	-----HsLeuLysSerLeuGlnIleuAsp	366
OY	13116	CTCAGTAGAAT-----GGCTTGAGATTTCAAGGTGTGCTGTTCTCAAGT	13160
Db	367	LeuSerGlnLeuMetValGlnGlnIleuIleuValAsnSerAlaCys-----	382
OY	13161	GATTTTGGGCAACACAGCCTAAAGTATTAGATCTGAGCTTCATGGTGTATTACCATG	13220
Db	383	GlnAspAlaIleProSerLeuGlnThrLeuIleLeuArgGlnAsn-----	397
OY	13221	AGTTCAAACTTCTGGGCTTAGAACAACTAGAACATCTGGATTTCCAGATTTCCAATTG	13280
Db	398	-----HisLeu-----AlaSerLeu-----	402
OY	13281	AAACAAATGATGATGATTTTCAGTATTCCTATGACCTCAGAAACCTCATTTACCTGACATT	13340
Db	403	GlnIleThrGln-----ThrLeuLeuThrLeuValAsnLeuThrAsnIleAspIle	420
OY	13341	TCTCATCTACACACAGAGTGTCTTCAATGGCATCTTCAATGGCTGTCCAGTCTGAA	13400
Db	421	SerLys-----	422
OY	13401	GTCCTGAAAATGGCTGCGCAATCTTTTCCAGGAAAACCTCTCCAGATATCTTCCACAGG	13460
Db	423	-----AsnSerPheHisSer-----MetProGlnThrCysGlnTrp	434
OY	13461	CTGAGAAACTGATCTTCCTGGACCTCTCTCAGTGTCACTGAGACAGATGTGCT-----	13514
Db	435	ProGlnIleMetLysIleuAsnLeuSerSerThrArgIleHisSerValThrGlnCys	454
OY	13515	---CCAAACAGCATTTAACTCACTCTCCAGCTCTTCAGCTCTTCAAGTAAATAGACCAAC---	13568
Db	455	IlePro-----LysThrLeuGlnIleLeuAspValSerAsnAsn	468
OY	13569	---AACTCTTTTCATTGCAAT-----	13586
Db	469	LeuAsnLeuPheSerLeuAsnLeuProGlnLeuLysGlnLeuLysIleSerArgAsnLys	488
OY	13587	-----ACGTTTCTCT---TATAAGTGTCTGAACCTCCCTCAGATTCTTGATTACAGTCTC	13637
Db	489	LeuMetThrLeuProAspAlaSerIleLeuLeuProMetLeuLeuValLeuLysIleSerArg	508
OY	13638	AATCACATTAATGACTCTCAAAAACAGAACTACAGACTTTTCCAAAGTAGTCACTTTC	13697
Db	509	AsnAlaIleThrThrPheSerLysGlnGlnLeuAspSerPhe---HisThrLeuLysThr	527
OY	13698	TTAAATCTTATCTGAAATGATCTTGTGTTGACTGTGTGAACACACAGATTTCTGCAATGG	13757
Db	528	LeuGlnAlaGlyIleAsnAsnPheIleCysSerCysGlnPheLeuSerPheThrGln---	546
OY	13758	ATCAAGACACAGAGGACGCTCTGTGGGAAGT-----GAACGATGGAA	13802
Db	547	-----GlnGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsnTrpLeu	563
OY	13803	TGTGCACACACCTTCATATGACAGGGCAGGCGCTGTGCTGATGTTGAATATACAC-----	13856
Db	564	CysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSerValSer	583
OY	13857	---TGTCAAGATGAATAAGACATCATTTGGTGTGTGCGGTCTTCAAGTGTGCTGTAGTATCT	13913
Db	584	GlnCysHisIleArgThrAlaLeuValIleSerGlyMetCysCysAlaLeuPheLeuIleLeu	603
OY	13914	GTTGTGACAGCTTGCTGATATAGTTCTAT-----TTTCACTGATGCTTCTGCTGGC	13967
Db	604	LeuThrGlyAlaLeuCysHisIleArgPheHisGlyLeuTrpTrpIleMetLysMetCysTrpAla	623
OY	13968	TGCATTAAGATAGTGTGATA-----GGTGAACAAACATC---TATGATGCC	14006
Db	624	TrpLeuGlnAlaIleArgLysProArgLysAlaProSerArgAsnIleCysIleThrAspAla	643
OY	14007	TTTGTATCTACTCAAGCAGATGAGACTGGGTGAAGATGAGCTAGTAAGAAATTTA	14066

```

Db      644 PheValSerTyrSerGluArgAspAlaTyrTrpValGluValLeuMeValGlnGluLeu 663
Qy      14067 GAAGAAGGGGTGCTCCATTTACAGCTGCTGCTTCACTACAGAGACTTTATTCGGGTGTG 14126
Db      664 GluAsnPheAsnProPheProPheLeuValCysLeuHisIleValArgAspPheIleProGlyLys 683
Qy      14127 GCCATTGCTGCACATCATCATGAGTTTCCATAAAGCCGAAGGTGATTTGTGTG 14186
Db      684 TrpIleIleAspAsnIleIle--AspSerIleGluLysSerHisIleValPheVal 702
Qy      14187 GTGTCCCACTCATTCATCCAGAGCCGCTGTGTATCTTGAATATGAGATTGCTCAGACC 14246
Db      703 LeuSerGluAsnPheValLysSerGluTrpCysLysTyrGluLeuAspPheSerHisPhe 722
Qy      14247 TGGCAGTTTTCAGACAGTCGCTGTGTATCATTTTCATTTGCTTCGACAGAGGTGAGAG 14306
Db      723 ArgLeuPheAspGluAsnAsnAspAlaIleIleuIleLeuLeuGluProIleGluLys 742
Qy      14307 ACCCTGCTCAGGACGACG--GTGAGCTGTACCGCTTCACACAGAACACTTACTCTG 14363
Db      743 LysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysThrTyrLeu 762
Qy      14364 GAGTGGAGAGACAGTGTCTGTGGCGGACATCTTCTTGAGACGACTCAGAAAGCCCTG 14423
Db      763 GluTrpProMetAspGluAlaGlnArgGluGlyPheTrpValAsnLeuArgAlaIle 782

RESULT 13
US-10-741-600-1390
; Sequence 1390, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARCILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: C1001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1390
; LENGTH: 784
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-741-600-1390

Alignment Scores:
Pred. No.: 1.55e-44 Length: 784
Score: 560.50 Matches: 220
Percent Similarity: 41.59% Conservative: 121
Best Local Similarity: 26.83% Mismatches: 260
Query Match: 1.70% Indels: 219
DB: 17 Gaps: 38

US-09-396-985B-47 (1-18989) x US-10-741-600-1390 (1-784)
Qy      12246 ATCCGAGAAATTGAAGATGGGGCATATACAGACCTTCTTACCTTATATATG 12305
Db      88 IleAsnThrIleGluGlnAspSerPheSerSerLeuGlySerLeuGlnIleAsnArgLeu 107
Qy      12306 ACAGGAACCCCATCAGAGTTTAGCCCTGGGAGCCTTTTTCGACATATCAAGTTTACAG 12365
Db      108 SerTyrAsnTyrLeuSerAsnLeuSerSerSerTrpPheLysProLeuSerSerLeuThr 127
Qy      12366 AAGCTG-----GTGCTGTGGAGACAAAT 12389
Db      128 PheLeuAsnLeuLeuGlyAsnProTyrLysThrLeuGlyGluThrSerLeuPheSerHis 147
Qy      12390 CTAGATCTCTTAGAAGAACTCCCATTTGGACATCTCAAAACT-----12431
Db      148 LeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspThrPheThrLysIleGlnArg 167
Qy      12432 -----TTGAAGAAGCTTAATGTGGCTCACAACTTATCCA 12467

```

```

Db      168 LysAspPheAlaGlyLeuThrPheLeuGluGluLeuGlnIleAspAlaSerAspLeuGln 187
Qy      12468 TCTTTCAAAATTAACCTGAGATTTTTCATCTATCTACCAATCTAGACACTTGACCTTCC 12527
Db      188 SerTyrGlu--ProLysSerLeuLysSerIleGlnAsnValSerHisIleuHis 206
Qy      12528 AGCAACAG-----ATTCAAAGTATTTATTTGC 12554
Db      207 MetLysGlnHisIleLeuLeuLeuGluIlePheValAspValThrSerSerValGluCys 226
Qy      12555 ACAGATCTGGGGTTTCTACATCAAAATGCCCTTACATCTCTTTTACAGCTGTCCCTG 12614
Db      227 LeuGluLeuArg-----AspThrAspLeu 234
Qy      12615 AACCCATGAACTTT-----ATCCAAACAGGTGCATTTAAAGAAATTAGGCTTCATAG 12668
Db      235 AspThrPheHisAspSerGluLeuSerThrGlyThrAsnSerLeu--IleLysLys 253
Qy      12669 CTGACTTTAAGAAAT-----AATTTGATAGTTTA--AATGTAATGAAGAACTGT 12716
Db      254 PheThrPheArgAsnValLysIleThrAspGluSerLeuPheGlnValMetLysLeuLeu 273
Qy      12717 -----ATTCAAGGTCTGCTGGTTTGAAGATCCATCGTTGGTTCG-----GGA 12761
Db      274 AsnGlnIleSerGlyLeuLeuGluLeuGluPheAspAspCysThrLeuAsnGlyValGly 293
Qy      12762 GAATTGAAAATGAGAAACTTGAAAAGTTTGACAAATCTGCTCTAGAGGCGCTGTGC 12821
Db      294 AspPheArgAlaSerAspAsnAspArgValIleAspProGlyLysValGlu-----310
Qy      12822 AATTGACCATTTGAAGAAATTCGATTAGCA-----TACTTAGACTACTACCTGATGAT 12875
Db      311 ThrLeuThrIleArgAlaLeuHisIleProArgPheLysLeuPheLys-----Asp 327
Qy      12876 ATTAATGACTTATTAATGTTTGACAAATGTTTCTTCATTTTCCCTGAGTGAAGTGAAT 12935
Db      328 LeuSerThrLeuTyrSerLeuThrGluArgValLys-----ArgIleThr 342
Qy      12936 ATTGAAGAGGTAAAGACTTTTCTTATTAATTTGCGATGGCAACTTGAATTAAGTTAAC 12995
Db      343 ValGluAsnSerLysValPhe-----LeuValPro 352
Qy      12996 TGTAATTTGAGACAGTTTCCACATTTGAACCTCAAACTCTCAAAAGCTTACTTCACT 13055
Db      353 CysLeuLeuSerGln-----357
Qy      13056 TCCAAAGAGTGGGATGCTTTTTCAGAAATTGATCTACCAAGCCTTGAAGTTTATGAT 13115
Db      358 -----HisLeuLysSerLeuGluTyrLeuAsp 366
Qy      13116 CTCAGTGAAGAT-----GGCTTGAGTTTCAAAAGTCTGTTCTCAAAAGT 13160
Db      367 LeuSerGluAsnLeuMetValGluGluTyrLeuLysAsnSerAlaCys-----382
Qy      13161 GATTTTGGGACACCAAGCCTTAAGTATTTAGATCTGATCTCAATGATGTTATATACATG 13220
Db      383 GluAspAlaTrpProSerLeuGlnThrLeuIleLeuArgGlnAsn-----397
Qy      13221 AGTTCAAACTTTTGAGCTTAGAACAACCTGAATCTGATTTCCAGATTTCCAAATTTG 13280
Db      398 -----HisLeu-----AlaSerLeu 402
Qy      13281 AAACAAATGAGTGAAGTTTTCAGATATCTTCACTACGAAACCTGATTTACCTTGACAT 13340
Db      403 GluLysThrGlyGlu-----ThrLeuLeuThrLeuLysAsnLeuThrAsnIleAspIle 420
Qy      13341 TCTCATACTCACACACAGATGCTTTCAATGGCATCTTCAATGGCTGTGCAAGCTCGAA 13400
Db      421 SerLys-----422
Qy      13401 GTCTTGAAGAAATGCTGGCAATTTCTTTCAGAGAAACTTCTTCAGATATCTTCACAGAG 13460

```

```

Db      423 -----AsnSerPheHisSer-----MetProGluThrCysGlnTrp 434
QY      13461 CTGGAAGAACTTGACCTTCTCGAGACTCTCTCAGTGTCACACGAGCACTTCTCT----- 13514
Db      435 ProGluYsMetLysTrpLeuAsnLeuSerSerThrArgIleHisSerValThrGlyCys 454
QY      13515 ---CCAACAGCACTTAACTCACTCTCCAGCTCTTCAGTCACTAATATGAGCCACAAAC--- 13568
Db      455 IlePro-----LysThrLeuGluIleLeuAspValSerAsnAsnAsn 468
QY      13569 ---AAGCTTTTCATTGGAT----- 13586
Db      469 LeuAsnLeuPheSerLeuAsnLeuProGluLeuLysGluLeuTrpLysArgAsnLys 488
QY      13587 -----ACGTTTCTCT---TATAAGTCTGAACTCCCTCCAGCTTCTTGATTAAGCTCTC 13637
Db      489 LeuMetThrLeuProAspAlaSerLeuLeuProMetLeuLeuValLeuLysIleSerArg 508
QY      13638 AATCACAATAATGACTTCCAAAAAACAAGAACTACAGCACTTTCACAGAGTTCCTGCAATGG 13697
Db      509 AsnAlaIleThrThrPheSerLysGluGlnLeuAspSerPhe---HisThrLeuLysThr 527
QY      13698 TTAAATCTTACTCAAAATGACTTCTTGTACTTGTAACAACAAGTTCCTGCAATGG 13757
Db      528 LeuGluIleaglYglAsnAsnPheIleCysSerCysGluPheLeuSerPheThrGln--- 546
QY      13758 ATCAGAGACCAAGAGCACTTCTTGGAAGTT-----GAAAGATGGA 13802
Db      547 -----GluGlnGlnAlaLeuAlaLysValLeuIleAspTrpProAlaAsnTrpLeu 563
QY      13803 TGTGCAACACCTTCAGATTAAGCAGCATGCTGCTGAGATTGGAATATCACC----- 13856
Db      564 CysAspSerProSerHisValArgGlyGlnGlnValGlnAspValArgLeuSerValSer 583
QY      13857 ---TGTCAATGAATAAGACCATCATTTGCTGTCTGCTGCTCACTGCTTGTAATCT 13913
Db      584 GluCysHisArgThrAlaLeuValSerGlyMetCysCysAlaLeuPheLeuIleLeu 603
QY      13914 GTTGACAGACTTCTGGTCTAATAGTTCTAT-----TTTCACTGATGCTTCTTGCTGGC 13967
Db      604 LeuThrGlyValLeuCysHisArgPheHisGlyLeuTrpTrpMetLysMetMetTrpAla 623
QY      13968 TGCATAGATGATGGTGA-----GGTGAATCATC---TATGATGCC 14006
Db      624 TrpLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTrpAspAla 643
QY      14007 TTTGTTATCTACTCAAGCCAGATGAGCACTGGGTAAAGCAATGAGCTTAAGCAATTTA 14066
Db      644 PheValSerTrpSerGluArgAspAlaIleTrpValGluAsnLeuMetValGlnGluLeu 663
QY      14067 GAAGAAGGGTGCCTCATTTCACTTCTGCTTCACTACAGACACTTTATCCGGGTGTG 14126
Db      664 GluAsnPheAsnProPheLysLeuCysLeuHisLysArgAspPheIleProGlyLys 683
QY      14127 GCCATTCTGCAACATCATTCATCAATGAAGTTTCCATAAAGCCAAAGGTGATGTTGTG 14186
Db      684 TrpIleIleAspAsnIleIle---AspSerIleGluLysSerHisLysTrpValPheVal 702
QY      14187 GTGTCCAGCACTTCATCAAGAGCCGCTGTGTATCTTTGAATATGAGATGCTCAGACC 14246
Db      703 LeuSerGluAsnPheValLysSerGluTrpCysLysTrpGluLeuAspPheSerHisPhe 722
QY      14247 TGGCAGTTTCTGAGCACTGCTGCTGTATCATTTTCTTCTGCTGCAAGAGTGGAGAG 14306
Db      723 ArgLeuPheAspGluAsnAsnAspAlaAlaIleLeuIleLeuGluProIleGlyLys 742
QY      14307 ACCCTGTACAGCAGAG---GTGAGCTGTACCGCTTCACAGCAAGAACTTACTCTG 14363
Db      743 LysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnTrpLysThrTrpLeu 762
QY      14364 GAGTGGAGAGACAGTGTCTGTGGGCGGACATCTTCTGAGACGACACTCAGAAAAAGCCCTG 14423
Db      763 GluTrpProMetAspGluAlaGlnArgGluGlyPheTrpValAsnLeuArgAlaAlaIle 782

```

```

RESULT 14
US-10-741-600-1391
; Sequence 1391, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0601499
; CURRENT APPLICATION NUMBER: US/10/741,600
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1391
; LENGTH: 784
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-741-600-1391

Alignment Scores:
Pred. No.: 1,55e-44 Length: 784
Score: 560.50 Matches: 220
Percent Similarity: 41.59% Conservative: 121
Best Local Similarity: 26.83% Mismatches: 260
Query Match: 1,70% Indels: 219
DB: 17 Gaps: 38

US-09-396-985B-47 (1-18989) x US-10-741-600-1391 (1-784)
QY      12246 ATCCAGCACTTGAAGATGGGGCATATCAGAGCTTAAGCAACCTCTACCTTAATATG 12305
Db      88 IleAsnThrIleGluGlnAspSerSerSerLeuLysLeuGluHisLeuAspLeu 107
QY      12306 ACAAGAAACCCATCCAGACTTAAAGCCCTGAGACCTTTCTGCACTATCAAGTTTACAG 12365
Db      108 SerTyrAsnTrpLysSerAsnLeuSerSerSerTrpPheLysProLeuSerSerLeuThr 127
QY      12366 AAGCTG-----GTGCTGTGGAGACAAAT 12389
Db      128 PheLeuAsnLeuLeuGluAsnProGlyLysThrLeuGlyLysThrSerLeuPheSerHis 147
QY      12390 CTAGCATCTCTAGGAACCTCCCATGGAACATCTCAAACT----- 12431
Db      148 LeuThrLysLeuGlnIleLeuArgValGlyAsnMetAspTrpPheThrLysIleGlnArg 167
QY      12432 -----TTGAAGAAGCTTAATGTGGCTCAAACTTTATCCAA 12467
Db      168 LysAspPheAlaGlyLeuThrPheLeuGluGlnLeuGluIleAspAlaSerAspLeuGln 187
QY      12468 TCTTTCAAAATTACCTGAGATTTTCTTAATCTGACCAATCTTAAGCACTTGAACCTTTCC 12527
Db      188 SerTyrGlu---ProLysSerLeuLysSerIleGlnAsnValSerHisLeuIleLeuHis 206
QY      12528 AGCAACAG-----ATTCAAAGATTTATTTGC 12554
Db      207 MetLysGlnHisIleLeuLeuLeuGluIlePheValAspValHisSerSerValGluCys 226
QY      12555 ACAGACTTGGGGTTCTACATCAAAATGCCCTACTCAATCTCTTTAGACCTGTCCCTG 12614
Db      227 LeuGluLeuArg-----AspTrpAspLeu 234
QY      12615 AACCTTAAGACTTT-----ATTCAAACAGGTGCACTTAAGAATAATGAGCTTCATAG 12668
Db      235 AspTrpPheHisAspSerGluLeuSerThrGlyLysThrAsnSerLeu---IleLysLys 253
QY      12669 CTGACTTTAAGAAAT-----AATTGATAGTTTA---AATGTAATGAAGAACTGT 12716
Db      254 PheThrPheThrAsnValLysIleThrAspGluSerLeuPheGlnValMetLysLeuLeu 273
QY      12717 -----ATTCAAGATCTGCTGCTGTGTAAGATGCATCGTTGGTCTG-----GGA 12761
Db      274 AsnGlnIleSerIleLysLeuLeuGluLeuGluPheAspAspCysThrLeuAsnGlyValGly 293

```



```

Db      604 LeuThrGlyValLeuCyHisArgPheHisGlyLeuTrpTyrMetLysMetMetTrpAla 623
QY      13968 TGCATAAAGTATGTTAGT-----GTTGAAAATC---TATGATGCC 14006
Db      624 TrpLeuGlnAlaLysArgLysProArgLysAlaProSerArgAsnIleCysTyrAspAla 643
QY      14007 TTTGTTATCTACTCAGACGAGATGAGACTGGGTAAAGATGAGCTAGTAAAGATTTA 14066
Db      644 PheValSerTyrSerGlnArgAspAlaTyrTrpValGluAsnLeuMetValGlnGluLeu 663
QY      14067 GAAGAAGGGGTGCTCCATTTCAGCTGTGCTGCTCACTACAGAGACTTTATTCCTGGTGTG 14126
Db      664 GluAsnPheAsnProPheLysLeuCyLeuHisLysArgAspPheIleProGlyLys 683
QY      14127 GCCATTGCTGCCAATCATCATGAAAGTTTCATAAAGCCGAAGGTGATTTGTTGTG 14186
Db      684 TrpIleIleAspAsnIleIle--AspSerIleGluLysSerHisLysTrpValPheVal 702
QY      14187 GTGTCCCAAGCACTTCATCTCAGAGCCGCTGTGTATCTTTGAATATGAGATTGCTCAGACC 14246
Db      703 LeuSerGluAsnPheValLysSerGluTrpCysLysTyrGluLeuAspPheSerHisPhe 722
QY      14247 TGGCAGTTTCTGAGCAGTCTGTGTATCATCTTCATTGTCTGCAGAAAGTGGAGAG 14306
Db      723 ArgLeuPheAspGluAsnAsnAspAlaAlaIleLeuIleLeuGluProIleGluLys 742
QY      14307 ACCCTGCTCAGGCGAGCAG---GTGAGAGCTGTACCGCTTCAGACGAGAACTTACCTG 14363
Db      743 LysAlaIleProGlnArgPheCysLysLeuArgLysIleMetAsnThrLysTrpTyrLeu 762
QY      14364 GAGTGGAGGAGCAGTGTCTCTGGGCGGACATCTTCTGAGAGCAGTCAAGAAAGCCCTG 14423
Db      763 GluTrpProMetAspGluAlaGlnArgGluGlyPheTrpValAsnLeuArgAlaAlaIle 782

```

Search completed: March 30, 2005, 08:08:43
 Job time : 903 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 30, 2005, 03:00:48 ; Search time 1865 Seconds
(without alignments)
17753.401 Million cell updates/sec

Title: US-09-396-985B-48
Perfect score: 86900
Sequence: 1 ttccatcatcatgtagtc.....catttagtatttccaga 50000

Scoring table: BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1407402 seqs, 331100923 residues
Total number of hits satisfying chosen parameters: 5629608

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame_n2p,model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09396985/funcat_28032005_155745_21245/app_query.fasta_1.85098
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blcsum62
-TRANS=human40.cdd -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HMAPSIZE=500 -MINLEN=0
-MAILEN=2000000000 -USER=US09396985@cgn2_1.1.3955@funcat_28032005_155745_21245
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result Query

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	2600.5	3.0	837	10	US-09-950-041-26	Sequence 26, App1
2	2591	3.0	799	10	US-09-950-041-8	Sequence 8, App1
3	2591	3.0	799	14	US-10-128-166-7	Sequence 7, App1
4	2591	3.0	799	16	US-10-732-563-8	Sequence 8, App1
5	2591	3.0	799	16	US-10-732-563-8	Sequence 8, App1
6	575.5	0.7	641	16	US-10-408-765A-181	Sequence 181, App
7	571.5	0.7	956	14	US-10-000-256A-153	Sequence 153, App
8	571.5	0.7	1275	14	US-10-025-201-3	Sequence 3, App1
9	568.5	0.7	1010	14	US-10-050-882-80	Sequence 80, App1
10	567.5	0.7	1275	17	US-10-800-322-34	Sequence 34, App1
11	559.5	0.6	1272	15	US-10-114-270-30	Sequence 192, App
12	548	0.6	1032	10	US-09-954-907B-192	Sequence 31, App1
13	548	0.6	1032	14	US-10-272-502B-31	Sequence 31, App1
14	548	0.6	1032	15	US-10-407-952-32	Sequence 32, App1
15	551.5	0.6	1274	16	US-10-415-615-3	Sequence 3, App1
16	541.5	0.6	240	15	US-10-094-749-2471	Sequence 2471, App
17	541.5	0.6	1018	15	US-10-085-198-156	Sequence 156, App
18	530.5	0.6	1041	9	US-09-168-978-3	Sequence 3, App1
19	530.5	0.6	1041	9	US-09-978-295A-498	Sequence 498, App
20	530.5	0.6	1041	9	US-09-978-697-498	Sequence 498, App
21	530.5	0.6	1041	9	US-09-978-192A-498	Sequence 498, App
22	530.5	0.6	1041	9	US-09-999-832A-498	Sequence 498, App
23	530.5	0.6	1041	10	US-09-978-189-498	Sequence 498, App
24	530.5	0.6	1041	10	US-09-978-608A-498	Sequence 498, App
25	530.5	0.6	1041	10	US-09-978-585A-498	Sequence 498, App
26	530.5	0.6	1041	10	US-09-978-191A-498	Sequence 498, App
27	530.5	0.6	1041	10	US-09-978-403A-498	Sequence 498, App
28	530.5	0.6	1041	10	US-09-978-564A-498	Sequence 498, App
29	530.5	0.6	1041	10	US-09-999-833A-498	Sequence 498, App
30	530.5	0.6	1041	10	US-09-981-915A-498	Sequence 498, App
31	530.5	0.6	1041	10	US-09-978-824-498	Sequence 498, App
32	530.5	0.6	1041	10	US-09-918-585A-498	Sequence 498, App
33	530.5	0.6	1041	10	US-09-999-834A-498	Sequence 498, App
34	530.5	0.6	1041	10	US-09-978-423A-498	Sequence 498, App
35	530.5	0.6	1041	10	US-09-978-193A-498	Sequence 498, App
36	530.5	0.6	1041	10	US-09-999-830A-498	Sequence 498, App
37	530.5	0.6	1041	10	US-09-978-757A-498	Sequence 498, App
38	530.5	0.6	1041	10	US-09-978-187A-498	Sequence 498, App
39	530.5	0.6	1041	10	US-09-978-643A-498	Sequence 498, App
40	530.5	0.6	1041	10	US-09-978-375A-498	Sequence 498, App
41	530.5	0.6	1041	10	US-09-978-298A-498	Sequence 498, App
42	530.5	0.6	1041	10	US-09-978-188A-498	Sequence 498, App
43	530.5	0.6	1041	10	US-09-978-681A-498	Sequence 498, App
44	530.5	0.6	1041	10	US-09-978-194A-498	Sequence 498, App
45	530.5	0.6	1041	10	US-09-999-829A-498	Sequence 498, App

ALIGNMENTS

RESULT 1
US-09-950-041-26
Sequence 26, Application US/09950041
Publication No. US2003032090A1
GENERAL INFORMATION:
APPLICANT: Hardiman, Gerard T.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
APPLICANT: Ho, Stephen W.K.
TITLE OR INVENTION: RECEPTOR PROTEINS, RELATED REAGENTS AND METHODS
FILE REFERENCE: EX0724XK1
CURRENT APPLICATION NUMBER: US/09/950,041
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 09/728,540
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/207,558
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 09/073,363
PRIOR FILING DATE: 1999-06-05
PRIOR APPLICATION NUMBER: 60/044,293

```

; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 837
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-950-041-26

Alignment Scores:
Pred. No.: 9,27e-192 Length: 837
Score: 2600.50 Matches: 526
Percent Similarity: 73.68% Conservative: 101
Best Local Similarity: 61.81% Mismatches: 171
Query Match: 2.99% Indels: 53
DB: 10 Gaps: 9

US-09-396-985b-48 (1-50000) x US-09-950-041-26 (1-837)

QY 37400 TGGAAAAATGCTAAATTAATCTAAGACTACTATCAATCACTGCTTTATGTAACCCA 37459
DB 25 TtqgluProCyvalGlu---ValProasnIleThrTyrGln----- 37
QY 37460 GTTATGATCTGAATGATTTTCTATGATTTGCTGCTGACATAGTGTATGATTT 37519
DB 38 CysMetGluLeuAsnPhenPheTyrLysIleProAsnAsnLeuPro----- 51
QY 37520 ATCATCACTGTAGCAAGTGTGAAAATGACAATCTGCAGAGTTCCTCTCTGCACACC 37579
DB 52 -----PheSerThrLysAsnLeuAsnLeuSerPheAsnProLeuArgHis--- 66
QY 37580 ATCATCACTGTTTCTCTGCTGCTGCTGCTTTCTTTACAAATACATGATATCATCT 37639
DB 67 -----LeuGlySerTyrSerPhe----- 72
QY 37640 GTTTGTATCATAGTATGTAGGAGCTGTATGATTAAGAAAGGTTTTTTTTCAGCAA 37699
DB 73 -----PheSerPheProGlu 77
QY 37700 AAATACATAATGTGATCTCTTTTGCCCATAGTGCTGTAATGAAACAATGAAGACACAG 37759
DB 78 LeuGlnValLeuAsnLeuSer-----ArgCysGluIleGlnThrIleGluAspGly 94
QY 37760 GCATGGCATGGCTTACACACACCTCTCAAACTTGTACTGACAGAAACCTATCCAGAGT 37819
DB 95 ALeTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSer 114
QY 37820 TTTTCCCAAGAGATTTCTCTGAGCTACATACAGTTTAGAGATCTGGCTGGAGACA 37879
DB 115 LeuAlaLeuGlyAlaPheSerGlyLeuSerSerLeuGlnIlybLeuValAlaValGluThr 134
QY 37880 AAATTTGGCTCTCTAGAAAGCTCCCTATTGAGACGCTTATACCTTAAAGAACTCAAT 37939
DB 135 AsnLeuAlaSerLeuGlnAsnPhenProIleGlyHisLeuLysThrIleuLysGluLeuAsn 154
QY 37940 GTGGCTCACAATTTATATCATCTCTGTAAGTTACCTGCATATTTTCCAAATCTGACGAC 37999
DB 155 ValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyrPheSerAsnLeuThrAsn 174
QY 38000 CTAGTACATGGAGATCTTTCTTATACATATTAATAATATTAATCTGTCAGACTTACAG 38059
DB 175 LeuGlnHisLeuAsnLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArg 194
QY 38060 TTTCTACCTGAAATTCACAAGTCAATCTCTTTAGACATGTCTTTGAACCCCAATGAC 38119
DB 195 ValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAsnLeuSerLeuAsnProMetAsn 214
QY 38120 TTCAATCAAGACCAAGCTTTTCAGGGAAATTAAGCTCCATGAACTGACTTAAAGAGTAT 38179

```

```

DB 215 PheIleGlnProGlyAlaPheLysGluIleArgLeuHisLysLeuThrIleuArgAsnAsn 234
QY 38180 TTTAATAGCTCAAAATTAATGAAGAACTGGCTTCAAAACCTGGCTGTTTACAGTCCAT 38239
DB 235 PheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeuAlaGlyLeuGluValHis 254
QY 38240 CCGTTGATCTTGGAGAAATTTAAAGATGAAGGAATCTGGAAATTTTGAACCTCTATC 38299
DB 255 ArgLeuValLeuGlyGluPheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAla 274
QY 38300 ATGGAAGCATATGTATGTATGACCATTTGATGATGATCTCAGGTTACATATACAAATGATTT 38359
DB 275 LeuGlnGlyLeuCysAsnLeuThrIleGlnGluPheArgLeuAlaTyrLeuAspTyrTyr 294
QY 38360 TCAGATGATTTGTAAAG--TTCCATGCTGGCGAAATTTTCTGCAATGTCTGGGCA 38416
DB 295 LeuPhePhePheIleLeuPheLeuPheAsnCybLeuThrAsnValSerSerPheSerLeuVal 314
QY 38417 GGTGTATCTATTAATAATATCTAGAAGATGTTCTTAAACATTTCAATGGCAATCTTATCA 38476
DB 315 SerValThrIleGluArgValLysAspPheSerTyrAsnPheGlyTtqglnHisLeuGlu 334
QY 38477 ATCATTAAGATGTCAACTTAAGCGCTTCCAACTCTGATCTACCCCTTTTAAAGATTG 38536
DB 335 LeuValAsnCybLysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeu 354
QY 38537 ACTTAACTATGAACAAGGGCTATCATCGTTTAAAAAAGTGCGCCCTACCAAGTCTCAGC 38596
DB 355 ThrPheThrSerAsnLysGlyGlyAsnAlaPheSerGlyValaLeuPheProSerLeuGlu 374
QY 38597 TATCTAGATCTTATAGTAAATGCACTGAGCTTATAGTGTGCTGTTCTTATTTGATTTG 38656
DB 375 PheLeuAsnLeuSerThrArgAsnGlyLeuSerPheLysGlyCysCysSerGlnSerAspPhe 394
QY 38657 GGAACAACAACGCTGAGACACTTAAGACCTCACTGATTCATATGTCCTCATTAATGATGCC 38716
DB 395 GlyThrThrSerLeuLysTyrIleuAsnLeuSerPheAsnGlyValIleThrMetSerSer 414
QY 38717 AATTTCATGGCTGTAGAGAGCTGCAGACCTGATTTTTCAGACACTTATTAATAAG 38776
DB 415 AsnPheLeuGlyLeuGluGlnLeuGlnHisLeuAsnPheGlnHisSerAsnLeuLysGln 434
QY 38777 GTCAACAATTTCTCAGGGTCTTATCCCTTGAAGACTATTTACCTTGAATCTGTAT 38836
DB 435 MetSerGluPheSerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHis 454
QY 38837 ACTTAACCAAAATTTGACTTCGATGTATATTTCTGGCTTACACAGTCTCAACACATTA 38896
DB 455 ThrHisThrArgValaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeu 474
QY 38897 AAATGGCTGGCAATTTCTTCAAGACACACACCTTTCAAAATGCTTTTGGCAACACACA 38956
DB 475 LysMetAlaGlyAsnSerPheGlnGlnAsnPheLeuProAspIlePheThrGluLeuArg 494
QY 38957 AACTTGCATCTCTGATCTTTCTTAAATGCAATTTGGAACAAATATCTTGGGGGTAATT 39016
DB 495 AsnLeuThrPheLeuAsnLeuSerGlnCysGlnLeuGlnIleuSerProThrAlaPhe 514
QY 39017 GACACCTCCATAGACTTCAATTAATTAATATGATGACAAACAATCTATTTGTTGGAT 39076
DB 515 AsnSerLeuSerSerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAsp 534
QY 39077 TCATCCCATATTAACAGAGTATTCCTCCAGACACTTGAATGGAGTTTCAATTCGCATA 39136
DB 535 ThrPheProTyrLysCysLeuAsnSerLeuGlnValaLeuAspTyrSerLeuAsnHisIle 554
QY 39137 GAGACATCT--AAAGATAATCTGCAACATTTTCCAAAGATCTTACCTTTCAATCTT 39193
DB 555 MetThrSerLysLysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeu 574
QY 39194 ACTTAACATTTCTGTTGTTGATATGATGAACATCAAGAAATTTCTGCAAGTGGCTCAAGAA 39253
DB 575 ThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheLeuGlnTtqglnLysAsp 594

```

```

QY 39254 CAGAGCAGTTCTTGGAATGTTGAACAATGACATGTGCAACCTGTAGATGAAT 39313
D 595 GlnArgGlnLeuLeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLeuGln 614
QY 39314 ACCTCCTTAGTGTGGATTTTAAATTAATTTCTACCTGTTATATGTACAAGACATCACTAGT 39373
D 615 GlyMetProValLeuSerLeu---AsnIleThrCysGlnMetAsnLysThrIleIleGly 633
QY 39374 GTGTCAGGTCAGTGTGATGTTGTGATCCACTGATGATTTCTGATATACCTTCAT 39433
D 634 ValSerValLeuSerValLeuValValSerValValAlaValLeuValTyrLysPheYr 653
QY 39434 TTTCACCTGATCTTATTTGCTGCTGTAAAAGTACAGAGAGAGAAAGCATCTATGAT 39493
D 654 PheIleSerMetLeuLeuAlaGlyCysIleLysTyrGlyArgGlyGlnMetIleTyrAsp 673
QY 39494 GCATTGTGATCTACTGAGTCAGATGAGAGACTGGGTGAGAAATGAGCTGTAAAGAT 39553
D 674 AlaPheValIleTyrSerSerGlnAspGlnAspIleTyrValAlaGlnGlnLeuValLysAsn 693
QY 39554 TTAAAGAGAGAGTCCCGCTTTCACCTGCTTCCTGCTACAGAGCTTATTCCTGCT 39613
D 694 LeuGlnGlnGlyValProProPheGlnLeuCysLeuHisTyrArgAspPheIleProGly 713
QY 39614 GTAGCCATTGCTGCACATCATCATCAGAGAGAGCTTCCACAGAGCCGGAAGTATTGTG 39673
D 714 ValAlaIleAlaAlaMetIleIleHisGlnGlyPheHisLysSerAspGlyValIleVal 733
QY 39674 GTAGTGTCTAGACATTTATTTCAAGCCGTTGTGTATCTTTGAATATGAGATTGCTCA 39733
D 734 ValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGlnIleValAlaGln 753
QY 39734 ACAAGGAGATTCTTGAGAGCCGCTCTGGCATCTTCAATTTGCTTGGAGAAGTTGAG 39793
D 754 ThrTyrGlnPheLeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGln 773
QY 39794 AAGTCCCTGCTGAGGAGCAGAGAGTGAATTTATGAGCTTTTACAGAGAAACCTATCTG 39853
D 774 LysThrLeuLeuArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeu 793
QY 39854 GAATGGAGAGACAATCTCTGGGAGAGCAATCTTGTGAGAGACTTAAATATGCCCTTA 39913
D 794 GluTyrGlnAspSerValLeuGlyArgHisIlePheTyrArgLeuArgLeuValAlaLeu 813
QY 39914 TTGATGGAAAAGCTCGAATCTTGAGCAACA 39946
D 814 LeuAspGlySerTyrAsnProGlnGlyThr 824

RESULT 2
US-09-950-041-8
; Sequence 8, Application US/09950041
; Publication No. US20030032090A1
; GENERAL INFORMATION:
; APPLICANT: Hardiman, Gerard T.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kaetelejn, Robert A.
; APPLICANT: Ho, Stephen W.K.
; APPLICANT: Liu, Yong-Jun
; TITLE OF INVENTION: RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
; FILE REFERENCE: DK0724XK1
; CURRENT APPLICATION NUMBER: US/09/950,041
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 09/728,540
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/207,558
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 09/073,363
; PRIOR FILING DATE: 1999-06-05
; PRIOR APPLICATION NUMBER: 60/044,293
; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212

```

```

; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-041-8

Alignment Scores:
Pred. No.: 4,97e-191 Length: 799
Score: 2591.00 Matches: 508
Percent Similarity: 79.76% Conservative: 95
Best Local Similarity: 67.20% Mismatches: 147
Query Match: 2,98% Indels: 6
DB: 10 Gaps: 4

US-09-396-985b-48 (1-50000) x US-09-950-041-8 (1-799)

QY 37685 TTTTCTTTCAGCAAAAATACATATTTGTAATCTTTTCCCATAGCTGTAATTTGAA 37744
D 35 PheSerPheProGlnLeuGlnValLeuAspLeuSer-----ArgCysGlnIleGln 51
QY 37745 ACAATTGAACAAGAGCATGAGCTTACACACCTCTCAACTGATATGACAGACAGA 37804
D 52 ThrIleGlnAspGlyAlaTyrGlnSerLeuSerHisLeuSerThrLeuIleLeuThrGly 71
QY 37805 AACCTATTCAGAGTTTTCCTCCAGAGAGTTTCTGTGACATTAACAATTTAGAAATCTG 37864
D 72 AsnProIleGlnSerLeuAlaLeuGlyAlaPheSerCylLeuSerSerLeuGlnLysLeu 91
QY 37865 GTGGCTGTGAGACAAATTTGGCTCTCTGGAAGCTTCCCTATTTGAGACGTTATACC 37924
D 92 ValAlaValGlnThrAsnLeuAlaSerLeuGlnAspPheProIleGlyHisLeuLysThr 111
QY 37925 TTTAAGAAATCTCAATGTGGCTGACAAATTTATATCTTCTGTAAGTTACCTGATATTTT 37984
D 112 LeuLysGlnLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGlyTyrPhe 131
QY 37985 TCCAACTGACGAACCTAGTACATGTGATCTTTCTTATATCATATATTCAACTATTACT 38044
D 132 SerAsnLeuThrAsnLeuGlnHisLeuAspLeuSerSerAsnLysIleGlnSerIleTyr 151
QY 38045 GTCAAGACCTTACAGTTTCTACGTGAATAATCCAAAGTCAATCTCTTTAGACATGCT 38104
D 152 CysThrAspLeuArgValLeuHisGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer 171
QY 38105 TTGAACCCATTTGACTTATTCAAGACCAAGACCTTTCAGGAGATTTAAGCTCCATGAACTG 38164
D 172 LeuAsnProMetAsnPheIleGlnProGlyAlaPheLysGlnIleArgLeuHisLysLeu 191
QY 38165 ACTCTAAGAGTAATTTTATAGCTCAATATATATGAAAATTGCCCTTCAAACTGGCT 38224
D 192 ThrLeuArgAsnAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGlyLeuAla 211
QY 38225 GGTTTACACGTCATGCGTTGATCTTGGAGAAATTTAAGATGAAAGAAATTCGAAATT 38284
D 212 GlyLeuGlnValHisArgLeuValLeuGlyGlnPheArgAsnGlnGlyAsnLeuGlnLys 231
QY 38285 TTTGAACCCCTTCATCATGGAAGACTATGATGATGCACTTATGATGTTAGGTTACAGTTTACA 38344
D 232 PheAspLysSerAlaLeuGlnGlyLeuCysAsnLeuThrIleGlnGlnPheArgLeuAla 251
QY 38345 TATACAAATGATTTTTCAGATGATTTGTTAAG---TTCCATTTGTTGGGAATGTTTCT 38401
D 252 TyrLeuAspLysTyrThrLeuAspPheIleIleAspLeuPheAsnCysLeuThrAsnValSer 271
QY 38402 GCATGTCTCTGCAAGTGTATCTATATTAATATCTAAGAGATGTTCTTAAACATTTCAA 38461
D 272 SerPheSerLeuValSerValThrIleGlnArgValLysAspPheSerTyrAsnPheGly 291

```

```
QY 38462 TGGCAATCCTTATGATCATTAAGTCAACCTTAAGCAAGTTCCAACTGATCTACCC 38521
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 292 TrglnhlsleuGluLeuValaAsnCysIysPheGlyGlnPheProthrlleuLysleuLys 311
QY 38522 TTTCTAAAGTTTGACTTTAAGTATGAACAAGGGCTCTACGTTTAAAAAAGTGGCC 38581
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 312 SerleuLysArgLeuThrPheThrSerAsnLysGlyAlaAsnAlaPheSerGluValAsp 331
QY 38582 CTACCAAGTCTCAGCTATCTAGATCTTATGTAAGAAATGACAGCACTTAAAGTGTGCT 38641
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 332 LeuProSerLeuGluPheLeuAspLeuSerArgAsnGlyLeuSerPheLysGlyCysCys 351
QY 38642 TCTTATCTGATTTGGGAACAACAAGCCTGAGACACTTGAAGCTCAGGCTCAATGAGTGC 38701
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 352 SerGlnSerAspPheGlyThrThrSerleuLysTyrLeuAspLeuSerPheAsnGlyVal 371
QY 38702 ATCATTTAGTGGCCAAATTTCAATGGGCTGTAAGAAGCTGACAGCACTTGAATTTTCAGAC 38761
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 372 IleThrMetSerSerAsnPheLeuGlyLeuGlnGlnLeuGlnIleLeuAspPheGlnHis 391
QY 38762 TCTTACTTAAAGGTCACAGAAATTCACAGCTTCTTATCCCTTGAAGACTATTAC 38821
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 392 SerAsnLeuLysGlnMetSerGlnPheSerValPheLeuSerLeuAspAsnLeuIleTyr 411
QY 38822 CTTGACATCTCTTACTTAAACCAACAATGACTTCGATGATATTCTTGGGCTTGACC 38881
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 412 LeuAspIleSerHisIleThrHisIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer 431
QY 38882 AGTCTCAACACATTTAAATGCGTGGCAATTTCTTCAAAAGCAACACCTTTCAATGTC 38941
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 432 SerleuGluValleuLysMetAlaGlyAsnSerPheGlnGlnAlaPheLeuProAspIle 451
QY 38942 TTTGCAAAACACAACAACTTACATCTCTGATCTTCTTAAATGTCATTTGGAACAATA 39001
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 452 PheThrGluLeuAspGlnMetLeuThrPheLeuAspLeuSerGlnCysGlnLeuGlnLeu 471
QY 39002 TCTTGGGGGATTTGACACCCCTCATGACTCTTCAATTTAAATATGAGTCACACAAT 39061
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 472 SerProthrlAlaPheAsnSerLeuSerleuGlnValleuAsnMetSerHisAsnAsn 491
QY 39062 CTATTTGTTTGGATTTCCCATTTAACAAGCTGTATTCCTCAGACACTTTGATTCG 39121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 492 PhePheSerLeuAspThrPheProTyrLysCysLeuAsnSerLeuGlnValleuAspTyr 511
QY 39122 AGTTTCATCGCATGAGACATCT---AAAGAAATACGCAACATTTCCAAAGCTTA 39178
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 512 SerleuAsnHisIleMetThrSerLysGlnGlnLeuGlnHisPheProSerSerleu 531
QY 39179 GCCTTCTTCAATCTTACTAACAATTTCTGTTCTGTATATGTGAACATCAGAAATTCCTG 39238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 532 AlaPheLeuAsnLeuThrGlnAsnAspPheAlaCysThrCysGlnHisGlnSerPheleu 551
QY 39239 CAGTGGGTCAAGAAACAGACAGAGTCTTGGTGAATGTTGAACAATGACATGTGCAACA 39298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 552 GlnTyrPheLysAspGlnArgGlnleuLeuValGlnValGlnArgMetGlnCysAlaIleThr 571
QY 39299 CCTGAGAGAGGAATACCTCCTTAGTGTGATTTTAATTTCTACCTGTATATATGAC 39358
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 572 ProSerAspLysGlnGlyMetCysProValIleuSerleu---AsnIleThrCysGlnMetAsn 590
QY 39359 AAGCAATCATCATGTCAGTGTGTCAGTGTGATGATGTCATGTCATGTCATGTCATGTCG 39418
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 591 LysThrIleIleGlyValSerValleuSerValleuValIleSerValAlaIleValleu 610
QY 39419 AATATTCATCTTATTTTCACTGATCTTATTTGCTGGCTGTAAAGATGACAGACAGGA 39478
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 611 ValTyrLysPheTyrPheHisIleMetSerleuMetIleAsnGlyCysIleTyrGlyArgGly 630
QY 39479 GAAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 39538
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 631 GlnAsnIleTyrAspAlaPheValIleTyrSerSerGlnAspGlnAspTyrValArgAsn 650
QY 39539 GAGCTGTAAAGAAATTTAGAAAGAGAGTGGCCCGCTTTCACCTTGCTTCACATACAGA 39598
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
Db 651 GlnLeuValLysAsnLeuGlnGlyValProProPheGlnLeuCysLeuHisTyrArg 670
QY 39599 GACTTTATCTCTGCTAGGATCTTGTGCTGCCAATCATATCCAGAAAGCTTCCCAAGAGC 39658
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 671 AspPheIleProGlyValAlaIleValAlaAsnIleIleHisGlnIlePheHisLysSer 690
QY 39659 CGAAGGTTATTTGGAGAGTGTCTAGACACTTATTCAGAGCGGTGGTGTATCTTTGAA 39718
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 691 ArgLysValIleValValValSerGlnHisPheIleGlnSerArgTyrCysIlePheGln 710
QY 39719 TATGAGATTTCTCAAAACATGAGCAAGTTTCTGAGCAGCGCTCTGACATCATCTTATGTC 39778
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 711 TyrGlnIleIleGlnThrTrpGlnPheLeuSerSerArgAlaIleIlePheIleVal 730
QY 39779 CTTGAGAAAGTTTGAAGAAGTCCCTGCTGAGGACAGCAGTGAATTTGATGCGCTTTTACG 39838
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 731 LeuGlnLysValIleLysThrIleLeuLeuAspGlnGlnIleValGlnLeuTyrArgLeuLeuSer 750
QY 39839 AGAAACACCTACCTGGAATGAGAGACAAATCCTCTGGGGAGGACATCTTCTGAGAGA 39898
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 751 ArgAsnThrTyrLeuGlnIleTrpGlnAspSerValleuGlyArgHisIlePheThrArg 770
QY 39899 CTTAAAAATGCCCTATTTGATGAGAAAAAGCTCGAATCTTGAGCAACA 39946
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 771 LeuArgLysAlaLeuLeuAspGlyLysSerTrpAsnProGlnIleThr 786

RESULT 3
US-10-128-166-7
; Sequence 7, Application US/10128166
; Publication No. US20030077279A1
; GENERAL INFORMATION:
; APPLICANT: ARDITI, MOSHE
; APPLICANT: RAJAVASHISTH, TRIPATHI
; APPLICANT: SHAH, PREDIMAN K.
; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITING
; FILE REFERENCE: 81476-025398
; CURRENT APPLICATION NUMBER: US/10/128,166
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 799
; TYPE: PRF
; ORGANISM: Homo sapiens
; US-10-128-166-7

Alignment Scores:
Pred. No.: 4,97e-191 Length: 799
Score: 2591.00 Matches: 508
Percent Similarity: 79.76% Conservative: 95
Best Local Similarity: 67.20% Mismatches: 147
Query Match: 2.98% Indels: 6
DB: 14 Gaps: 4

US-09-396-985b-48 (1-50000) x US-10-128-166-7 (1-799)
QY 37685 TTTTCTTTCAGCAAAAATCATTAATGGTATCTCTTTGCCCCATAGCTGTGAATGAA 37744
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 35 PheSerPheProGlnLeuGlnValleuAspLeuSer-----ArgCysGlnIleGln 51
QY 37745 ACAATTGAACAAGAGCATGGCTTACACACCTCTCAAACTGATTAAGTGAAGAGA 37804
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 52 ThrIleGlnAspGlyAlaTyrGlnSerLeuSerHisIleuSerThrLeuIleuThrGly 71
QY 37805 AACCTATCCAGAGTTTTCGCCAGAGTTCCTGCACTTAACAAGTTTGAAGAAATCTG 37864
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 72 AsnProIleGlnIleSerleuAlaLeuGlyAlaPheSerGlyLeuSerSerleuGlnLysleu 91
QY 37865 GTGGCTGTGAGACAAAAATTTGGCTCTTGAAGAAAGCTTCCCTTATTTGAGACCTTATTAAC 37924
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 92 ValAlaValGlnThrAsnLeuAlaSerleuGlnAsnPheProIleGlyHisLeuLysThr 111
```



```
FILE REFERENCE: 58183W0003
CURRENT APPLICATION NUMBER: US/10/732,563
CURRENT FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 799
TYPE: PR1
ORGANISM: Homo sapiens
US-10-732-563-8

Alignment Scores:
Pred. No.: 4,97e-191 Length: 799
Score: 2591.00 Matches: 508
Percent Similarity: 79.76% Conservation: 95
Best Local Similarity: 67.20% Mismatches: 147
Query Match: 2,98% Indels: 6
DB: 16 Gaps: 4

US-09-396-985b-48 (1-50000) x US-10-732-563-8 (1-799)

QY 37685 TTTTTCGACGAAATATCATATGCTATCTCTTGGCCATAGGTGTAATGGA 37744
DB 35 PheSerPheProGluLeuGlnValLeuAspLeuSer-----ArgCyGluIleGln 51
QY 37745 ACAATTGAAGACAAAGCATGGCATGGCTTACACACACCTTCGAACCTTGATATGACAGGA 37804
DB 52 ThrIleGluAspGlyAlaIleArgIleSerIleuSerIleuSerIleuIleuSerIleuIleu 71
QY 37805 AACCTATCCAGAGTTTTCGCCAGAGTTTCTCTGACTATGACAGATTTAGAGAACTG 37864
DB 72 AsnProIleGlnSerIleuAlaIleuGlyAlaPheSerGlyLeuSerSerIleuGlnIleu 91
QY 37865 GTGGCTGTGGAGCAAAATTTGGCTCTTACGAAAGCTTCCCTATTGACACCTTATACC 37924
DB 92 ValAlaValGluThrAsnLeuAlaSerIleuGlnAsnProIleGlyIleuLeuThr 111
QY 37925 TTAAGAACCAATGAGTGGCTCACAAATTTATACATCTCTGTAATGCTGACATATTTT 37984
DB 112 LeuIleuGlnLeuAsnValAlaIleAsnLeuIleGlnSerPheIleuProGluIleuPhe 131
QY 37985 TCCAACTGACGAACCTATGATCATGTGGATCTTTCTTAACTATATTCGAACCTATTA 38044
DB 132 SerAsnLeuThrAsnLeuGlnIleuIleuAspLeuSerSerIleuGlnSerIleuIleu 151
QY 38045 GTCAACGACTTACAGATTTCTACGTGAAATTCACAGATCATCTCTTATGACATGCT 38104
DB 152 CysThrAspLeuArgValIleuIleGlnMetProLeuLeuAsnLeuSerIleuAspLeuSer 171
QY 38105 TTGAACCAATGATCTTCAATCAAGACCAAGCCTTCAGGAATTAAGCTCCATGAACTG 38164
DB 172 LeuAsnProMetAsnPheIleGlnProGlyAlaPheIleuGluIleuGlnIleuIleu 191
QY 38165 ACTTAAAGAGTAATTTATATAGCTCAATATATATGAATAACTTGCCTTCAAAAGCTGCT 38224
DB 192 ThrIleuArgAsnAsnPheAspSerIleuAsnValMetIleuIleuGlnIleuIleu 211
QY 38225 GGTTCACGCTTCATCGCTGATCTTGGAGAAATTTAAAGATGAAGAAGATCTGAAATT 38284
DB 212 GlyIleuGlnValIleuAspIleuValIleuGlnIleuPheArgAsnGlnIleuGlnIleu 231
QY 38285 TTGAACCTCATATGAGGAAGGACTATGATGATGACATTTGAGATGAGTTAGCTTACA 38344
DB 232 PheAspIleuSerAlaIleuGlnIleuIleuIleuIleuIleuIleuIleuIleuIleu 251
QY 38345 TATACAAATGATTTTTCAGATGATATGTTAAG--TTCCATTTGCTGGCGAATGTTCT 38401
DB 252 TyrIleuAspIleuIleuIleuAspIleuIleuIleuAspIleuIleuIleuIleuIleu 271
QY 38402 GCAATGCTCTGGGAGGCTGTATCTATAAATATCTAGAAAGATTTCTTAAACATTTCAA 38461
DB 272 SerPheSerIleuValSerValThrIleuIleuIleuIleuIleuIleuIleuIleu 291
```

```
QY 38462 TGGCAATCCTTATCATATCATATGATGCACTTAAAGCAAGTTTCCAACTGTGATTAACC 38521
DB 292 TrpGlnIleuGlnIleuValAsnCyIlePheGlyGlnPheProIleuIleuIleuIleu 311
QY 38522 TTTCTTAAAGTTTGAACCTTAACTATGACAAAGGCTATACGTTTAAAGGAGGCC 38581
DB 312 SerIleuIleuArgLeuThrPheThrSerAsnIleuGlyGlyAsnAlaPheSerGlnValAsp 331
QY 38582 CTACCAAGCTCAGCTATCATAGATCTTATGAGAAAGCACTGAGCTTATAGGTGCTGT 38641
DB 332 LeuProSerIleuGlnIleuAspLeuSerIleuAsnGlyLeuSerPheIleuGlyCyGAs 351
QY 38642 TCTTATCTGATTTGGGACAAACAGCCTGAGACCTTACAGCTTCAATGCTGCC 38701
DB 352 SerGlnSerAspPheGlyThrIleuIleuIleuIleuIleuIleuIleuIleuIleu 371
QY 38702 ATCATTTAGAGTCCAAATTTACGCTGTAGAAAGCTGACAGACCTGATTTTACGAC 38761
DB 372 IleThrMetSerSerAsnPheLeuGlnIleuGlnIleuGlnIleuIleuAspPheGlnIle 391
QY 38762 TCTACTTAAAGAGGTCACAGAAATCTCAGCCTTATCCCTGAAAAGCTACTTAC 38821
DB 392 SerAsnLeuIleuGlnMetSerGlnPheSerValPheLeuSerIleuIleuIleuIleu 411
QY 38822 CTTGACATCTCTTATATACACCAAAATGACTTCGATGATATTTCTTGGCTTGACC 38881
DB 412 LeuAspIleuSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 431
QY 38882 AGTCTCAACATTTAAATGCTGCGCAATTTCTTCAAGACAAACACCTTTCAATGTC 38941
DB 432 SerIleuIleuValIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 451
QY 38942 TTTGCAAAACAAACAACTGACATCTCCGATCTTTCAATGATGTCATTTGGAACAAATA 39001
DB 452 PheThrGluLeuArgAsnLeuThrPheLeuAspLeuSerIleuIleuGlnIleu 471
QY 39002 TCTTGGGGGATTTTGAACACCTCCATAGACTTCAATATTAATGATGTCACAAACAT 39061
DB 472 SerProThrAlaPheAsnSerIleuSerSerIleuGlnIleuIleuIleuIleuIleu 491
QY 39062 CTATGTTTGGATTCATCCATTAATACCAAGCTGATTCCTCAGACACTTGTATGC 39121
DB 492 PhePheSerIleuAspThrPheProIleuIleuIleuIleuIleuIleuIleuIleu 511
QY 39122 AGTTCAATGCGATAGAGACATCT--AAAGAAATATGCAACATTTCCAAAGAGCTA 39178
DB 512 SerIleuAsnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 531
QY 39179 GCTTCTTCAATCTTACTAACAATTCGTGCTGTATGATGTAACATCAGAAATTCCTG 39238
DB 532 AlaPheLeuAsnLeuThrIleuIleuIleuIleuIleuIleuIleuIleuIleu 551
QY 39239 CAGTGGTCAAGACAGAAAGAGTCTTGGTGAATTTGAACAATGACATGTCACAA 39298
DB 552 GlnIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 571
QY 39299 CCTGTAGATGAATTAACCTCTTAAGTGTGATTTTAATTAATCTACCTGTATATGATAC 39358
DB 572 ProSerAspIleuGlnIleuMetProValIleuSerIleu--AsnIleuIleuIleuIleu 590
QY 39359 AAGACATCACTAGTGTGTCAGTGTGATGATGATGATGATGATGATGATGATGATGAT 39418
DB 591 LysThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 610
QY 39419 ATATACCACTTATATTTTCACTGATATCTTATGCTGCTGTAAGAAAGTACAGACAGGA 39478
DB 611 ValTyrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 630
QY 39479 GAAAGCATCTATGATGATTTTGGATCTTACTCAGTACAGAAATGAGGCTGGGTAGAAAT 39538
DB 631 GluIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 650
QY 39539 GAGCTGTAAAGAAATTTAGAAAGAGAGTCCCGCTTTCACCTCTTCACTACAGAG 39598
```


Db	651	GIuueVallVbshnLeuGIuGIuLYaLPbPbPheGInLeuSyLeuHsIYrAg	670
Qy	39599	GACTTAAATTCGGGTGTAGCCATTGCTGCCAATCATCCAGAGAGGCTTCCACAAGAC	39658
Db	671	AspHeIlePbPbGlyValAlaAlaIleAlaAlaAlaIleIleIleGIuLYrPheHsIlybSer	690
Qy	39659	CGAAGGTTATTGTGTAGTGTCTAGACACTTTATTACAGCCGGTGGTGATCTTTGAA	39718
Db	691	ArgIySVaIIleValValSerGIuHsIbPheIleGIuSerIgrIbPbSyIlePheGIu	710
Qy	39719	TATGAGATGCTCAACATGGCACTTTCTAGACGCCCTCTGGCATCATTTCAATGTGC	39778
Db	711	TyrGIuIleAlaGIuHrIbPbInPheLeuSerSerArgIaGIuIleIlePheIleVal	730
Qy	39779	CTTAGAAGGTTGAGAAAGTCCCTCTGTAGGACAGAGGTGAATTGATAGCTTCTTAC	39838
Db	731	LeuGIuIySVaIIGIuIySbHrIleuArgIuGIuIuValGIuDeuIyIArgIeLeuSer	750
Qy	39839	AGAAACCTTACCTCGAATGGAGAGAAATCCCTCTGGGAGGACATCTTTTGAGAGAA	39898
Db	751	ArgSbHrIyIleuGIuIbPbIuAspSerValLeuGIuYArgHsIlePheIbPbArgG	770
Qy	39899	CTTAAATATGCCCTATTGATGGAGAAAGCCGCAATCCGAGAGAAACA	39946
Db	771	LeuArgIySVaIIeLeuLeuAspGIuLYbSerIbPbAsbPbIuGIuLYbHr	786

RESULT 5
IIS-10-73

; Sequence 8, Application US/10732796A
; Publication No. US20040197865A1

GENERAL INFORMATION:

;; APPLICANT: Gupta, Shalley K
; APPLICANT: Ghosh, Tarun K.

APPLICANT: Fink, Jason R.

; TITLE OF INVENTION: Gene Expr
; FILE REFERENCE: 58182US004

CURRENT APPLICATION NUMBER:

CURRENT FILING DATE: 2003-12-10
NUMBER OF SEQ ID NOS. 23

SOFTWARE: Patent in years

COL INTRAC. FACCHETTI VERBOSI 3:2
; SEQ ID NO 8
LENGTH: 700

LENGTH: 799

```

; TYPE: PRI
; ORGANISM: Homo sapiens
;

```

US-10-732-796A-8

Alignment Scores:

Pred. No.: 4.

Score: 25
Percent similarity: 79

Best Local Similarity: 67

Query Match: 2.0
DB: 16

100

US-09-396-985B-48 (1-50000) x US-10-732-796A-8 (1-799)

2025-01-27 10:00:00

QY 3/685 IIII CAGCAAAATACATAATGGTATCCTTTG
::: ::::: ::::III

Db 35 PheSerPheProGluLeuGlnValLeuAspLeuSer-----

37745 ACAATTGAGACAAGGCATGGCATGGCTTACACCACTCTT

B

Db 52 ThrIleGluAspGlyAlaTyrGlnSerLeuSerHisLeuS

37805 AACCTATCCAGAGTTTTCCTCTGGA

```

72 AsnProteinInsertion[all]a[all]v[all]a[all]b[all]c[all]d[all]e[all]f[all]g[all]h[all]i[all]j[all]k[all]l[all]m[all]n[all]o[all]p[all]q[all]r[all]s[all]t[all]u[all]v[all]w[all]x[all]y[all]z[all]
Db

```

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

37865 GTGGCTGTGAGACAAAATTGGCCTCTAGAAAGCTTCC

2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841

92 VARAIAVAIGIUNIFASHLEUAIASEILEUGIUAABNPHET

QY	37925	TTAAAGAAACTGCAATGCGGTCAATTTTATACATTCCTGTGTAAGTACTGCAATTTT	37985
Db	112	LeuLyseGluLeuAsnValAlaHisAsnLeuIleGlnSerPheLysLeuProGluTyrPhe	131
QY	37985	TCCAAATCGACGAACCTGACATGAGATGCGGATCTTTCTTAATCAATATTCCTAACTAAT	38044
Db	132	SerAsnLeuThrAsnLeuGlnHisIleAspLeuSerSerAsnLysIleGlnSerIleTyr	151
QY	38045	GTCAACGACTTACAGTTTCTACGCTGAAAAATCCACAGTCATCTCTCTTACAGCATGTC	38104
Db	152	CythrThrAspLeuArgValLeuHisIleGlnMetProLeuLeuAsnLeuSerLeuAspLeuSer	171
QY	38105	TTGAACCCCAATTGACATTCCTTACATTCAGACCAAGCCTTTACAGGAATTAACTCCATGAAC	38164
Db	172	LeuAsnProMetSerAsnPheIleGlnProGlyAlaPheLysGluIleArgLeuHisIleLysLeu	191
QY	38165	ACTGTAGAGGTAAATTTTAAATAGCTCAAAATATATAGAAAATTCGCTTCGCAAAACCGGCT	38224
Db	192	ThrLeuArgAsnAsnPheAspSerLeuAsnValMetLysThrCysIleGlnGluLeuAla	211
QY	38225	GGTTTACACGTCCTCAGTGGTTGATCTTGGAGAAATTTAAAGATGAAGAATCTGGAATT	38284
Db	212	GlyLeuGluIuValHisArgLeuValLeuGlyGluPheArgAsnGluLysLeuLeuGluLys	231
QY	38285	TTTGAACCCCTCTATCATGGAAGACATATGATGTACCATGATGAGATTCACGTTTACAC	38344
Db	232	PheAspLysSerAlaLeuGluGluLysLeuCysAsnLeuThrIleGluGluIuPheArgLeuAla	251
QY	38345	TATACAAATGATTTTTCAGATGATATGTGTTAAG--TTCATGTCTGGCGAATGTTCT	38404
Db	252	TyrLeuAspTyrTyrTyrLeuAspAspIleIleAspLeuPheAsnCysLeuThrAsnValSer	271
QY	38402	GCAATGCTCTCGGACAGGTGATCTATATAAATATCTGAAGAGTTCCTAAACATTTTCAAA	38461
Db	272	SerPheSerLeuValSerValThrIleGluArgValLysAspPheSerTyrAsnPheGly	291
QY	38462	TGGCAATCTTATCAATCATTAAGATGTCAACTTAAGCAGTTTCAACTGTGATCTACCC	38521
Db	292	TyrGlnHisIleGluGluIuLeuValAsnCysLysPheGlyGlnPheProThrLeuLysLeuLys	311
QY	38522	TTTTCTTAAAGTTTGACTTAACTTAATGAACAAAGGCTCATACGTTTAAAAAAGTCGCC	38581
Db	312	SerLeuLysArgLeuThrPheThrSerAsnLysGlyLysAsnAlaPheSerIuValAsp	331
QY	38582	CTACCAAGTCTCAGCATCTAGATCTTAATAGAAAATGACAGCTTGTGTGTTGCTGCT	38641
Db	332	LeuProSerIleuGluIuPheLeuAspLeuSerAlaGAsnGlyLeuSerPheLysGlyCys	351
QY	38642	TCTTAATCTGATTTGGGAAACAAACAGCCTGAGACATTAGACCTCAGCTTCAATGAGTGC	38701
Db	352	SerIleuSerAspPheGlyThrThrSerIleuLysTyrLeuAspLeuSerPheAsnGlyVal	371
QY	38702	ATCATTAATGATGCCAATTTTCATGGGTCTAAGAAAGCTGCACACCTGGATTTTACAGAC	38761
Db	372	IleThrMetSerSerAsnPheLeuGluLysGluGlnLeuGlnHisIleuAspPheGlnHis	391
QY	38762	TCTACTTTAAAAAGGCTCAGAGAAATCTCAGCGTCTTATCCCTGAAAAAGCTACTTTAC	38821
Db	392	SerAsnLeuLysGlnMetSerGluPheSerValPheLeuSerIleuArgAsnLeuIleTyr	411
QY	38822	CTTGACATCTCTTAATCTACACCAAAATGACTTCGATGTATATTTCTTGAGCTTGACC	38881
Db	412	LeuAspIleSerHisIleThrHisIleThrArgValAlaPheAsnGlyIlePheAsnGlyLeuSer	431
QY	38882	AGTCTCAACCACTTAAAAATGGCTGGCAATTTCTTCAAAGACAAACACCTTTCAATGTC	38941
Db	432	SerLeuGluIuValLeuLysMetAlaGlyAsnSerPheGlnLysAsnPheLeuProAspIle	451
QY	38942	TTTGGCAAAACCAACCAACTTGACATCTCCGGAATCTTTCTTAATGTCAATTTGGAACAAAT	39001
Db	452	PheThrGluIuLeuArgAsnLeuThrPheLeuAspLeuSerGlnCysGlnLeuGluIuLeu	471
QY	39002	TCTTGGGGGGATTTTGACACCTCCATAGACTTCAATTAATTAATATGATCACAACAT	39061

```

Db      472 SerProthralAphadenSerleuSerleuInValleuAmenSethiAaphsn 491
Qy      39062 CTATGTTTGGATTCATCCATTATACCAAGCTGTATTCCTTCAGACATCTTGATTGC 39121
Db      492 PheheserleuAapthPheProTylrCyseuAensSerleuInValleuAapTyr 511
Qy      39122 AGTTTCATCCCATGAGACATCT--AAAGAAATACGCAATTTTCCAAAGCTA 39178
Db      512 SerleuAenhiSilemetThSerlySerlySgIngluInhiSphneProSerleu 531
Qy      39179 GCCTTTCATCTTACTAACAATTCCTGTATGTATGTGAACATCAGAAATCTCTG 39238
Db      532 AAlpheuAenleuThInGlnAenAphheAlCystrhCySgInhiSgInSerPheleu 551
Qy      39239 CAGTGGGTCAGAAACAGACAGACTTGGTGAATGTGAACAAATGACATGGCAACA 39298
Db      552 GlntrpIlelyAaSerGlnArgGlnleuValGlnValGlnArgMetGlnCyAlaThr 571
Qy      39299 CCTGTAGAGATGAAATACCTCTTGTAGTGGATTTTAATATGTAACCTGTATATGAC 39358
Db      572 ProSerApylSgInglyMetProValleuSerleu--AanIlethCySgInMetAasn 590
Qy      39359 AAGCAATCATCAGTGTGTGTCAGTGTGTCAGTGTGATGTGATCCATGACATTTCTG 39418
Db      591 LysThrIleIleGlyValSerValleuSerValleuValSerValAlaIleValleu 610
Qy      39419 ATATACCACTTGTATTTTACCTGTACTTATGTGCTGTAAAGTACAGACAGAGA 39478
Db      611 ValTyrLysPheTyrPhehiSleuMetleuAglCyS1IelyTyrG1YArgG1Y 630
Qy      39479 GAAAGCATCTATGATGATTTGTGATCTACTGATCGATCGATGAGAACTGGTGAGAAAT 39538
Db      631 GlnAenIleTyrAaPheAlaPheValIleTyrSerSerGlnAaPheGlnAaPheTyrValArgasn 650
Qy      39539 GAGCTGTAAAGAAATTTGAGAAAGAGAGTGCCTTCCTTCATCTGTGCTTCATACAGA 39598
Db      651 GluLeuValLysAenleuGlnGlnGlyAlaProPheGlnleuCySleuhiS1YArg 670
Qy      39599 GACTTATTCCTGTGTGTCATGTCATGTCCTCAACATCATCATCAAGAAAGCTTCCACAGAGC 39658
Db      671 AspPheIleProGlnYValAlaIleAlaAanIleIleIleSgIngluYrPhehiS1YSer 690
Qy      39659 CGGAAGGTATTTGGTGTGTGTATGACATCTTATTCAGACCTGTGTGTATCTTTGAA 39718
Db      691 ArgLysValIleValValSerGlnhiSphneIleGlnSerArgTyrCyS1IephGln 710
Qy      39719 TATGATTTGCTCAACATGTCAGTGTGTGACAGCCCTGTGACATCATCTTATGTC 39778
Db      711 TyrGlnIleAlaGlnThrTrrPglInPheleuSerArgAlaGlyIleIlePheIleVal 730
Qy      39779 CTTGAGAAAGTTGAGAAAGTCCCTGTGTGAGCAGCAGGTGTGAATGTATGCGCTTTAGC 39838
Db      731 LeuGlnLysValGlnLysThrleuAenArgGlnGlnValGlnleuTyrArgleuLeuSer 750
Qy      39839 AGAAACACTTCCTGTGTGTGAGAGAGCAATCTCTGGAGAGCAGCATTTCTGGAGAGAA 39898
Db      751 ArgAenhiTyrleuGlntrpGlnAaPheSerValleuGlnYArgGlnhiS1IephtrIrrgArg 770
Qy      39899 CTTAAAAATGCCCTATTTGATGTGAAAAGCCTCGATTCCTGAGCAAAACA 39946
Db      771 LeuArgLysAlaIleleuAaPhePolYlysSerTrpAenProGlnGlyThr 786

```

RESULT 6
US-10-408-765A-181
; Sequence 181, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Boi D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.

```

; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale R.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ. ID NOS: 3077
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 641
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-408-765A-181

```

```

Alignment Scores:
Pred. No.: 4,81e-34 Length: 641
Score: 575.50 Matches: 110
Percent Similarity: 72.73% Conservative: 34
Best Local Similarity: 55.56% Mismatches: 53
Query Match: 0.66% Indels: 2
DB: 16 Gaps: 1

```

US-09-396-985B-48 (1-50000) x US-10-408-765A-181 (1-641)

```

Qy      36378 ATTGAAAAATGGGGGTACAGACCTAAAGAAAGAAATTCCTCACTGAGGAATACATGATGACT 36319
Db      435 ILeuLysTrrPAlaLysAaPheMetAaArghiSphSerlySgInSpleTyrAlaAla 454
Qy      36318 GAAAGTACCTAAAAAAATGTTTACATCTTATGATCATCAGGAGAAATGCAAAATCAAAACA 36259
Db      455 LysLysHiSmetLysLysCySsSerSerSerleuAlaIleArgGlnMetGlnIleYThr 474
Qy      36258 ACCCTGATATTCATCTTACACACAGTCAGATGACATGATCAAAATCTAAGTACAGC 36199
Db      475 ThmetArgTyrhiSleuThrProValArgMetAlaIleIleLysSerGlyAaAasn 494
Qy      36198 AGATGCTCCGAGAG-1GTAGAGAGAGAGAACTCTTCATGCTGGGCAACTGTAA 36140
Db      495 ArgGyTrrPArgLysGlyGlnIleGlyThrleuAenhiS1YStrPrrAaPcySlys 514
Qy      36139 CTGATATACCACTCTGGAATGCAATGATGTGTGCTCTCAGAAATTTGACATGTACTA 36080
Db      515 LeuValGlnProleuTrrPlySsSerValTrrArgPheleuAaArgSpleuGlnleuIle 534
Qy      36079 CTTGAGGATCCAGCATACCATCTTCAAGGCAAAATATCCAGATAT--GCTTCACTTGT 36023
Db      535 ProPheAaPrrAlaIleProleuAenGlyIleTyrProAaAaPrrTyrLysSerCyS 554
Qy      36022 AATPAGGACACATGCTCTACTATGTTCAATGACAGTTTATTTAATPAGCCAGATGCTTG 35963
Db      555 TyrLysAaPrrhrcyStrhArgMetPheIleAlaIleuPhehiS1YThrTrr 574
Qy      35962 AAAGAACTTGAATGTCCTTCAACAGAGAAATGAGATCAAAAATATGTGATCATTTGACA 35903
Db      575 AaGlnPrrLysCySProthrmctIleAaPrrIleLysLysMetTrrPheIleTyrThr 594
Qy      35902 GTGAGATCTATGACATGATATTAACAGTGAATCTATGACATTTCTTAGCAAAATGAATG 35843
Db      595 MetGlnTyrTyrAlaAlaIleLysAaAaPrrGlnPheMetSerPheValGlyThrTrrMet 614
Qy      35842 GACTGGAGGACATCATCTGAGTGAATGACCAACCAAGTCAATMAAAGAGACACAT 35789
Db      615 LysleuGlnThrIleIleleuSerLysleuSerGlnGlnLysThrlyS1Yhis 632

```

RESULT 7
US-10-000-256A-153
; Sequence 153, Application US/10000256A
; Publication No. US20030039983A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Yongsung
; APPLICANT: Recipon, Herwe
; APPLICANT: Chen, Sel-Yu

APPLICANT: Liu, Chenghua
 TITLE OF INVENTION: Compositions and Methods Relating to Prostate Specific Genes and
 FILE REFERENCE: DEX-0259
 CURRENT APPLICATION NUMBER: US/10/000,256A
 PRIOR FILING DATE: 2001-11-01
 PRIOR APPLICATION NUMBER: 60/244,782
 NUMBER OF SEQ ID NOS: 240
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 153
 LENGTH: 956
 TYPE: PRT
 ORGANISM: Homo sapien
 US-10-000-256A-153

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1.14e-33	571.50	72.22%	55.56%	14	956	110	33	54	2	1

US-09-396-985B-48 (1-50000) x US-10-000-256A-153 (1-956)

QY 36378 ATTGAAAATGGGTACAGAACTAAAGAAATTCCTCACTGAGAACTGATGACT 36319
 Db 750 ILeYslystrpAlaYsAspMetAsnArgHisPheSerlySGluSepIleTyAlaAla 769
 QY 36318 GAAAGTACCTAAATAATGTTTACATCTTACATCAAGGAAATGCAATCAAAACA 36259
 Db 770 LyshishmetlyslsYsSerSerSerleuAlaIleArglumeGlnIlelythr 789
 QY 36258 ACCCTGATATTCCTCACTCAACAGCTGAGTGAATGACTAAGTCAAACTCAAGTACAGC 36199
 Db 790 ThreterArglyrHisleuthrProvalArgMetAlaIleIlelyslsSerGlyAsnAsn 809
 QY 36198 AGATGCTCGCAAGA-TGTAGAGAGAGAGAACACTCTTCATTCCTGGCAGACTGTAA 36140
 Db 810 ArgCysrtpArglyGlyGlyGlyIleThrclyThreleuuhisCysrtpTrpAspCyslye 829
 QY 36139 CTGATATTAACCACTCGGAAATCAAGTTGTGTTCTCAGAAAATTGACATGCTACTA 36080
 Db 830 leuAlaGlnProleuthrlyPlySerValTrpArgPheleuArgAspLeuGlnle 849
 QY 36079 CCTGAGATCCAGCAATACCACTCCAGGCAAAATTCAGATGAT--GCTTCACTTGT 36023
 Db 850 ProheAspProAlaIleProleuLeuglyIleTyProGlnAspTyrlsSerCysCys 869
 QY 36022 AATNAGACACATGCTCTACTATGTTGATGCTTATTTATTAATAGCCAGATGCTG 35963
 Db 870 TyrlsAspThrCysrtpArgMetPheIleAlaIleuethrIleAlaIlyThrTrp 889
 QY 35962 AAAGAACCTAGATGCTCCCTCAACAGAGAAATGATATCAAAAATATGTCATTTGACA 35903
 Db 890 AsnGlnProlyscsPpThrIleIleAspTrpIlelyslsMetTrpHisIleTyThr 909
 QY 35902 GTGAGTACTATGACGCTATTTAAACAGTAACTATGATCTTATGAGCAAAATGATG 35843
 Db 910 MetGlnTyrlsAlaIleIlelyAsnAspGlnPheIleSerPheValGlyThrTrpMet 929
 QY 35842 GACCTGAGGGCATCATCTGAGTGAAGGTAAACCATATTAAGAGACACAT 35789
 Db 930 LyshleuGlnIleIleIleleuSerlyleuSerGlnGlnIlyThrHis 947

RESULT 8

US-10-025-201-3
 Sequence 3, Application US/10025201
 Publication No. US20030003468A1
 GENERAL INFORMATION:
 APPLICANT: Crow, Mary K.
 TITLE OF INVENTION: MARKERS FOR DISEASE SUSCEPTIBILITY AND TARGETS FOR THERAPY
 FILE REFERENCE: 5983/2H567

CURRENT APPLICATION NUMBER: US/10/025,201
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/256,673
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 3
 LENGTH: 1275
 TYPE: PRT
 ORGANISM: Homo sapiens
 PUBLICATION INFORMATION:
 DATABASE ACCESSION NUMBER: GenBank Accession No. US20030003468A1 U09116
 DATABASE ENTRY DATE: 1995-02-02
 RELEVANT RESIDUES: (1)..(1275)
 US-10-025-201-3

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1.28e-33	572.50	72.73%	55.05%	14	1275	109	35	53	2	1

US-09-396-985B-48 (1-50000) x US-10-025-201-3 (1-1275)

QY 36378 ATTGAAAATGGGTACAGAACTAAAGAAATTCCTCACTGAGAACTGATGACT 36319
 Db 1069 ILeYslystrpAlaYsAspMetAsnArgHisPheSerlySGluSepIleTyAlaAla 1088
 QY 36318 GAAAGTACCTAAATAATGTTTACATCTTACATCAAGGAAATGCAATCAAAACA 36259
 Db 1089 LyshishmetlyslsYsSerSerSerleuAlaIleArglumeGlnIlelythr 1108
 QY 36258 ACCCTGATATTCCTCACTCAACAGCTGAGTGAATGACTAAGTCAAACTCAAGTACAGC 36199
 Db 1109 ThreterArglyrHisleuthrProvalArgMetAlaIleIlelyslsSerGlyAsnAsn 1128
 QY 36198 AGATGCTCGCAAGA-TGTAGAGAGAGAGAACACTCTTCATTCCTGGCAGACTGTAA 36140
 Db 1129 ArgCysrtpArglyGlyGlyGlyIleThrclyThreleuuhisCysrtpTrpAspCyslye 1148
 QY 36139 CTGATATTAACCACTCGGAAATCAAGTTGTGTTCTCAGAAAATTGACATGCTACTA 36080
 Db 1149 leuValGlnProleuthrlyPlySerValTrpArgPheleuArgAspLeuGlnle 1168
 QY 36079 CCTGAGATCCAGCAATACCACTCCAGGCAAAATTCAGATGAT--GCTTCACTTGT 36023
 Db 1169 ProheAspProAlaIleProleuLeuglyIleTyProGlnAspTyrlsSerCysCys 1188
 QY 36022 AATNAGACACATGCTCTACTATGTTGATGCTTATTTATTAATAGCCAGATGCTG 35963
 Db 1189 TyrlsAspThrCysrtpArgMetPheIleAlaIleuethrIleAlaIlyThrTrp 1208
 QY 35962 AAAGAACCTAGATGCTCCCTCAACAGAGAAATGATATCAAAAATATGTCATTTGACA 35903
 Db 1209 AsnGlnProlyscsPpThrIleIleAspTrpIlelyslsMetTrpHisIleTyThr 1228
 QY 35902 GTGAGTACTATGACGCTATTTAAACAGTAACTATGATCTTATGAGCAAAATGATG 35843
 Db 1229 MetGlnTyrlsAlaIleIlelyAsnAspGlnPheIleSerPheValGlyThrTrpMet 1248
 QY 35842 GACCTGAGGGCATCATCTGAGTGAAGGTAAACCATATTAAGAGACACAT 35789
 Db 1249 LyshleuGlnIleIleIleleuSerlyleuSerGlnGlnIlyThrHis 1266

RESULT 9

US-10-050-882-80
 Sequence 80, Application US/10050882
 Publication No. US20030104400A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: 27 Human secreted proteins

FILE REFERENCE: P2038P1
CURRENT APPLICATION NUMBER: US/10/050,882
CURRENT FILING DATE: 2002-01-18
PRIOR APPLICATION NUMBER: 09/661,453
PRIOR FILING DATE: 2000-09-13
PRIOR APPLICATION NUMBER: PCT/US00/06783
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/125,055
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 156
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
LENGTH: 1010
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (125)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (104)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (194)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (362)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (525)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (643)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (643)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (643)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (656)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (660)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (711)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (770)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (777)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (790)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (800)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (825)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (987)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (996)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (1003)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-050-882-80

Alignment Scores:

Pred. No.: 2e-33 Length: 1010
Score: 568.50 Matches: 109
Percent Similarity: 71.72% Conservative: 33
Best Local Similarity: 55.05% Mismatches: 55
Query Match: 0.66% Indels: 2
DB: 14 Gaps: 1
US-09-396-985b-48 (1-50000) x US-10-050-882-80 (1-1010)
QY 36378 ATTGAATAATGGGTACAGAACTTAAGAGAAATTCAGCTAGGAGTAATGATGACT 36319
DB 804 TLeYsLsYsTPrLaLsYsApMeLsAeNArgHsPheSeTysGluNpLlEYrAlaAla 823
QY 36318 GAAAGTACCTAAATAATGTTTAACATCTTAGCTACGAGGAAATGCAATCAAAACA 36259
DB 824 Lys**HisMetYsLsYsCySsSerSerLeuAlaIlleArgLsMetGlnIlleYsThr 843
QY 36258 ACCCTGATATTCACCTTCACACCGATGACAGATGACTAAGATCAAAAATCTGACGACG 36199
DB 844 ThrMetArgTyHisLeuThrProValArgMetAlaIlleIlleYsLsSerGlyAAsn 863
QY 36198 AGATGCTCGAAGA-TGTAGAGAAGAGAACTCTTCATGCTGCGCAAGCTGTAA 36140
DB 864 ArgCyStrParGlyCySglYgLuIlleGlyThrLeuNuhIsCyStrPrPaSbCySlys 883
QY 36139 CTGATATTAACCACTGCAAAATGATTTGGTGTCTTCAGAAAATTTGACATGTACTA 36080
DB 884 LeuValGlnProLeuThrTyrSsSerValTTrParGPhenLeuArgSbPLeuGluLe 903
QY 36079 CTGAGAGTCACGAATATCACTTCAGAGCAAAATATTCAGATAT--GCTTCACTTGT 36023
DB 904 ProPheSbProAlaIlleProLeuLeuGlyIleTyProLysSbPtyrLysSerCySlys 923
QY 36022 AATAGGACACAGCTCTACTATGTTCAATGACGTTTATTAATAGCAGATGCTTG 35963
DB 924 TyTrLysAspThrCyStrNArgMetPheIlleAlaLeuPheThrIlleAlaYsThrTrp 943
QY 35962 AAAGAACCTAGATGTCCTTCACACAGAAATGATCAAAAATATGATGATTTGCACA 35903
DB 944 AsnGlnProLysCySbProThrMetIlleAspTrpIlleYsLysMetTrpHisIleYrThr 963
QY 35902 GTGGAGTACTATGACAGCTATTAATAACAGTGAATCTATGACATTTTAGCAATGAATG 35843
DB 964 MetGluTyTrYrAlaAlaIlleLysAsnAsbPgluPheSerPheValGlyThrTrpMet 983
QY 35842 GACCTGAGGCGCATTCCTGAGTGAAGGTAAACCAAGTCAAAAAGAACACAT 35789
DB 984 LysLeuGluN**IlleIlleLeuSerLysLeuSerGln**GlnYsThrLysHis 1001
RESULT 10
US-10-800-322-34
; Sequence 34, Application US/10800322
; Publication No. US20050053967A1
; GENERAL INFORMATION:
; APPLICANT: MEDIMOLECULAR PTY LTD
; TITLE OF INVENTION: NOVEL MARKERS AND USES THEREOF
; FILE REFERENCE: 2558321/TDO
; CURRENT APPLICATION NUMBER: US/10/800,322
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/322228
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 1275
; TYPE: PRT
; ORGANISM: mammalian
US-10-800-322-34
Alignment Scores:
Pred. No.: 3.12e-33 Length: 1275
Score: 567.50 Matches: 108
Percent Similarity: 72.73% Conservative: 36

QY 36022 AATAAGACACAGTCGTCTACTAGTGTACATAGCAGTTTATTATTAATAGCCAGA----- 35969
DB 1180 TyrllysasprlnrCysrlrhHmeCpHeleAlaaleuPheHrlleGlualrGleuGly 1199
QY 35968 -----TCCTGAAAGAACTAGATGTCCCTCAACAGAAATGATGATCAAAA 35921
DB 1200 ThrAnProLysrHrTrPrAnInLPrOlyeCysProthrmelLeaPrTrlLeLyls 1219
QY 35220 ATATGACATTTGACAGTGGAGTACTATGACGTATTAAAAACAGTAACTATGACA 35861
DB 1220 MetrhPslleTyrlrHmeGlulrTyrlAlaAlaIleLysAaNgluGluPheMetSer 1239
QY 35860 TTCTTAGCAATGATGAGCAGGAGCATCATCTCGATGATGAGTAAACCAGTCAATA 35801
DB 1240 PheValglYhrTrPrMetLysLeuGlulIlelleleuSerLysLeuSerGluGlu 1259
QY 35800 AAGAAGACACAT 35789
DB 1260 LysThrLysHis 1263
RESULT 12
US-09-954-987B-192
Sequence 192, Application US/09954987B
Publication No. US20030104523A1
GENERAL INFORMATION:
APPLICANT: Stefan Bauer
APPLICANT: Grayson B. Lipford
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
FILE REFERENCE: C1041/7016 (AMS)
CURRENT APPLICATION NUMBER: US/09/954,987B
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/233,035
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/263,657
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: US 60/291,726
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/300,210
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 230
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 192
LENGTH: 1032
TYPE: PRT
ORGANISM: Mus musculus
US-09-954-987B-192
Alignment Scores:
Pred. No.: 1,31e-32 Length: 1032
Score: 548.00 Matches: 219
Percent Similarity: 42.89% Conservative: 149
Best Local Similarity: 25.52% Mismatches: 298
Query Match: 0.63% Indels: 192
DB: 10 Gaps: 35
US-09-396-985B-48 (1-50000) x US-09-954-987B-192 (1-1032)
QY 37721 TTTCGCCATAGGTGTAATTGAACAATGAGACAGATGGCATGCTTACACCA 37780
DB 223 PheLeuSerAaAlaLysIleMetAsnIleThrGlnGluAaPheLysGlyLeuGluAa 242
QY 37781 CTCTCAAACTTGATACAGAGAAAC----- 37807
DB 243 LeuThrLeuLeuAaPheLysSerGlyAaCysProArgCysTyrlAaAlaProPheProCys 262
QY 37808 ---CCTATCCAGAGCTTTTCC-----CCAGAACTTTCTGAGACTACA 37849
DB 263 ThrProCysLysGluAaSerSerIleHisIleHisProLeuAlaPheGlnSerLeuThr 282
QY 37850 AGTTTAGAGAACTCTGTGGCTGTGGAGACAAATTTGGCCTCTTAGAAAGCTTCCCTATT 37909

DB 283 GlnLeuLeuTyrlLeuAaLeuSerSerThrSerLeuAaGhrIleProSerThrTrpPhe 302
QY 37910 GGAACGTTTAAACCTTAAAGAAACCTAATGTCGCTCACAATTT---ATACTTCTCT 37966
DB 303 GluAaLeuSerAaLeuLysGluLeuHrIleGluPheAaSerLysLeuValGlnIle 322
QY 37967 AAGTTACCTGCATATTTTTCATCTGACAGACCTAGTACATGGATCTTCTTATAC 38026
DB 323 AlaSerGlyAlaPheLeuTrLysLeuProSerLeuGlnIleLeuAaPheLeuAa 342
QY 38027 -----TATATCAAACTATTACTGTC---AAGCACTTACAGTTTTCAGT 38068
DB 343 PheGlnTyrlLysGluTyrlLeuGlnPheIleAaHrIleSerSerAaPheSerLysLeuAa 362
QY 38069 GAAATTCACAAAGTCAATCTC----- 38089
DB 363 SerLeuLysLysLeuHisLeuAaGlyTyrlValPheAaGluLeuLysLysHisAaPhe 382
QY 38090 -----TCTTAGACATGCTTTGAACCAATGAC 38119
DB 383 GluHisLeuGlnSerLeuProAaLeuAlaThrIleAaLeuGlyIleAaPheIleGlu 402
QY 38120 TTCAATTCAGACCAAGCTTTCAAGGAATT---AAGCTCCATGACTGACTTAAGAGT 38176
DB 403 LysIleAaPheLysAlaPheGlnAaPheSerLysLeuAaPheValIleTyrlLeuSerGly 422
QY 38177 AATTTTAAATGCTCAATTAATGAAGAAACTGCTTCAAAACCTGGCTGTTTACAGTC 38236
DB 423 AaAaHrIleAaSerValLeuAaPglYhr----- 432
QY 38237 CATGGTGAATCTGGAGAAATTAAGATGAAGAAATCTGGAATTTTGAACCTCT 38296
DB 433 -----AaPtyrSerSerTrpAaAa---ArgLeuAaGlyLysProLeu 445
QY 38297 ATCATGAGACATAGTGAATGACCATGATGATGAGTTCAGGTTAACAATATACAT 38356
DB 446 SerThrAaPhePhe-----AaPgluAaPhe---ProHisValAaPhe 458
QY 38357 TTT-----TCAGATGATATTGTTAAAGTTCATGCTGGCGAATGTTTTCGAATGCT 38410
DB 459 TyrHisSerThrLysProLeuIleLysProGlnCysThrIaTyrlGlyValAaLeuAa 478
QY 38411 CTGGCAGGTGATCTAATAAATATCTGAAGATGTCCTTAAACATTTCAATGAGCAATCC 38470
DB 479 Leu-----SerLeuAaAaenIlePheIleIleGlyLysSer---GlnPheGluGly 494
QY 38471 TTATCAATCATTAAGATGTCAACTTAACAGCTTCCAACTGTGATTAACCTTTCTTAA 38530
DB 495 PheGlnAaPheIleAaCys----- 500
QY 38531 AGTTGACTTTAACTAATGAACAAAGGCTCATACGTTTAAAAAAGTG-----GCC 38581
DB 501 ---LeuAaLeuSerPheAaAlaAaSerThrGlnValPheAaGlnTyrlrGluPheSerSer 519
QY 38582 CTACCAAGTCTGACGTATCTAGATCTTAGTGAAGAACTGACGCTTATGATGCTGT 38641
DB 520 MetProHisIleLysTyrlLeuAaPheLeuThrAaAaHrGluAaPheAaPheAaAaAa 539
QY 38642 TCTTATTCTGATTTGGGACAAACAGCCTGAGACACTTGAACCTCACTCAATGAGTGCC 38701
DB 540 AlaPheSerAaPheLeu-----HisAaPheGluValLeuAaPheLeuSerHisAaAlaHis 557
QY 38702 ATCATTAAGAGTGCAT-----TTCATGGCTCTGAAGAGCTG 38740
DB 558 TyrPheSerIleAlaGlyValThrHisAaGluGlyPheIleGlnAaLeuAaHisLeu 577
QY 38741 CAGACCTGATTTTACGACTCTACTTAAAGGCTCACAGA----- 38785
DB 578 ArgValLeuAaLeuSerHisAaGlyIleTyrlThrLeuThrGlnGluSerGluLeuLys 597
QY 38785 ----- 38785

```

Db      598 SerIleSerLeuValGluLeuValPheSerGluValAsnArgLeuAspHisLeuTrpAsnAla 617
Qy      38786 -----TTCTGAGCGTTCTTATCCCTGAAAGACTTACTTACCTGACATC 38830
Db      618 AsnArgGluValTyrTrpSerIlePheLeuSerLeuGlnAsnLeuIleValGluLeuAspLeu 637
Qy      38831 TCTTATACTACACCAAAATGACTCGATGATATTTATTTGGCTTG---ACCAAGTCTC 38887
Db      638 SerTyrAsnAsnLeuGlnGlnIleProAsnGluAlaPheLeuAsnLeuProGlnSerLeu 657
Qy      38888 AACACATTAATAAGGCTGGCAATTTCT-----TTCAAGACAAACCCCTTCAAAATGTC 38941
Db      658 GlnIleLeuLeuIleSerGluValAsnLeuValArgPheAsnTrpIleLeuGlnTyr 677
Qy      38942 TTTCGAAACACAAACAACTTACATTCCTGATCTTTTAAATGATTCGAAACAAATA 39001
Db      678 Phe-----ProIleValHisLeuLeuAspLeuSerArgAsnGluLeuTyrPheLeu 694
Qy      39002 TCTTGGGGGATATTGACACCCCTGCATAGACTTCATATTATTAATGATGACACAAAT 39061
Db      695 ProAsnGluSerLeuValPheAlaHisSerLeuGlnIleLeuLeuLeuSerHisAsnHis 714
Qy      39062 CTATGTTGTTGGATGATCCCATTAATACACAGCTGATTCCTGCAGACCTTGGATTC 39121
Db      715 PheSerHisLeuProSerGluPheLeuSerGluAlaArgAsnLeuValHisLeuAspLeu 734
Qy      39122 AGTTTCATGCGATAGAG---ACATCTTAAGGAATACGCAACCTTTCCAAAG---AGT 39175
Db      735 SerPheAsnThrIleLeuMetIleAsnLeuSerLeuGlnIleTyrMetLeuTyrAsn 754
Qy      39176 CTACGCTTCTTCATCTTACTACAAATCTGCTGTTGATATGCAATCAACAATTC 39235
Db      755 LeuSerIleLeuGluLeuHisGluValAsnTyrPheAspGlyAsnArgIleSerAspPhe 774
Qy      39236 CTGACGTGGCTCAAGAAACAGAGAGAGTTC-----TTGGTGAATGTTGAACAA 39283
Db      775 ArgSerTrpLeuAspArgGluAsnLeuAsnIleThrIleProValLeuValAsnVal----- 792
Qy      39284 ATGACATGTGCAACACCTGATAGATGAATACCTCTTATGTTGATTTTAATTAATTC 39343
Db      793 ---IleCysSerAsnProGluValAspGlnLeuSerLeuSerIleMetSerLeuAspLeuThr 811
Qy      39344 ACCTGTTATATGATCAAGACAAATCATCATGCTGTCAGTGCATGTCATGTCGATCC 39403
Db      812 ThrCysValSerAspThrThrAlaValLeuPheLeuThrPheLeuThrSer 831
Qy      39404 ACTGTA-----GCATTTCTGATATACAC-----TTCTATTTT 39436
Db      832 MetValMetLeuAlaIleValHisIleValPheTyrTrpAspValTrpPheIleTyr 851
Qy      39437 CACCTG-----ATACTTATGCTGGCTGTAAAGAAAGTACAGAGAGAAAGCATCTAT 39490
Db      852 HisMetCysSerAlaValLeuValGluTyrArgThrSerSerThrSerGlnThrPheTyr 871
Qy      39491 GATGCAATTTGATGATCTGAGTCAAGTCAAT-----GAGACCTGGGTGAGAAATAG 39541
Db      872 AspAlaTyrIleSerTyrAspThrLeuAspAlaSerValThrAspTrpValIleAsnGlu 891
Qy      39542 CTGCTAAAGAAATTTAAGAAAGAGAGTCCCGC---TTTCACTCTGCTTCACTACAGA 39598
Db      892 LeuArgTyrHisLeuGlnGluSerGluAspValSerValLeuLeuValGluGlnArg 911
Qy      39599 GACTTATTCCTGCTGATGATGATGCTGCGCAACATCATCCAGAAAGCTTCCAAAGAGC 39658
Db      912 AspTrpAspProGluLeuProIleIleAspAsnLeuMetGln---SerIleAsnGlnSer 930
Qy      39659 CGAAGGATTTGCTGATGATGCTTACACACTTTATGACAGCCCTGGTGTATTTGAA 39718
Db      931 LysLeuThrIlePheValLeuThrLeuValTyr----- 941
Qy      39719 TATAGATTGCTCAACAGTCTTCTGAGC----- 39751
Db      942 -----AlaLysSerTrpAsnPheThrAlaPheTyrIleAlaIleGlnArgLeu 958

```

```

Qy      39752 -----AGCCGCTCGGATCATCTTATTCCTTGAAGAGTTGAGAACTCCCTG 39802
Db      959 MetAspGluAsnMetAspValIleIlePheIleLeuLeuGlnProValLeuGln----- 976
Qy      39803 CTGAGCAGCAGCAGGATGAAATTTGATTCGCTTTTACGAGAAACCTTACCTGGAATGGAG 39862
Db      977 TyrSerGlnTyrLeuArgLeuArgGlnArgIleCysLysSerSerIleLeuGlnTrpPro 996
Qy      39863 GACAACTCTCTGGGAGAGCAGATCTTGTGAGAGAACTTAATAATGCCCTATTG 39916
Db      997 AsnAsnProValAlaGluAsnLeuPheTrpGlnSerLeuLysAsnValValLeu 1014

RESULT 13
US-10-272-502A-31
: Sequence 31, Application US/10272502A
: Publication No. US20030139364A1
: GENERAL INFORMATION:
: APPLICANT: Krieg, Arthur M.
: APPLICANT: Schetter, Christian
: APPLICANT: Bratzler, Robert L.
: APPLICANT: Volmer, Jorg
: APPLICANT: Bauer, Stefan
: TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
: FILE REFERENCE: IMIDAZOQUINOLINE COMPOUNDS
: CURRENT APPLICATION NUMBER: US/10/272,502A
: PRIORITY FILING DATE: 2002-10-15
: PRIOR APPLICATION NUMBER: 60/329,208
: NUMBER OF SEQ ID NOS: 31
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 31
: LENGTH: 1032
: TYPE: PRT
: ORGANISM: Mus musculus
US-10-272-502A-31

Alignment Scores:
Pred. No.: 1,31e-32 Length: 1032
Score: 548.00 Matches: 219
Percent Similarity: 42.89% Conservative: 149
Best Local Similarity: 25.52% Mismatches: 198
Query Match: 0.63% Indels: 192
DB: 14 Gaps: 35

US-09-396-985B-48 (1-50000) x US-10-272-502A-31 (1-1032)
Qy      37721 TTGGCCATGAGTGTGAATTTGAACAATGAAGACAGGACGATGCTTACACACC 37780
Db      223 PheLeuSerAsnAlaValIleMetAsnIleThrGlnIleAspPheLysGluLeuAsn 242
Qy      37781 CTCTCAAACTTGATCTACAGAGAAAC----- 37807
Db      243 LeuThrLeuLeuAspLeuSerGluValAsnCysProArgCysTyrTrpAsnAlaPheProCys 262
Qy      37808 ---CTATCCAGAGTTTTC-----CCAGAACTTCTCTGAGCTPACA 37849
Db      263 ThrProCysLeuValGluAsnSerSerIleHisIleIleProLeuAlaPheGlnSerLeuThr 282
Qy      37850 AGTTTGAAGAACTGCGTGTGAGACAAATTTGGCCCTCGACAAAGCTTCCCATAT 37909
Db      283 GlnLeuLeuTyrIleValAsnLeuSerSerThrSerLeuArgThrIleProSerThrTrpPhe 302
Qy      37910 GACAGCTTAATACTTAAAGAACTCAATGTGCTCACAATTT---ATACTTCCTGT 37966
Db      303 GluAsnLeuSerAsnLeuLysGluLeuHisLeuGlnPheAsnTyrIleValGlnIle 322
Qy      37967 AAGTTACCTGCATATTTTTCATCTGACAGAACTTGTATACATGATCTTCTTATAC 38026
Db      323 AlaSerGluAlaPheLeuThrLysLeuProSerLeuGlnIleLeuAspLeuSerPheAsn 342

```

QY	38027	-----TATATTCACAACTATTACTGTC-----AAGCACTTACAGTTTCTAGT	38068
Db	343	PheGlnIYrYsgIuYrIeugInPheIleAsnIleSerSerAsnPheserIYsleuArg	362
QY	38069	GAANAATCCACAAGCAATCTC-----	38089
Db	363	SerIeulYsIeulSleuAsIeulArgGlyTrValPheArgGluLeulYsIeulSleuPhe	382
QY	38090	-----TCTTAGACATGCTTTGAACCAATTGAC	38119
Db	383	GluHISleuGInSerIeulProAsnLeuAlaThrIleAsnLeuGlyIleAsnPheIleGlu	402
QY	38120	TTCAATTCAAGACCAAGCTTTCCAGGGAATT--AAGCTCAAGAACTGACTTAAGAGT	38176
Db	403	LysIleAspPheYsIaIaPheGlnAsnPheserIYsIeulAspValIleTrYserIeulArg	422
QY	38177	AATTTTAATAGCTCAAAATATTAAGAAGAACTGGCTTCAAAACCTGGCTGTTACAGTC	38236
Db	423	AsnArgIleAlaSerValIeulAspGlyThr-----	432
QY	38237	CATCGGTTGATCTTGGGAAATTTAAAGATGAAGAATCTGGAATTTTGAACCTCT	38296
Db	433	-----AspIYrSerSerTrpArgAsn--ArgIeulArgIysProIeul	445
QY	38297	ATCATGGAAGACTATGTGATGTGACCAATGATGAGTTCAGTTAACATATACAATGAT	38356
Db	446	SerThrAspAsp-----AspGluPheAsp--ProHISValAsnPh	458
QY	38357	TTT-----TCAGATGATATTGTTTAAGTTCATGCTGGTGGCAATCTTCTGCATATGCT	38410
Db	459	TrYHISerThrIYsPProIeulIeYsPProGInCysThrAlaTrYgIYsAlaIeulAsp	478
QY	38411	CTGGCAGGTGATCTATTAATAATATCTGAAGATGTTCTTAACATTTCAATGACCAATCC	38470
Db	479	Leu-----SerIeulAsnAsnIlePheIleIleGlyIYsSer--GlnPheGluGly	494
QY	38471	TTATCAATCATTTAGATGTCAACTTAAGCAGTTTCAACTCTGGATCTACCCTTTCTTAA	38530
Db	495	PheGlnAspIleAlaCys-----	500
QY	38531	AGTTGACTTAACTATGAACCAAGGCTCATACGTTTAAAAAATG-----GCC	38581
Db	501	---LeuAsnIeulSerPheAsnAlaAsnThrGlnValPheAsnGlyThrGluPheSerSer	519
QY	38582	CTACCAAGTCTCAGCTATCTAGATCTTAAGAGAAAGCACTGAGTCTAGTGGTGGCTGT	38641
Db	520	MetProHISleIeulYrIeulAspIeulThrAsnAsnArgIeulAspPheAspAsnAsn	539
QY	38642	TCTTATTTCTGATTTGGAAACAACAGCTGAGACACTTAGACCTCAATGATGGTGCC	38701
Db	540	AlaPheSerIeulAspLeu-----HISAspIeulGluValIeulAspIeulSerHISAsnAlaHIS	557
QY	38702	ATCATTTATGATGCCAAT-----TTCAATGGGCTTGAAGAAGCTG	38740
Db	558	TrYPheSerIleAlaGlyValThrHISArgIeulGlyPheIleGlnAsnIeulIeAsnLeu	577
QY	38741	CAGCACTCGGATTTTTCAGACTCACTACTTTAAAAAGGCTCAAGAA-----	38785
Db	578	ArgValIeulAsnIeulSerHISAsnGlyIleTrYThrIeulThrGluIeulSerGluIeulS	597
QY	38785	-----	38785
Db	598	SerIleSerIeulYsGluIeulValPheSerGlyAsnArgIeulAspHISleulTrpAsnAla	617
QY	38786	-----TTCTCAGGCTTCTTATCCCTTGAAGAAAGTACTTTAACCCTTGACATC	38830
Db	618	AsnAspGlyYrYrTrpSerIlePheIYsSerIeulGlnAsnIeulIeArgIeulAspLeu	637
QY	38831	TCTTATACTACACCAAAATGACTTGAGATGATATTTTGGGCTTG---ACCAGTCTC	38887
Db	638	SerTrYsAsnIeulGInGlnIleProAsnGlyAlaPheIeulAsnIeulProGInSerIeul	657
QY	38888	AACCATTTAAAAATGGCTGGCAATTC-----TTCAAGACAAACCCCTTCAATATGC	38941

D6		677
	658	GlnGluLeuLeuIleSerGlyAsnLysLeuAArgPhePheAsnTrpThrLeuLeuGlnTyr		
OY	38942	TTTGAACAAACAACAATCGATTCCTGGATCTTTCTTAATTGTCAATTGACAATA	39001	
		: :	: :	:
D6	678	Phe-----ProHisLeuHISLeuLeuAAspLeuSerArgAsnGluLeuTyrPheLeu	694	
OY	39002	TCCTTGAGGGGATATTGACACCCTCCATAGACTTCAAATTATTAATAATGAGTCACAACAT	39061	
		:::: ::::	: :	: :
D6	695	ProAlaCysLeuSerLysPheAlaHisSerLeuGlnThrLeuLeuLeuSerHisAsnHis	714	
OY	39062	CTATTGTTTTGGATTTCATCCCATTATTAACAAGCTGTATTCCCTCAGACTGTGATTGC	39121	
D6	715	PheSerHisLeuProSerGlyPheLeuSeuGluAlaArgAsnLeuValHisLeuAspLeu	734	
OY	39122	AGTTTCAATCGCATTAGAG--ACATCTMAAAGAAAGTAAGTACTCAACATTTCCAAG--	39175	-AGT
		: :		
D6	735	SerPheAsnThrIleLeuMetIleAlanLysSerSerLeuGlnThrLysMetLysThrAsn	754	
OY	39176	CTAGCCTTCTTCAATCTTATCAAAATTCGTGTTGCTGTATATGACAATCAGAAAATTC	39235	
		:		
D6	755	LeuSerIleLeuGlnLeuHisGlyAlaAnTyrPheAspCysThrCysAspLysSerAspPhe	774	
OY	39236	CTGCAGTGGGTCAAGAACAGAAAGACTTC-----TTGTTGAATGTGGAACA	39288	
		:		
D6	775	ArgSerThrLeuAspGlnAAsnLeuValIleThrIleProLysLeuValAsnVal-----	792	
OY	39284	ATGCATGTGCAACAACCTGATAGATGAATACCTCTTGAAGTGGATTATTAATTC	39343	
		: :		
D6	793	--LleCysSerAsnProGlyAspGlnLysSerLysSerIleMetSerLeuAspLeuThr	811	
OY	39344	ACCTGTATATATGACAAAGACATCATCATGCTGTCACTGTCAGTGTGAATTGTGTATCC	39403	
D6	812	ThrCysValSerAspThrThrAlaAlaValLeuPhePheLeuThrPheLeuThrThrSer	831	
OY	39404	ACTGTA----GCATTTCTGATATACCC-----TTCATTTT	39436	
		: :		
D6	832	MetValMetLeuAlaAlaLeuValHisHisLeuPheTyrTrpAspValTrpPheIleTyr	851	
OY	39437	CACCTG-----ATACTTATGCTGGCTGTTAAAAAGATACAGAGAGAACATCACTAT	39490	
		: :		
D6	852	HisMetCysSerAlaLysLeuLysGlyTyrArgThrSerSerThrSerGlnThrPheTyr	871	
OY	39491	GATCATTTGTGATCTACTGAGTCAGAAAT-----GAGGACTCGGTGAGAAATGAG	39541	
		: :		
D6	872	AspIleTyrLieserTyrAspThrLysAspAlaSerValThrAspTrpValIleAsnGln	891	
OY	39542	CTGTAAAGAATTTAGAAAGAGGCCCGC---TTTCACTCTGCTTCACTACACAA	39599	
		: :		
D6	892	LeuArgTyrHisLeuGlnGluInuSerGluAspLysSerValLeuLeuCysLeuGlnGluArg	911	
OY	39599	GACTTTATCTGGTGTAGCACCTGTCGCCAATCATCATCAGAGAACGCTTCCACAGAG	39656	
		: :		
D6	912	AspTrpAspProGlyLeuProIleIleAspAsnuMetCin---SerIleAsnGlnSer	930	
OY	39659	CGGAAGGTATTATGTGATGTCTAGACACTTATTACAGACCGGTGTGTATCTTTGAA	39718	
		: :		
D6	931	LysLysThrIlePheValLeuThrLysLysTy-----	941	
OY	39719	TATGAGATTGCTCAACATGGCAGTTTGTAGC-----	39753	
		: :		
D6	942	-----AlaLysSerTrpAsnPhelysThrAlaPheTyrLeuAlaLeuGlnArgLeu	958	
OY	39752	-----AGCGCGCTCGGCAATCATCTTCATGTCCTTGAGAAAGGTGAGAACGCCCG	39800	
		: :		
D6	959	MetAspGluAsnMetAspValIleIlePheIleLeuLeuGlnProValLeuGln-----	976	
OY	39803	CTGAGCAGCAGCAGGTGATATGTATCGCTTTTAGAGAGAAACCACTCACTGATAGATGGAG	39862	
		: :		
D6	977	TyrsertGlnTyrLeuArgLeuArgGlnArgIleCylasLysSerSerIleLeuGlnIntPrco	996	
OY	39863	GACAATCTCTGGGGAGGACATCTTTGTGAGAGAAAGCTTAAAAATGCCCTATTG	39916	
		::: : :		


```

Db      997 AsnAsnProlysaIaGluAsnLeuPheTrpGlnSerLeuLysAsnValValIleu 1014
RESULT 14
US-10-407-952-32
; Sequence 32, Application US/10407952
; Publication No. US20030232074A1
; GENERAL INFORMATION:
; APPLICANT: Lipford, Grayson
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides
; FILE REFERENCE: C01041.70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1032
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-407-952-32

Alignment Scores:
Pred. No.: 1,31e-32 Length: 1032
Score: 548.00 Matches: 219
Percent Similarity: 42.89% Conservative: 149
Best Local Similarity: 25.52% Mismatches: 192
Query Match: 0.63% Indels: 192
DB: 15 Gaps: 35

US-09-396-985b-48 (1-50000) x US-10-407-952-32 (1-1032)
QY      37721 TTGCCCATAGCTGTGAATTGAAACAATTGAAAGACAGAGTCGCTTAACACCAC 37780
Db      223 PheuserAenAlaIylleEmeLasnIleThrgIngluAepHelyglYleuGluasn 242
QY      37781 CTCGCAACTGTGATACGACAGGAAC----- 37807
Db      243 LeuThreuleuAepLeuserGlyAsnCyProArgCysTyraAnaIaProPheProCys 262
QY      37808 ---CCATCCAGAGTTTTC-----CCAGAGAGTTTCTCGACTACA 37849
Db      263 ThrProCylysGluAsnSerSerIleHisIleHisProLeuAlaPheGlnSerLeuThr 282
QY      37850 AGTTAGAAATCTGTGGCTGTGGAGACAAATTTGCGCTCTAGAAAGCTCCCTAAT 37909
Db      283 GlnLeuLeuTyrlleuAsnLeuserSerTherSerleuArgThrIleProSerThrTriPhe 302
QY      37910 GGACAGCTTAATACCTTAAGAAACTCAATGTGCTCACAATTTT---ATACATTCCTGT 37966
Db      303 GluAsnLeuserAenLeuLysGluLeuHisIleuGlnPheAsnTyrlleuValGlnGluIle 322
QY      37967 AAGTTACCTGATATTTTCCAAATCTGACGAAACCTAGACATGAGATCTTTCTTATAC 38026
Db      323 AlaSerGlyAlaPheLeuThrlYleuProSerLeuGlnIleLeuAepLeuserPheAsn 342
QY      38027 -----TATATCAACTATTAAGTCTC---AAGCACTTAAGTTCTTACGT 38068
Db      343 PheGlnTyrlYlsGluTyrlleuGlnPheIleAsnIleSerSerAenPheSerLysLeuArg 362
QY      38069 GAAATTCACAAAGTCATCTC----- 38089
Db      363 SerLeuLysLysLeuHisIleuArgGlyTyrlValPheArgGluLeuLysLysHisPhe 382
QY      38090 -----TCTTAGACATGTCTTGAACCAATGAC 38119
Db      383 GluHisLeuGlnSerLeuProAsnLeuAlaThrIleAsnLeuGlyIleAsnPheIleGlu 402
QY      38120 TTCAATTCAGACCAAGCTTTCAAGGAAT---AAGTTCATGAATGACTTAAAGAGT 38176

```

```

Db      403 LysIleAspPheLysAlaPheGlnAsnPheSerLysLeuAspValIleTyrlLeuSerGly 422
QY      38177 AATTTAATAGCTCAAAATATATATGAAACCTTGCTCAAAACCGGTGGTTACAGTC 38236
Db      423 AsnArgIleAlaSerValIleAspGlyThr----- 432
QY      38237 CATCGTTGATCTTGGAGAAATTTAAAGATGAAAGATCTGAAATTTTGAACCTCT 38296
Db      433 -----AspTyrlSerSerTriPheArgAsn---ArgLeuArgLysProLeu 445
QY      38297 ATCATGAGAGCACTATGTGATGTCACCAATTGATGATGATTCAGGTTAAACATATACAAATGAT 38356
Db      446 SerThrAspAsp-----AspGluPheAsp---ProHisValAsnPhe 458
QY      38357 TTT-----TCAGATGATATTTGTAAGTTCATTCATTCATTCGTTGGAGATGTTTCGCAATGCT 38410
Db      459 TyrHisSerThrLysProLeuIleLysProGlnLysThrAlaTyrlYlsAlaLeuAsp 478
QY      38411 CTGGCAGGTGATATATATAATATCTAGAAAGATGTTCTTAACATTTCAATGGCAATCC 38470
Db      479 Leu-----SerLeuAsnAsnIlePheIleIleGlyLysSer---GlnPheGlnGly 494
QY      38471 TTATCAATCATTTAGATGTCAACTTAAGACAGTTTCCAACTGTGATCACTTCTTAA 38530
Db      495 PheGlnAspIleAlaCys----- 500
QY      38531 AGTTTGACTTAACTATGAAACAAAGGCTATACGTTTAAAAAAGTG-----GCC 38581
Db      501 ---LeuAsnLeuserPheAsnAlaAsnThrGlnValPheAsnGlyThrGluPheSerSer 519
QY      38582 CTACCAAGTCTCAAGCTATCTAGATCTTATGATGAAAGATGACAGTCTTATAGTGTGTGT 38641
Db      520 MetProHisIleLysTyrlleuAepLeuThrAsnAsnArgLeuAspPheAspAspAsn 539
QY      38642 TCTTATTTGATTTTGGGACAAACAGCTGAGACACTTAACCTCAGCTTCAATGTCGCC 38701
Db      540 AlaPheSerAspLeu-----HisAspLeuGluValLeuAepLeuserSerHisAsnAlaHis 557
QY      38702 ATCATTTATGAGTGCAT-----TTCAATGGCTTAAAGAGCTG 38740
Db      558 TyrPheSerIleAlaGlyValThrHisArgLeuGlyPheIleGlnAsnLeuIleAsnLeu 577
QY      38741 CAGCACCTGATTTTGCACACTCTACTTAAAGGCTACACAGA----- 38785
Db      578 ArgValLeuAsnLeuserHisAsnGlyIleTyrlThrLeuThrGlnGlnSerGluLeuLys 597
QY      38785 ----- 38785
Db      598 SerIleSerLeuLysGluLeuValPheSerGlyAsnArgLeuAspHisLeuTriPheAsnAla 617
QY      38786 -----TTCACAGGCTCTTATCCCTTGAAGAAAGCTATTTACCTTGAACATC 38830
Db      618 AsnAspGlyLysTyrlTriPheSerIlePheLysSerLeuGlnAsnLeuIleArgLeuAspLeu 637
QY      38831 TCTTATCTACTACACAAATTTGACTTGATGATATTTCTTGCGCTGG---ACCAGCTTC 38887
Db      638 SerTyrlAsnAsnLeuGlnGlnIleProAsnGlyAlaIlePheLeuAsnLeuProGlnSerLeu 657
QY      38888 AACACATTAATAATGGCTGSCAATCT---TTCAAGACAAACACCTTTCAATGTC 38941
Db      658 GlnGluLeuLeuIleSerGlyAsnLysLeuArgPhePheAsnLeuTriPheLeuGlnTyrl 677
QY      38942 TTTCGAAACACAAACAACTTGACATTCCTGTGATCTTTCTTAATGTCAATTTGAAACAATA 39001
Db      678 Phe-----ProHisLeuHisIleuLeuAspLeuserTrgAsnGlnLeuTyrlPheLeu 694
QY      39002 TCTTGGGGGTATTTGACACCTTCATAGACTTCATATTAATTAATAGATCAACAAT 39061
Db      695 ProAsnCyLysLeuserLysPheAlaHisSerLeuGlnThrLeuLeuLeuserHisAsnHis 714
QY      39062 CTATGTTGTTTGAATTCATCCATTAATACACAGCTGATATTCCTCAGACACTTGTGATGC 39121
Db      715 PheSerHisLeuProSerGlyPheLeuserGlyAlaArgAsnLeuValHisIleAspLeu 724

```

QY	39122	AGTTTCAATGCGATAGG---	ACATCTAAGAAATCTGCAACATTTTCCAAG--	AGT	39175
Db	735	SerPheAsnThrIleuValMetIleAsnValSerSerLeuGlnThrLysMetLysThrAsn			754
QY	39176	CTACCCCTTCTTCATCTTAAACAATTCCTGTGCTTGTAATGTGAACATCAAGAAATTC			39235
Db	755	LeuSerIleLeuGluLeuHisGlyAsnTyrPheAspCysThrCysAspIleSerAspPhe			774
QY	39236	CTGCATGGCGCTCAAGAGACAGACAGCTTC-----	TTGGTAATGTTGAACA	39283	
Db	775	ArgSerTyrLeuAspGluAsnLeuAsnIleThrIleProLysLeuValAsnVal-----			792
QY	39284	ATGCACTGGTGAACACCTGGTAAGATGAATATACCTCCCTTAGTGTTGAATTTTAATAATCT			39343
Db	793	---IleCysSerAsnProGlyAspGlnLysSerLysSerIleLeuSerLeuAspLeuThr			811
QY	39344	ACCTGTATATATGTAACAAGACATCATCATGTGTCTCATGTGTGATTTGTGTATCC			39403
Db	812	ThrCysValSerAspThrThrAlaIleValIleuPhePheLeuThrPheLeuThrThrSer			831
QY	39404	ACTGTA-----GCATTTCTGATATACAC-----	TTCTATTTT	39436	
Db	832	MetValMetLeuAlaIleValHisIleValPheTyrTrpAspValTrpPheIleTyr			851
QY	39437	CACCTG-----ATACCTTATTTGCTGGCTGTAAAGATGACAGACAGAGAGACATCTAT			39490
Db	852	HisMetCysSerAlaLysLeuLysGlyTyrArgThrSerSerThrSerGlnThrPheTyr			871
QY	39491	GATGCATTTTGATCTCTACTGCAGTCAGAAAT-----	GAGCAGCTGGCTGAGAAATGAG	39541	
Db	872	AspAlaTyrIleSerTyrAspThrLysAspAlaSerValThrAspThrValIleAsnGlu			891
QY	39542	CTGGTAAAGATTTTGAAGAAGAGATGCCCCC-----	TTTACCTCTGCTTCACTACACAA	39598	
Db	892	LeuArgTyrHisLeuGluGlnSerGluAspLysSerValLeuLeuLysLeuGluArg			911
QY	39599	GACTTTATTCCTGGTGTAGCCATGTGTCGCAACATCATCCAGAGAGGCTTCCACAGAGC			39658
Db	912	AspTrpAspProGlyLeuProIleIleAspAsnLeuMetGln---SerIleAsnGlnSer			930
QY	39659	CGGAAGGTTATTTGTGTAGTGTCTAGACACTTTATTCAGAGCCGTTGGTGTATCTTTGAA			39718
Db	931	LysIleThrIlePheValIleuThrLysLysTyr-----			941
QY	39719	TATGAGATTTGCTCAACATGCGACGTTTCTGAC-----			39753
Db	942	-----AlaLysSerTyrAspAsnLysPheLysThrAlaPheTyrLeuAlaLeuGlnArgLeu			958
QY	39752	-----AGCCCGCTCGGCATCATCTTCAATTTGCTTGAGAGAGGTTGAGAGTCCCTG			39802
Db	959	MetAspGluAsnMetAspValIleIlePheIleLeuLeuGlnProValLeuGln-----			976
QY	39803	CTGAGCGACGAGGTGGAATGTATGCGCTTTCAGAGAAACACTTACCTCGAATGGGAG			39862
Db	977	TySerGlnTyrLeuArgLeuArgAlaGlyIleCysLysSerSerIleLeuGlnTyrPro			996
QY	39863	GACATCTCTCTGGGGAGGACATCTTCTTGAGAGAACTTAAATGCGCATTTG			39916
Db	997	AsnAsnProLysAlaGluAsnLeuPheTyrGlnSerLeuLysAsnValValLeu			1014
RESULT 15					
US-10-415-615-3					
; Sequence 3, Application US/10415615					
; Publication No. US20040101943A1					
; GENERAL INFORMATION:					
; APPLICANT: INCYTE CORPORATION					
; APPLICANT: BAUGHN, Mariah R.					
; APPLICANT: YUB, Henry					
; APPLICANT: LU, Yan					
; APPLICANT: DING, Li					
; APPLICANT: TANG, Y. Tom					
; APPLICANT: GANDHI, Ameena R.					

```

1  APPLICANT:  HAFALIA, April J.A.
2  APPLICANT:  LAH, Preeti G.
3  TITLE OP INVENTION:  NUCLEIC ACID MODIFICATION ENZYMESS
4  FILE REFERENCE:  PI-0280 USN
5  CURRENT APPLICATION NUMBER:  US/10/415, 615
6  CURRENT FILING DATE:  2003-04-29
7  PRIOR APPLICATION NUMBER:  PCT/US01/46301
8  PRIOR FILING DATE:  2001-11-01
9  PRIOR APPLICATION NUMBER:  US 60/245,458
10 PRIOR FILING DATE:  2000-11-02
11 PRIOR APPLICATION NUMBER:  US 60/255,107
12 PRIOR FILING DATE:  2000-12-12
13 NUMBER OP SEQ ID NOS:  6
14 SOFTWARE:  PERL Program
15 SEQ ID NO 3
16
17 LENGTH:  1274
18
19 TYPE:  PRT
20 ORGANISM:  Homo sapiens
21 FEATURE:
22 NAME/KEY:  misc feature
23 OTHER INFORMATION:  Incyte ID No:  1258887CD1
24
25 US-10-415-615-3

```

Alignment Score

Pred. No.:	3, 47e-32	Length:	1274
Score:	551.50	Matches:	36
Percent Similarity:	69.61%	Conservative:	106
Best Local Similarity:	51.96%	Mismatches:	61
Query Match:	0.64%	Indels:	2
DB:	16	Gaps:	1

US-09-396-985B-48 (1-50000) X US-10-415-615-3 (1-1274)

QY	36378	ATTGAAAAATGGGGTACAGACTTAAAGAAAGAAATTTCTCACTGAGGAATATCTGATGACT	36313
Db	1068	leamstgtrpVallylsaspmleaaanagserPheSerIyglulubspileTyralaala	1087
QY	36318	GAAAAGTAACTTAAAAAATGTTTAAATCCTTGTGATCAGGGAATATGCAATCAAAACA	36255
Db	1088	AsmtrgtsmetelyblybCysserSerSerleuValValarglmetcglilleysttr	1107
QY	36258	ACCTGATATTCACCTTCAACCCAGTCAGAAATGACTAAGATCAAAAATCTCAAGTACACG	361995
Db	1108	ThmetargtlyrhlsleuthrProVallylsmetalaleilelyblysergilyAaen	1127
QY	36198	AGATGCTTCGCAAGATGT-AGAGAAGAGCAACCTTCTCATTTGCTGCGAAGACTTAA	36144
Db	1128	ArgCystrprrggllyargllyglumetgIyThrleuLeuhlieCystrprrpCyblyb	1147
QY	36139	CTGATATTAACACCTCGGAATACAGTTGGTGGTCTCGAAGAAATATGGACATGACATCA	36080
Db	1148	LeuValGlnProleuthrlybsserValTrrpArgPheleudrghspleuGlulile	1167
QY	36079	CCTGAGGATCCAGCAATATACACTCCAAAGCAATATACAGATGAT--GCTTCACTTGT	36023
Db	1168	ProheasprrhoalaleProleuLeuGllyleTyProlyasprrlyrlybsserCyblyb	1187
QY	36022	AATAGACACACAGCTCTACTANGTTCATrAGCAGTTTATTTATATAGCCAGATCCTTG	35966
Db	1188	TyrlybsaprrileCystrhCybValPheillealaleuPheThrillealalystrhrrp	1207
QY	35962	AAAGAACCTTGAGTCCCTCCACAGAGAATATGATCAAAAATATAGrACATTTGCACA	35904
Db	1208	AasmGlnProlybCybPrrhoImetlleasrrprrilelyblybssertrprrshetCystrh	1227
QY	35902	GTGGAGTACTATGACAGCTATTAAAAACAGGAATCTrAGCATTTCTTAGGCAATAGTATG	35843
Db	1228	MetclulurlyrrhlaalaalelybAaenaspGluPhehmetSerhethalarghrrtrpmet	1247
QY	35842	GACCTGGAGGGCATCATCTCTGAGTGAAGTAAACCAGCTCATAAAGAAACACATGATATG	35788
Db	1248	LyseleuGlnhrilleileleuserrlybValleuGlnGlyglulnlysserlybshlybCybmet	1267

OY 35782 CACTTAATCTG 35771

Db 1268 PheSerLeuIle 1271

Search completed: March 30, 2005, 15:34:07
Job time : 4042 secs

This Page Blank (uspto)

SUMMARIES

No.	Score	Match Length	DB	ID	Description
1	2844	47.9	837	10	US-09-960-041-26
2	2726	45.9	799	10	US-09-950-041-8
3	2726	45.9	799	14	US-10-128-166-7
4	2726	45.9	799	16	US-10-732-563-8
5	2726	45.9	799	16	US-10-732-796A-8
6	609	10.2	661	13	US-10-114-893-10
7	609	10.2	661	15	US-10-038-854-134
8	597.5	10.1	661	15	US-10-038-854-135
9	597.5	10.1	661	15	US-10-037-417-107
10	575	9.7	1032	15	US-09-954-987B-192
11	575	9.7	1032	14	US-10-272-502A-31
12	575	9.7	1032	15	US-10-407-952-32
13	559	9.4	1050	10	US-09-954-987B-175
14	559	9.4	1050	14	US-10-272-502A-22
15	559	9.4	1050	15	US-10-407-952-26
16	548	9.2	1059	15	US-09-954-987B-187
17	548	9.2	1059	15	US-10-407-952-30
18	548	9.2	1059	17	US-10-753-267-30
19	541.5	9.1	859	14	US-10-125-692-6
20	541	9.1	1041	9	US-09-168-978-3
21	541	9.1	1041	9	US-09-978-295A-498
22	541	9.1	1041	9	US-09-978-657-498
23	541	9.1	1041	9	US-09-978-192A-498
24	541	9.1	1041	9	US-09-999-832A-498
25	541	9.1	1041	10	US-09-978-189-498
26	541	9.1	1041	10	US-09-978-608A-498
27	541	9.1	1041	10	US-09-978-585A-498
28	541	9.1	1041	10	US-09-978-191A-498
29	541	9.1	1041	10	US-09-978-101A-498
30	541	9.1	1041	10	US-09-978-603A-498
31	541	9.1	1041	10	US-09-978-564A-498
32	541	9.1	1041	10	US-09-999-833A-498
33	541	9.1	1041	10	US-09-981-915A-498
34	541	9.1	1041	10	US-09-978-824-498
35	541	9.1	1041	10	US-09-918-585A-498
36	541	9.1	1041	10	US-09-999-834A-498
37	541	9.1	1041	10	US-09-978-423A-498
38	541	9.1	1041	10	US-09-978-193A-498
39	541	9.1	1041	10	US-09-999-830A-498
40	541	9.1	1041	10	US-09-978-757A-498
41	541	9.1	1041	10	US-09-978-187B-498
42	541	9.1	1041	10	US-09-978-633A-498
43	541	9.1	1041	10	US-09-978-375A-498
44	541	9.1	1041	10	US-09-978-298A-498
45	541	9.1	1041	10	US-09-978-188A-498
					Sequence 498, App

```

; PRIOR FILING DATE: 1997-05-07
; PRIOR APPLICATION NUMBER: 60/072,212
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/076,947
; PRIOR FILING DATE: 1998-03-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 837
; TYPE: PR1
; ORGANISM: Homo sapiens
; US-09-950-041-26

Alignment Scores:
Score: 2,45e-262 Length: 837
Percent Similarity: 2844.00 Matches: 558
Best Local Similarity: 80.10% Conservative: 114
Query Match: 47.85% Mismatches: 159
DB: 10 Gaps: 8

US-09-396-985b-5 (1-3395) x US-09-950-041-26 (1-837)

QY 263 ATGCTCTCTGCATCTGGCTGGACTGTGATCATGGCATG--TTCCCTTTCCTGCTG 319
Db 1 MetSerAlaSerArgLeuAlaGlyThrLeuIleProAlaMetAlaPheLeuSerCysVal 20
QY 320 AGACAGGAAGCTGGAATCCCTGCATAGAGGACTCTCTAATATATACCTACCAATGCATG 379
Db 21 ArgProGlnSerThrProGlnProCysValGlnVal--ProAsnIleThrTyGlnCysMet 39
QY 380 GATGAGATCTCAGCAAAATCCCTGCATAGACATCCCTTATTCACCAAGAACTGATCTG 439
Db 40 GluLeuAsnPheTyrluSileProAspAsnLeuProPheSerThrTySAsnLeuAspLeu 59
QY 440 AGCTTCAACCCCTGAAGATCTTAAGAAGCTTAAGCTTCAACCAATTTCTCACAATTCAG 499
Db 60 SerPheAsnProLeuAlaGHisLeuGlySerTySerPheSerPheProGlnLeuGln 79
QY 500 TGGCTGATTTATTCAGATGTGAATTTAGACATTTGAACAATGACAGCATGGAGCTTA 559
Db 80 ValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaTyGlnSerLeu 99
QY 560 AACGAGCTCTCAACCTTGTACTGACAGAAACCTTACAGAGTTTTCCTCCAGAGAGT 619
Db 100 SerIleSerThrIleLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGlyAla 119
QY 620 TTTTCTGACTACAAATTTAGAAATCTGGTGGCTGTGAGACAAAAATGACCTCTCTA 679
Db 120 PheSerGlyLeuSerSerLeuGlnLeuValAlaValGlnThrAsnLeuAlaSerLeu 139
QY 680 GAGGTTTCCATATTTGACAGCTTATATCCTTAAGAAATGAAATGTGGCTCAATATCTT 739
Db 140 GluAsnPheProIleGlyHisLeuIleThrLeuIleGlyLeuAsnValAlaHisAsnLeu 159
QY 740 ATACATCTCTTAAGTGGCTGATATTTTCTAATCTGACAAACCTAGAACTGATGAGAT 799
Db 160 IleGlnSerPheIleuSleuProGlnIleTyPheSerAsnLeuThrAsnLeuGlnHisLeuAsp 179
QY 800 CTTCCTTAATACTATTTCAACTATTTCTGTGCAAGAATTACAGTTTCTACGTAAGAAAT 859
Db 180 LeuSerSerAsnIleGlnSerIleTyCysThrAspLeuArgValLeuHisGlnMet 199
QY 860 CCCCAAGTCATCTCTCTTGAACCTGTCTTAAACCAATGACCTGCATTCAGAGCCAA 919
Db 200 ProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnProGly 219
QY 920 GCTTTTCAAGGAATTAAGCTCCATGATTAATGACTTAAGAAGTAATTTTAATAGCTCAAT 979
Db 220 AlaPheIleGlyGlnIleGlnLeuHisIleTyLeuThrIleuArgAsnAsnAspSerLeuAsn 239
QY 980 GTACTGAATATGTGCTTCAAAACATGACTGGTTTACATGTCATCGGTTGATCTTGGA 1039

```

```

Db 240 ValMetIleThrCysIleGlnGlyLeuAlaGlyLeuGlnValHisArgLeuValLeuGly 259
QY 1040 GAATTTAAAGAAAGAAATCGAAGCTTGTGACCGTTCTGTGATGGAAGGACTATGC 1099
Db 260 GluPheArgAsnGlnIleGlnAsnLeuGlnIlePheAspIleSerAlaLeuGlnGlyLeuCys 279
QY 1100 AATGTAGCATTTGATGATTCAGGTTTACATATATTAATCATTTTTCAGATGATTTAT 1159
Db 280 AsnLeuThrIleGlnIleuPheArgLeuAlaTyLeuAspTyTyTyLeuAspPheIleIle 299
QY 1160 AATCTC---AATGCTTGGCAATATTTCTGCAGATGCTTTTCACAGGTGATCATTAATA 1216
Db 300 AspLeuPheAsnIleCysLeuThrAsnValIleSerPheSerLeuValIleValThrIleGly 319
QY 1217 CACATAGCAGATGTCCTTAGCATTTCAATGGAATCCCTTATTCATCATTTAGATGCAT 1276
Db 320 ArgValIleAspPheSerTyTrAsnProGlyTyProGlnHisLeuGlnLeuValAsnCysIle 339
QY 1277 CTTAAGCTTTTTCCAAGCTGACTTACCTTTTCTTAAGAATGGACTTTTACATCAAC 1336
Db 340 PheGlyGlnPheProThrIleuSleuTySleuTySleuTyLeuArgLeuThrPheThrSerAsn 359
QY 1337 AGAAGAGATTAACGCTTTTGCTCAGTTGGCTCTGCCAAGTCTCAGATATCTTAAT 1396
Db 360 LysGlyGlyAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeuSer 379
QY 1397 AGAAATGCCATGAGCTTTAGAGGTGCTGTCTTATTCGATTTTGAACAACAACCTG 1456
Db 380 ArgAsnGlyLeuSerPheIleGlyCysCysSerGlnSerAspPheGlnThrThrSerLeu 399
QY 1457 AAGTACTTAACCTCAGCTTCAATGCTGATCATCTGATGATGATGATGATGATGATGATGAT 1516
Db 400 LysTyLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGlyLeu 419
QY 1517 GAAGAGCTGGAATTAACCTGACCTTTCAGACATCCACTTTAAAGGTCACAGAAATCTCA 1576
Db 420 GluGlnLeuGlnIleuIleuAspPheGlnHisSerAsnLeuIleGlnSerGlnPheSer 439
QY 1577 GTGTCTTATCTCTGAAAACCTTCTTACCTTGCATCTTCACTTACATAACCAAAAT 1636
Db 440 ValPheLeuSerLeuArgAsnLeuIleTyLeuAspIleSerHisThrHisArgVal 459
QY 1637 GACTTTGATGAGCATATTTCTTGTGCTGATCAGTCAACACTTTAAAGTGGGCAAT 1696
Db 460 AlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuIleuSleuMetAlaGlyAsn 479
QY 1697 TCTTTCAAGACAAACCTTTTCAATATGCTTTTACAAACAACAACCTTAAACCTTCTG 1756
Db 480 SerPheGlnIleuAsnPheLeuProAspIlePheThrGlyLeuArgAsnLeuThrPheLeu 499
QY 1757 GATCTTTCTAAAGGCAACCTGAAACAGATCTTAGAGGGGATTTTGAACAACCTTACAGA 1816
Db 500 AspLeuSerGlnCysGlnLeuGlnIleuSerProThrAlaPheAsnSerLeuSerSer 519
QY 1817 CTCAGTTATTAACAATGAGTCAACAACCTATCTGTTCTGATCCATCCATTAATAA 1876
Db 520 LeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyIle 539
QY 1877 CAGCTGATCTCCCTCAGGACTCTTGATGCAATTTCAATGCAATGACATGCAATCC--AAA 1933
Db 540 CysLeuAsnSerLeuGlnValIleuAspTySerLeuAsnHisIleMetCThrSerTyIle 559
QY 1934 GGAATCTGCAACATTTTCCAAAGAGCTAGCCGTCTTCAATGCAATTAATATTCGTT 1993
Db 560 GlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAspPhe 579
QY 1994 GCTTTATATGATTAATGAAATTTCTTCAAGTGGCTCAAGGACCAAGAAATGTTCTTG 2053
Db 580 AlaCysThrCysGlnIleGlnSerPheLeuGlnIleThrIleuSAspGlnArgGlnLeu 599
QY 2054 GTGAAATTTGAACAATGAATGATGCATCACTTATAGACATGAAGGCTCCCTGGTGTG 2113
Db 600 ValGlnValGlnIleuArgMetGlnCysAlaThrProSerAspIleGlnIleMetProValLeu 619

```

```

QY 2114 GATTTCAGAAATTCACCTGTTATATATACAGACTATCATAGTATCGGTGCTGT 2173
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 620 Serleu---AsnIleThrCysGlnMetCasnIleThrIleGlyValSerValleuSer 638
QY 2174 GTGCTTGTTGTTAGGACCTGTAGACATTTTGTATATACACTTCTATTTTTCACCTGATCTT 2233
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 639 ValIeuValValSerValValAlaValIeuValTyrLysPheTyrPheIleIleuMetIeu 658
QY 2234 ATTGCTGCTGTAAATAAGTACAGACAGAGAGAAAGCATCTATGATGCTTTGTATCTAC 2293
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 659 LeuIaGlyCysIleLysTyrGlyTyrGlyGluMetIleTyrAspAlaPheValIleTyr 678
QY 2294 TCGAGCCGAAATGAGGACCTGGGTGAGAAACGAGCTGTAAAGAAATTTAGAAAGAGAGCTG 2353
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 SerSerGlnMetPheGluMetPheTyrValIlePheAsnIleuValIlePheMetGluGlyVal 698
QY 2354 CCCCCTTTGAGCTTTGCTTTCATTTACAGGACCTTATTCCTGTGTAGCCATGCTGCC 2413
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 699 ProProPheGlnIleuCysLeuIleTyrGlyTyrGlyPheIleProGlyValAlaIleIleAla 718
QY 2414 AACATCATCCAGAAAGCTTCCACAAAGCCGGAAGATTATGTGTGTGTGTGTGTGTGTGTGT 2473
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 719 AsnIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 738
QY 2474 TTATCCAGAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2533
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 739 PheIleGlnSerIleTyrCysIleIlePheIleValIleGlnIleIleIleIleIleIleIle 758
QY 2534 AGTACCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2593
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 759 SerSerArgIleGlyIleIleIlePheIleValIleGlnIleValIleGlyIleIleIleIle 778
QY 2594 CAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2653
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 779 GlnGlnValGlnIleTyrArgIleuSerIleuSerIleuSerIleuSerIleuSerIleuSer 798
QY 2654 GCTCTGGGAGGACATCTTGTGAGAGACTCAAAAAGCCCTGTGTGTGTGTGTGTGTGTGTGT 2713
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 ValIeuGlyArgIleIlePheIleTyrArgIleuMetGlyValIleuMetGlyLysSer 818
QY 2714 TTGAATCCAGAT-----GAAACATCAGAGGAAAGACAAAGCAACTTTG 2761
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 819 TrpAsnProGlnGlyThrValGlyThrCysAsnTrpGlnGlyAlaThrSerIle 837

```

```

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-950-041-8

Alignment Scores:
Score: 4.63e-251 Length: 799
Percent Similarity: 2726.00 Matches: 532
Best Local Similarity: 80.38% Conservative: 111
Query Match: 66.50% Mismatches: 151
DB: 45.87% Indels: 151
Gaps: 4

US-09-396-985b-5 (1-3395) x US-09-950-041-8 (1-799)

QY 377 ATGGATCAGAAATCTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGACATGAT 436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MetGluIleuAsnPheTyrLysIleProAspAsnIleuProPheSerThrLysAsnIleuAsp 20
QY 437 CTGAGCTTCAACCCCTGAAAGATCTTAAAGACTATAGCTTACCAATTTCTCAAACTT 496
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 LeuSerPheAsnProIleuArgIleIleGlySerTyrSerPhePheSerPheProGluIleu 40
QY 497 CAGTGGCTGATTTATTCAGGTGTGAATTTGAGACATTTGAGACAAAGCAGGACATGGC 556
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41 GlnValIleuAsnIleuSerIleuGlyIleGlnIleIleGlnIleIleGlnIleIleGlnIle 60
QY 557 TTAACCAAGCTCTCAACCTTGATCTGACAGAAACCTTATTCAGAGATTTTCCCAAGA 616
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 LeuSerIleIleuSerThrIleuIleIleuThrClyAsnProIleGlnSerIleuAlaGly 80
QY 617 AGTTTCTGTGACTTAAATTTTGAAGATCTGGTGGCTGTGGAGCAAAATATGACCTCT 676
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 AlaPheSerGlyLeuSerSerIleuGlnIleuValAlaValGlnThrAsnIleuAlaSer 100
QY 677 CTAGAGGTTTCCATATTTTGGACAGCTTATATCCCTTAAAGAAATTTGAGCTCATAT 736
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 101 LeuGlnAsnPheProIleGlyIleIleIleIleIleIleIleIleIleIleIleIleIle 120
QY 737 CTATATCATCTTTAAGTTCCTGAAATTTTCTAATTTTCTATGACAAACCTAAGACATGTG 796
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 LeuIleGlnSerPheLysIleuProGlyTyrPheSerIleuIleuThrAsnIleuGlnIle 140
QY 797 GATTTTCTTATTAATCTATTAATCAACTATTTCTGTCAAAAGCTTACAGTTTCTACGTGAA 856
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 141 AspLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValIleuIleGln 160
QY 857 AATCCCAAGCAATCTCTTTAGACCTGTCTTAAACCAATGCTCCATCCAAAGCC 916
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 161 MetProIleuIleuAsnIleuSerIleuAspLeuSerIleuAsnProMetAsnPheIleGlnPro 180
QY 917 CAAGCTTTCAAGGAAATTAGGCTCCATGAAATTTGACTAAGAAATTTTATTAAGCTCA 976
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GlyAlaPheLysGlnIleArgIleuIleIleIleIleIleIleIleIleIleIleIleIle 200
QY 977 AATGTACTGAAATATGTCCTTCAAAACATGATGCTTTTACATGCTCCATCGGTATCTTG 1036
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 201 AsnValMetLysThrCysIleGlnIleuAlaGlyIleuGlnValIleIleAspLeuValIleu 220
QY 1037 GGAGAAATTTTAAATGAAAGAAATCTGAAAGATTTTACAGCTTTTCTGACAGAAAGACTA 1096
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 221 GlyIleIleuPheArgAsnGlnGlyAsnIleuGlnIleuPheAspLysSerIleAlaGlnIleu 240
QY 1097 TGCAGTGTGACATTTGATGAGTTTCAGGTTAACTATTAATCAATTTTTCAGATGATAT 1156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 CysAsnIleuThrIleGlnIleuIleuArgIleuAlaTyrIleuSerGlyTyrIleuAspAspIle 260
QY 1157 TATATATCTC--AATGCTTGGCAAAATATTTTGCAGATGCTTTTACAGAGTGTACATATA 1213
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 261 IleAspIleuPheAsnIleuThrAsnValIleSerSerPheSerIleuValIleThrIle 280

```

QY	1214	AAACACATGACGATGTTCTTAGGCACTTCAATGGCACTCTTATCATATTAATGATGT	1273

Db	281	GIUUAAGLVLVAAAPRPheserTyrAsnHegLyrTrpGlnIshLeuValAsnCyS	300
QY	1274	CATGTTAGCCCTTTTCCAAAGCTAGCTACTCTTTCTTAAAGTTGAGCTTTAACTAC	1333
Db	301	LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysValGlyLeuThrPheThSer	320
QY	1334	AACAGAGAGATATCAAGCTTTGGTCAGTGGCTGGCCCAAGTCCAGATATCTAGATCTT	1393

Db	321	AsnLysGlyGlnAsnAlaPheSerGlnValAspLeuProSerLeuGlnPheLeuAspLeu	340
QY	1394	AGTAGAAATGSCATGAGCTTTAGAGGTTGCTGTCTTATTTGTGATTTTGGAAACAACAC	1453

Db	341	SerTrpGanGlyLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrThSer	360
QY	1454	CTGAAGTACTTAGACCTCAGCTTCAATGGTGATCTCGATAGAGGCCAATTCATGGGT	1513

Db	361	LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerAspPheLeuGly	380
QY	1514	CTAGAAGCTGGAATATCTGGACTTTGACAGCTCCACTTTAAAGGTCAACAATTC	1573

Db	381	LeuGlnGlnLeuGlnIshLeuAspPheGlnIshSerAsnLeuLysGlnMetSerGlnPhe	400
QY	1574	TCAGTGTCTTATCTCTTGGAAAACTTTTAACTCTTGACATCTCTTAACTAAATCCAAA	1633

Db	401	SerValPheLeuSerLeuAlaGlyAsnLeuIleLysTyrLeuAspIleSerIshIshThrArg	420
QY	1634	ATTTGACTTGAATGGCATTTCTTGGCTGATGCTGACATGCTTCAACACTTTAAAGTGGTC	1693

Db	421	ValAlaPheAsnGlyLysPheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly	440
QY	1694	AATTTCTTCAAGACACACACCCCTTTCACAAATGTCTTTACAAACACAACTTTAACTTC	1753

Db	441	AsnSerPheGlnGlnIshAsnPheLeuProAspIlePheThrGlnLeuAlaGlyAsnLeuThrPhe	460
QY	1754	CTGGATCTTTTCTTAAATGCCAATGGAACAGATATGTAGGGGGGATTTTGACACACTTAC	1813

Db	461	LeuAspLeuSerGlnCysGlnLeuGlnIshLeuSerProThrAlaPheAsnSerLeuSer	480
QY	1814	AGACTCCAGTATTAACATGATGATGACAAACAACCTAGTCTTGGAGTCCATCCATAT	1873

Db	481	SerLeuGlnValLeuAsnMetSerIshAsnAsnPhePheSerLeuAspThrPheProLys	500
QY	1874	AAACAGCTGTACTCCCTCAGACACTTTGATTTGCACTTTCAATGCCATPAGACATCC---	1933

Db	501	LysCysLeuAsnSerLeuGlnValLeuAspLysSerLeuAsnIshIleMetThrSerLys	520
QY	1931	AAAGGAATATGCAACATTTTCCAAAGAGCTAGCCGCTTCCATCTGACATTAATCT	1990

Db	521	LysGlnGlnLeuGlnIshPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp	540
QY	1991	GTTGGCTTGATATGGAATATGAGAATTTCTTGGAGTGGTGCACAGACAAATGTTTC	2050

Db	541	PheAlaCysThrCysGlnIshGlnSerPheLeuGlnTrpIleLysAspGlnIshGlnLeu	560
QY	2051	TTGTGTAATGTTGAACAATGAAATGTCATCACTATAGACATGAAGCCCTCCGTGTG	2110

Db	561	LeuValGlnValGlnArgMetGlnCysAlaThrProSerAspLysGlnGlyMetProVal	580
QY	2111	TTGGATTTTTCAGATTCACCTGTTATATATACAAAGACTATCATCATGTATGGTGTC	2170

Db	581	LeuSerLeu---AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValIsh	599
QY	2171	AGTGGCTTGGTGGTGGCCACTGTACATTTCTGATATACACTTATATTTTCACTGATA	2230

Db	600	SerValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheIshLeuMet	619
QY	2231	CTTATTTGCTGCTGTAAAAAGTACAGCAGAGAGAAAGACATGTATGATGATTTTGTGATC	2290

Db	620	LeuLeuAlaGlyCysAlleLysTyrGlyArgGlyGlnAsnIleTyrAspAlaPheValIle	639
QY	2291	TACTGAGCCAGAAATGAGACTGGGTGAGAAAAGACTGTGTAAGAAATTTAGAAAGGA	2350

Dd		640	TyrSerSerGlnAerPTrValArgSerGluLeuValLysAsnLeuGluGly	659
Oy		2351	GTCGCCCGCTTCAAGCTTTGGCTTCATTACAGGACTTAATTCGTGTGAACCATTCGT	2411
Dd		660	ValProProPheGlnLeuCysLeuHieIeYrArGAsPheHeIleProGlyValAlaIleAla	679
Oy		2411	GCCAAATCATCCAGAAAGGCTTCCACAAGAACCAGAAAGTTATTTGGTGCTGTACGA	2477
Dd		680	AlaasnIleIleHieIeGluGlyPheHieIlysSerArgLysValIleValValSerGln	699
Oy		2471	CACCTTATCCAGACCCGTGGTGTATCTTTGAATATATGATGATTCGCACAGATGGCAGTTT	2533
Dd		700	HispheIleGlnSerArGTrPCysIlePheGluTyrguIleAlaGlnThrTriPoleInPhe	719
Oy		2531	CTGAGTAGCCGCTCTGGCATCATCTTCATTGTCCTTGAAGAAAGTGAAGAGTCCCTGCTG	2590
Dd		720	LeuSerSerArGalAglIyleIleIlePheHeIleValLeuGlnLysValGluLysThrLeuLeu	739
Oy		2591	AGGACAGCAGTGCATATGTATTCGCTTTTACAGAAAACCTTACCTGCAGTGGAGAAC	2655
Dd		740	ArgGlnGlnValIGluLeuTyraArgLeuLeuSerArGaenThrTyraLeuGluTrpGluAsp	759
Oy		2651	AATGCTCTGGGAGAGCACATCTTCTGCAGAGACCTCAAAAAAGCCGTGGATGGAGAA	2711
Dd		760	SerValLeuGlyArgHisIlePheThrArgArGLeuArgLysAlaLeuLeuAspGlyLys	779
Oy		2711	GCCCTTGAATCCAGAT-----GAAACATCCAGAGAAACAGAGAACAACTTTG	2765
Dd		780	SerTrpAsnPProGluGlyThrValGIdgLythrGlyCysAsnTrpGlnGluAlaThrSerIle	799
 RESULT 3 US-10-128-166-7 ; Sequence 7, Application US/10128166 ; Publication No. US2003077279A1 ; GENERAL INFORMATION: ; APPLICANT: AKDITI, MOSHE ; APPLICANT: RAJAVASHISTH, TRIPATHI ; APPLICANT: SHAH, PREMDHAN K. ; TITLE OF INVENTION: METHODS FOR TREATING VASCULAR DISEASE BY INHIBITTING ; FILE REFERENCE: 81476-0255398 ; CURRENT APPLICATION NUMBER: US/10/128.166 ; CURRENT FILING DATE: 2002-04-23 ; NUMBER OF SEQ ID NOS: 7 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 7 ; LENGTH: 799 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-128-166-7				
 Alignment Scores:				
Pred. No.:	4.63e-251	Length:	799	
Score:	2726.00	Matches:	532	
Percent Similarity:	80.38%	Conservative:	111	
Best Local Similarity:	66.50%	Mismatches:	151	
Query Match:	45.87%	Indels:	6	
DB:	14	Gaps:	4	
 US-09-396-985B-5 (1-3395) x US-10-128-166-7 (1-799)				
Oy		377	ATGATTCAGATATCTCAGCAAATCCCTCATGACATCCCTTATTCACAAGAACTAGAT	436
Dd		1	MetGluLeuAsnPhenTyraIleIleProAspAsnLeuProPheSerThrIlysAsnLeuAsp	20
Oy		437	CTGAGCTTCAACCCCCTGAGAGATCTTAAAGAACTATAAGCTTACCAATTTCTCACAATT	496
Dd		21	LeuSerPheAsnPProLeuArgHisLeuGlySerTyraPhePheSerPheProGluLeu	40
Oy		497	CAGTGGCTGATTTATTCAGGTGTGAATTTGAGACAAATTTGAAGACAAGCAATGGCATGGC	556
Dd		41	GlnValLeuAspLeuSerArgCysGluIleGlnThrIleGluAspGlyAlaItyrGlnSer	60

557 TTAACGAGCTCTCAACCTGGTACTGACAGAAACCCATCAAGATTTCGCCAGCA 616
61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
617 AGTTTTCGTGACCTAACAAATTTAGAGAATCGTGAGCTGTGAGACAAATAAGCACTCT 676
81 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValGluThrAsnLeuLaser 100
677 CTAGAGGTTTCCATATTCGACAGCTTATTCCTTAAAGAACTAAAGTGGCTCATAT 736
101 LeuGluAsnProIleGlyHisLeuLysThrLeuLysGluLeuAsnValAlaHisAsn 120
737 CTATATACATCTTAAAGTGGCTGAATATTTTCTATATTCGACAAACCTGAACATGTG 796
121 LeuIleGlnSerPheLeuLeuProGluThrPheSerAsnLeuThrAsnLeuGlnHisLeu 140
797 GATCTTTCTTATATCTATATTCAAACTATTTCTGTCAAGACTTACAGTTTCTACGTGA 856
141 AspLeuSerSerAsnLysIleGlnSerIleThrCysThrAspLeuArgValLeuHisGln 160
857 AATCCCAAGTCAATCTCTCTTTAGACCTGTCTTAAACCCATGAGTCCATTCAGACC 916
161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
917 CAAGCTTTCAGGGAATAGGCTCCAGATTCGATTCAGAGATTTTAAATTTTAAATTCCTCA 976
181 GlyAlaPheLysGluIleArgLeuHisLysLeuThrLysAlaGluAsnPheAspSerLeu 200
977 AATGTAATGAAATGTGCTTCAAAACATGACTGTGTTTACATGTCCATCGGTGATCTTG 1036
201 AsnValMetLysThrCysIleGlnIleGluLeuAlaGluLeuValHisArgLeuValLeu 220
1037 GGAGATTTTAAATGAAAGAAATTCGAAAGATTTCACCTGTCTGTATGGAAGAGATA 1096
221 GlyIlePheArgAsnGluGlyAsnLeuGluLysPheAspLysSerAlaLeuGlnGlyLeu 240
1097 TGCATGTGAGACATGATGAGTTCAGGTTTAAATATTAATCAATTTTTCAGATGATTT 1156
241 CysAsnLeuThrIleGlnGluPheArgLeuAlaThrLysLeuAspLysIleLeuAspPheIle 260
1157 TATATATCTC--AATGTCTTGCAAAATATTTCTGCATGTCTTTCACAGGTGTACATATA 1213
261 IleAspLeuPheAsnCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
1214 AAAACATGACGATGTTCTTACGAGCTTCAAAATGCGCATCTTATCATATTAATGATGT 1273
281 GluArgValLysAspPheSerLysAsnPheGlyThrGlnHisLeuGluLeuValAsnCys 300
1274 CATCTTAAGCTTTTCAAGAGTGTACCTTTTCTTAAAGTTGAGCTTAACTTACATAC 1333
301 LysPheGlyGlnPheProThrLeuLysLeuLysSerLysLysAlaGluLeuThrPheThrSer 320
1334 AACAGAGATATACGCTTGTGTCAGTGTGCTGCGCAAGTTCAGATATCTAGATCTT 1393
321 AsnLysGlyLysAlaPheSerGluValAspLeuProSerLeuGluPheLeuAspLeu 340
1394 AGTGAAGATGCCATGAGCTTTAGAGCTTGTCTTATTTCTGATTTTGAACAACAAC 1453
341 SerArgAsnGlyLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrThrSer 360
1454 CTGAAGATCTAAGACCTGAGCTCAATGGTGCATCCGATGAGAGGCCAATTCATAGGCT 1513
361 LeuLysThrLeuAspLeuSerPheAsnGlyAlaIleMetSerSerAsnPheLeuLys 380
1514 CTGAAGAGCTGATATCTGAGCTTTCAGACCTCCATTTAAATAAGTCAAGATTC 1573
381 LeuGluGlnLeuGluHisLeuAspPheGlnHisSerAsnLeuLysGlnMetSerGluPhe 400
1574 TCAGTGTCTTATCTCTTGAATAACTTTTATCTTGAACATCTCTTACATTAATACCAA 1633
401 SerValPheLeuSerLeuArgAsnLeuIleThrLeuAspIleSerHisThrHisThrArg 420

1634 ATTGACTTTCAGTGCATATTTCTTGCGTTCATGATCAGTCTCAACATTTAAATAAGCTGCGC 1693
421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGluValLeuLysMetAlaGly 440
1694 AATCTTTCAAGACAAACACCTTTTCAATGCTTTTCAAAACAAACAAACTTAAATTC 1753
441 AsnSerPheGlnGluAsnPheLeuProAspIlePheThrGluLeuArgAsnLeuThrPhe 460
1754 CTGATCTTTCTAAATGCGCACTGGAACAGATATCTGAGGGGGGATTTGACACACTGAC 1813
461 LeuAspLeuSerGlnCysGlnLeuGlnGlnLeuSerProThrAlaPheAsnSerLeuSer 480
1814 AGACTCCAGTATTAACATGATGATCACAACAACTTACTGTTTCTGATCCATCCATATAT 1873
481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPheSerLeuAspThrPheProThr 500
1874 AAACAGCTGATCTCCCTGAGACTTTCGATTCGAGTTTCAATGSCATAGACATCC-- 1930
501 LysCysLeuAsnSerLeuGlnValLeuAspLysSerLeuAsnHisIleMetThrSerLys 520
1931 AAAGAAATACGCAACATTTTCCAAAGCTACCGCTTCATCTGACTGAATTAATCT 1990
521 LysGlnGluLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
1991 GTTGCTGTATATGTGAATATCAGAAATTTCTTGACGTGGTCAAGACCAAGAAATGTTTC 2050
541 PheAlaCysThrCysGluHisGlnSerPheLeuGlnIleProIleLysAlaArgGlnLeu 560
2051 TTGGTGAATGTTGAACAAATGAATGTGCATCACTTATACATGAAGGCTCCCTGCTG 2110
561 LeuValGluValGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal 580
2111 TTGATTTTACGATTCACCTGTTATATATACAGACTATCATCAGTATCGGTGCTC 2170
581 LeuSerLeu--AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu 599
2171 AGTGTCTGTGTGAGACACTGTGATCTTGCATATACCACTTATTTTCACTGATA 2230
600 SerValLeuValValSerValValAlaValLeuValLysThrPheThrPheHisLeuMet 619
2231 CTATTCCTGCTGTAAAGTAAAGTACAGACAGAGAGAAACATATGATTCATTTGTGATC 2290
620 LeuLeuAlaGlyCysIleLysGlyArgGlyGluAsnIleThrAspAlaPheValIle 639
2291 TACTCGACCAAGATGAGCTGGGTGAGAAACAGCTGTGTAAGATTTTGAAGAAAGA 2350
640 TyrSerSerGlnAspGluAspThrValArgAsnGluLeuValLysAsnLeuGlnGly 659
2351 GTGCCCCGCTTTCAGCTTTCCTTCATTAACAGGACTTTATTCCTGGTGTAGCATTTGCT 2410
660 ValProProPheGlnLeuCysValLeuHisLysThrArgAspPheIleProGlyValAlaIleAla 679
2411 GCGAATCATTCACAGAAAGCTTCCACAAGAGCCGGAAGATTAATGTTGGTGTCTAGA 2470
680 AlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValAlaIleSerGln 699
2471 CACTTTATCCAGAGCCGTGTGTGATTTTGAATATAGATGTGTCAGACATGCACTT 2530
700 HisPheIleGlnSerArgThrCysIlePheGluThrGluIleAlaGlnThrThrGlnPhe 719
2531 CTGAGTACGCGCTGACATCATCTTCAATTCCTTGAAGAAAGGAGAGAGTCTTCTGTG 2590
720 LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGluLysThrLeuLeu 739
2591 AGGCAAGAGCTGAATGTATTCGCTTTTACAGAAACAACCTTACAGTGGAGAGAC 2650
740 ArgGlnGlnValGluLeuThrArgLeuLeuSerArgAsnThrThrLysGluThrArgLysPhe 759
2651 AATGCTGTGGGAGGACATCTTCTGAGAAAGCTCAAAAAGCCCTGTGAGAGGAAA 2710
760 SerValLeuGlyArgHisIlePheThrArgArgLeuArgLysValAlaLeuAspGlyLys 779
2711 GCCTTGATCCAGAT-----GAAACATCAGAGGAAACAAAGCAACAACTTTC 2761

```
Db      780 SertrpansPrgIngluGlyThrValGlyThrGlyCysAsnTrpGlnGluAlaThrSerIle 799
      ::|||::|
RESULT 4
US-10-732-563-8
; Sequence 8, Application US/10732563
; Publication No. US20040132079A1
; GENERAL INFORMATION:
; APPLICANT: Gupta, Shalley K.
; APPLICANT: Ghosh, Tatum R.
; TITLE OF INVENTION: Assays Relating to Toll-Like Receptor Activity
; FILE REFERENCE: 58183WO003
; CURRENT APPLICATION NUMBER: US/10/732,563
; SOFTWARE: Patent version 3.2
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 8
; LENGTH: 799
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-732-563-8

Alignment Scores:
Pred. No.:      4.63e-251      Length:      799
Score:          2726.00      Matches:      532
Percent Similarity: 80.38%      Conservative: 111
Best Local Similarity: 66.50%      Mismatches: 151
Query Match:    45.87%      Indels:      6
                Gaps:      4

US-09-396-985b-5 (1-3395) x US-10-732-563-8 (1-799)
QY      377 ATGATCAGATCTCAGAGAAATCCCTCATGACATCCCTTATTGACCAAGAACCTTAAAT 436
      ::|||::|
Db      1 MetGluLeuAsnPheTyrLysAlaProAspAsnLeuProPheSerThrLysAsnLeuAsp 20
QY      437 CTGAGCTTCAACCCCTGAGATCTTAAAGACTATAGACTTACCAATTTCTCAACAATT 496
      |||||::|
Db      21 LeuSerPheAsnProLeuArgHisLeuGlySerTyrSerPhePheSerPheProGluLeu 40
QY      497 CAGTGGCTGATTTATCCAGGTGTGAAATTGAGACAAATTGAAAGCAAGCAGTCATGGC 556
      |||||::|
Db      41 GlnValLeuAspLeuSerArgCysGlnIleGlnThrIleGlnAspGlyAlaTyrGlnSer 60
QY      557 TTTAAACCAAGCTCTCAACCTTGGTACTGACAGAAACCTTATCAAGAGTTTCCCGCAGA 616
      |||||::|
Db      61 LeuSerHisLeuSerThrLeuIleLeuThrGlyAsnProIleGlnSerLeuAlaLeuGly 80
QY      617 AGTTTCTGAGACTAACAATTTAGAGATCTGGGTGCTGAGAGACAAAAATGACCTCT 676
      ::|||::|
Db      81 AlaPheSerGlyLeuSerSerLeuGlnIleValAlaValAlaGlnThrAsnLeuAlaSer 100
QY      677 CTAGAGGGTTTCATATTGACAAGCTTATCTCTTAAAGAACTTAAATGTGGCTCATAT 736
      |||||::|
Db      101 LeuGlnAsnPheProIleGlyHisLeuLysThrLeuLysGlnLeuAsnValAlaHisAsn 120
QY      737 CTTATACCTTCTTAAATGCTGCTGCAATATTTTCTATCTGACAAACCTTGAACATGTG 796
      |||||::|
Db      121 LeuIleGlnSerPheLysLeuProGlnIlePheSerAsnLeuThrAsnLeuGlnHisLeu 140
QY      797 GATCTTCTTAAATCTAATATTCAACTATTTCTGCAAGACTTACCAATTTCTACGTGA 856
      |||||::|
Db      141 AsnLeuSerSerAsnLysIleGlnSerIleTyrCysThrAspLeuArgValLeuHisGln 160
QY      857 AATCCCAAGTCAATCTCTTTAGACCTGTCTTTAAACCAATTTGACTCTCAATTCAGCC 916
      |||||::|
Db      161 MetProLeuLeuAsnLeuSerLeuAspLeuSerLeuAsnProMetAsnPheIleGlnPro 180
QY      917 CAAGCTTTCAAGGGAATTAGGCTCCATGAATTTGACTTGAAGAATTTTAAATATAGCTCA 976
      |||||::|
Db      181 GlyAlaPheLysGlnIleArgLeuHisIleLysLeuThrIleArgAsnAsnPheAspSerLeu 200
```

```
QY      977 AATGACTGAAAAATGTCCTTCAAAAATGACATGCTGTTACATGTCATCGGTGATCTTG 1036
      |||||::|
Db      201 AsnValMetLysThrCysIleGlnGlnLeuAlaGlyLeuGlnIleValHisArgLeuValLeu 220
QY      1037 GGAAGATTTAAAAATGAAAGAAATCTGAAAGATTTTGACCGCTTGTGTCATGAAAGACTA 1096
      |||||::|
Db      221 GlyIlePheArgAsnGlnGlnIleAsnLeuGlnLysPheAspLysSerAlaLeuGlnGlnLeu 240
QY      1097 TGCAGTGTGAGCATGATGAGTTCAGGTTCATATATATAATCATTTTTCAGATTTAT 1156
      |||||::|
Db      241 CysAsnLeuThrIleGlnGlnIlePheArgLeuAlaIleLeuAspTyrTyrLysAspAspIle 260
QY      1157 TATATATCTC--ATTGCTTGGCAAAATATTCTGCAATGTCTTTCACAGGTGATACATA 1213
      ::|||::|
Db      261 IleAspLeuPheAsnGlySerLeuThrAsnValSerSerPheSerLeuValSerValThrIle 280
QY      1214 AAACACATGACGACATGTTCTCTAGACATTTAAATGCGATCTTATTCATATTAAGTGT 1273
      ::|||::|
Db      281 GlnArgValLysAspPheSerTyrAsnPheGlyTyrGlnHisIleLeuGlnLeuValAsnCys 300
QY      1274 CATCTTAAAGCTTTCCAAAGCTGAGTCTACCTTTCTTAAAGTTGAGTCTTAAATACATAC 1333
      |||||::|
Db      301 LysPheGlyGlnPheProThrLeuLysLeuLysSerLeuLysArgLeuThrPheThrSer 320
QY      1334 AACAGAGAGATATACAGCTTTGGTCAAGTGTGCTGTGCACAGTCTCAGATATCTAGATCTT 1393
      |||||::|
Db      321 AsnLysGlyGlyLysAsnAlaPheSerGlnValAspLeuProSerLeuGlnIlePheLeuAspLeu 340
QY      1394 AGTGAAGATCCCATGAGCTTTTAAAGTGTGCTGTCTTATTTCTGATTTTGAACAAACAC 1453
      |||||::|
Db      341 SerArgAsnGlyLeuSerPheLysGlyCysSerGlnSerAspPheGlyThrThrSer 360
QY      1454 CTGAGACTTACAGCTCAGCTCAATGCTGATCTCATCTGATGAGTCACTTCAATCATGAGGT 1513
      |||||::|
Db      361 LeuLysTyrLeuAspLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly 380
QY      1514 CTAGAGAGCTGGAATACCTGACTGACTTTCAGACACTCCACTTAAAAAAGTCAAGAAATTC 1573
      |||||::|
Db      381 LeuGlnIleLeuGlnIleAsnAspPheGlnHisSerAsnLeuLysGlnMetSerGlnPhe 400
QY      1574 TCGAGTCTTATATCTCTTGA AAACTTTTACCTTACATCTCTTACATTAATACCAA 1633
      |||||::|
Db      401 SerValPheLeuSerLeuArgAsnLeuIleTyrLeuAspIleSerHisThrHisIleThrArg 420
QY      1634 ATTGACTTATGAGCAATATTTCTTGGCTGATGAGTCTCAACCTTAAAAAAGGCTGGC 1693
      ::|||::|
Db      421 ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValLeuLysMetAlaGly 440
QY      1694 AATCTTTCAAAAGCAACACCTTTCAATATGCTCTTTCAAAACACAACTTAACATTC 1753
      |||||::|
Db      441 AsnSerPheGlnGlnIleAsnPheLeuProAspIlePheThrGlnLeuArgAsnLeuThrPhe 460
QY      1754 CTGAGATCTTTCTAATGCCAATCTGGAACAGATATCTAGGGGGGATTTTGACACACTTAC 1813
      |||||::|
Db      461 LeuAspLeuSerGlnCysGlnLeuGlnIleLeuSerProThrAlaPheAsnSerLeuSer 480
QY      1814 AGACTCAGTTATTAACATGAGTCAACAACCTATGTTTCTGATCCATCCCATAT 1873
      |||||::|
Db      481 SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAspThrPheProTyr 500
QY      1874 AAACAGCTGACTCCCTCAGAGACTCTGATGTCAGTTTCAATGACATGACATGACATCC-- 1930
      |||||::|
Db      501 LysCysLeuAsnSerLeuGlnValLeuAspTyrSerLeuAsnHisIleMetThrSerLys 520
QY      1931 AAAGAAATCTGCAACATTTTCCAAAGAGTCTAGCGCTTTCATCTGACTATATATTC 1990
      |||||::|
Db      521 LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAsp 540
QY      1991 GTTGCTGTATATGATGATATGCAATTTCTGACAGGGGATTCAGACGCAAAATGTTTC 2050
      |||||::|
Db      541 PheAlaCysThrCysGlnHisGlnSerPheLeuGlnIleThrLysAspGlnHisGlnLeu 560
QY      2051 TTGGTGAATGTTGAACAAATGAATGTGACTACCTTATGACATGAAGGCTCCCTGTGTG 2110
```

	Db	561	LeuValIGluValIGluArgMetGluCysAlaThrProSerAspLysGlnGlyMetProVal	580
Qy	2111	TTGATATTTTTCAGAAATTCACCTGTTATATATATACAAAGACTATCATGATGATCGGTGTC	2170	TTGATATTTTTCAGAAATTCACCTGTTATATATATACAAAGACTATCATGATGATCGGTGTC
Db	581	LeuSerLeu---AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu	599	LeuSerLeu---AsnIleThrCysGlnMetAsnLysThrIleIleGlyValSerValLeu
Qy	2171	AGTGGCTTGTGGTGGTGGCCACTGTAGACATTTTTCGATATATACACTTCTATTTTTCACCTGATA	2233	AGTGGCTTGTGGTGGTGGCCACTGTAGACATTTTTCGATATATACACTTCTATTTTTCACCTGATA
Db	600	SerValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMet	619	SerValLeuValValSerValValAlaValLeuValTyrLysPheTyrPheHisLeuMet
Qy	2231	CTTATGTGCGCTGTAAAAAGTACAGCAGAGAGAAAGACATCTATGATGACATTTGTGATC	2290	CTTATGTGCGCTGTAAAAAGTACAGCAGAGAGAAAGACATCTATGATGACATTTGTGATC
Db	620	LeuLeuAlaGlyCysIleLysTyrIleLysGlnGlnSerIleTyrAspIlePheValIle	639	LeuLeuAlaGlyCysIleLysTyrIleLysGlnGlnSerIleTyrAspIlePheValIle
Qy	2291	TACTGCAGCCAGATAGAGACTGGGTGAGAAACGAGCTGGTAAAGATTTTGAAGAAAGAA	2350	TACTGCAGCCAGATAGAGACTGGGTGAGAAACGAGCTGGTAAAGATTTTGAAGAAAGAA
Db	640	TyrSerSerGlnAspGlnAspTyrPalaArgAsnGlnLeuValLysAsnLeuGlnGlnGly	659	TyrSerSerGlnAspGlnAspTyrPalaArgAsnGlnLeuValLysAsnLeuGlnGlnGly
Qy	2351	GTGCCCGCGCTTTCAGCTTTGCTTTCATTACAGGACCTTATTCCTGTGGTGGCCATTGCT	2410	GTGCCCGCGCTTTCAGCTTTGCTTTCATTACAGGACCTTATTCCTGTGGTGGCCATTGCT
Db	660	ValProProPheGlnLeuCysLeuHisTyrLysAspPheIleProGlyValAlaIleAla	679	ValProProPheGlnLeuCysLeuHisTyrLysAspPheIleProGlyValAlaIleAla
Qy	2411	GCCAAACATCATCCAGGAAGGCTCCACAAAGCCGGAAGAGTATGTGNGTGGTGTCTGA	2470	GCCAAACATCATCCAGGAAGGCTCCACAAAGCCGGAAGAGTATGTGNGTGGTGTCTGA
Db	680	AlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValValSerGln	699	AlaAsnIleIleHisGlnGlyPheHisLysSerArgLysValIleValValValSerGln
Qy	2471	CACCTTATTCACAGAGCCGTGGTGTATCTTTGATATGATGATGCTCAGACATGACATTT	2530	CACCTTATTCACAGAGCCGTGGTGTATCTTTGATATGATGATGCTCAGACATGACATTT
Db	700	HisPheIleGlnSerAsnArgTyrCysIlePheGlnGlyArgIleAlaGlnIleThrTyrPheGln	719	HisPheIleGlnSerAsnArgTyrCysIlePheGlnGlyArgIleAlaGlnIleThrTyrPheGln
Qy	2531	CTGAGTACCGCGCTCTGGCATCATCTTCATCTGTCTTGAGAAAGTGAAGAACTCTTGCTG	2590	CTGAGTACCGCGCTCTGGCATCATCTTCATCTGTCTTGAGAAAGTGAAGAACTCTTGCTG
Db	720	LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeu	739	LeuSerSerArgAlaGlyIleIlePheIleValLeuGlnLysValGlnLysThrLeuLeu
Qy	2591	AGGACAGCAGGTGCGAATTTGATCGCCTTTTGACGAACACCTACTCGAGTGGAGAGAC	2650	AGGACAGCAGGTGCGAATTTGATCGCCTTTTGACGAACACCTACTCGAGTGGAGAGAC
Db	740	ArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrPheGlnAsp	759	ArgGlnGlnValGlnLeuTyrArgLeuLeuSerArgAsnThrTyrLeuGlnTyrPheGlnAsp
Qy	2651	AATGCTCTGGGAGGAGCAGCATCTTCTGAGAGAAAGCTCAAAAAAGCCTGTGGATGGAAGA	2710	AATGCTCTGGGAGGAGCAGCATCTTCTGAGAGAAAGCTCAAAAAAGCCTGTGGATGGAAGA
Db	760	SerValLeuGlnGlyArgHisIleIlePheThrArgArgLeuAlaGlyValAlaLeuLeuAspGlyLys	779	SerValLeuGlnGlyArgHisIleIlePheThrArgArgLeuAlaGlyValAlaLeuLeuAspGlyLys
Qy	2711	GCCTTGAATCCAGAT-----GAAACATCAGAGGAAGAACAAAGAACCACTTGG	2761	GCCTTGAATCCAGAT-----GAAACATCAGAGGAAGAACAAAGAACCACTTGG
Db	780	SerTyrAsnProGlnGlnGlyThrValGlnGlyThrGlyCysAsnTyrPheGlnGlnAlaThrSerIle	799	SerTyrAsnProGlnGlnGlyThrValGlnGlyThrGlyCysAsnTyrPheGlnGlnAlaThrSerIle
RESULT 5				
US-10-732-796A-8				
: Sequence 8, Application US/10732796A				
: Publication No. US20040197865A1				
: GENERAL INFORMATION:				
: APPLICANT: Gupta, Shelley K.				
: APPLICANT: Ghosh, Tatum K.				
: TITLE OF INVENTION: Gene Expression Systems and Recombinant Cell Lines				
: FILE REFERENCE: 58182US004				
: CURRENT FILING DATE: 2003-12-10				
: NUMBER OF SEQ ID NOS: 23				
: SOFTWARE: PatentIn version 3.2				
: SEQ ID NO 8				
: LENGTH: 799				
: TYPE: PRT				
: ORGANISM: Homo sapiens				
US-10-732-796A-8				
Alignment Scores:				
Pred. No.: 4.63e-251 Length: 799				
Score: 2726.00 Matches: 532				
Percent Similarity: 80.38% Conservative: 111				
Best Local Similarity: 66.50% Mismatch: 151				
Query Match: 45.87% Indels: 6				

DB:	16	Gaps:	4
US-09-396-985B-5 (1-3395) x US-10-732-796A-8 (1-799)			
QY	377	ATGATTCAGATTCATCAGCAAAATCCCTCATGACATCCCTTATTTCACCAAGAACTGAT	436
Db	1	MetGluLeuAanPheTyLysIleProkAspAenLeuProPheSerThrIlyAsnLeuAap	20
QY	437	CTGAGCTTCAACCCCTGAGAGATCTTAAAGACTATAGCTTCACCAATTTCTCACACTT	496
Db	21	LeuSerPheAanProLeuAArgHileuGIyertyrSerPhePheSerPheProGluLeu	40
QY	497	CAGTGGCTGATTTATTCAGGTGTGAATTGAGACAAATTGAAGACAAGCAGTCGTCG	556
Db	41	GlnValLeuAapLeuSerAArgCysGlnIleGlnThrIleGluAspGlyAlaTyrgInser	60
QY	557	TTAAACCAAGCTCTCAACCTTGATGACAGAAACCCATCAAGATTTTCCCAAGA	616
Db	61	LeuSerHileuSerThrLeuIleleuThrGlyAanProIleGlnSerLeuAlaGluGly	80
QY	617	AGTTTTCTGACATCAACAAATTTAGAGATCTGTGGCTGTGAGACAAATATGACTCT	676
Db	81	AlaPheSerGlyLeuSerSerLeuGlnIlySerValAlaValGluThrAsnLeuAlaSer	100
QY	677	CTAAGAGGTTTCCATATTGACAGCTTATTCCTTAAAGAACTAAATGGCTCATAT	736
Db	101	LeuGluAanPheProIleGlyHileuTySerLeuIlyGluLeuAsnValAlaHileAan	120
QY	737	CTTATACATCTCTTAAAGTTGCTGAATATTTTGTATCTGACAAACCTAGACATGTG	796
Db	121	LeuIleGlnSerPheIlySerProGluTyrrPheSerAanLeuThrAsnLeuGlnIleu	140
QY	797	GATCTTCTTAACTATATTCAACTATTTCTGTCAAAAGACTTACAGTTTCTAGCTGA	856
Db	141	AspLeuSerSerAanIlyIleGlnSerIleTyrrCysThrAapLeuAArgValLeuHileGln	160
QY	857	AATCCCAAGTCATCTCTCTTATGACCTGTCTTTAAACCCATAGCTCCATTCAGGC	916
Db	161	MetProLeuLeuAanLeuSerLeuAapSerLeuAanProMetAanPheIleGlnPro	180
QY	917	CAAGCTTTCAAGGGAATTAGGCTCCATGAAATAGTCTGAAGAAATTTTAATAGCTCA	976
Db	181	GlyAlaPheIlyGlnIleArgLeuHileuIlyAsnThrLeuAArgAsnAapPheAspSerLeu	200
QY	977	AATGACTGAAATATGTGCTTCAAAACAATCTGCTGTATTCATATGTCATCGTTGATCT	1033
Db	201	AsnValMetIlySerThrCysIleGlnIlyLeuAlaGlyLeuGluValAlaHileArgLeuValLeu	220
QY	1037	GGAGAAATTTAAATGAAAGGAATCTGGAAAGTTTGAACCGTCTGTCAATGGAAGACTA	1099
Db	221	GlyGluPheAArgAanGluGlyAsnLeuGluIlyPheAapIlySerAlaIleuGluGlyLeu	240
QY	1097	TGCAATGTGAGACTTATGAGATTCAAGTTAACATATATTAATCATTTTTCAGATGATAT	1155
Db	241	CysAsnLeuThrIleGluGlnPheAArgLeuAlaTyrrLeuAapIlyTyrrLeuAspIle	260
QY	1157	TATATATCTC--AATTGGCTTGGCAAAATTTTCTGCAATGTCTTTCAAGTTCATATTA	1211
Db	261	IleAspLeuPheAanCysLeuThrAsnValSerSerPheSerLeuValSerValThrIle	280
QY	1214	AAACACATAGACAGATGTTCTCAGCAATTCAAATGGCAATCTTATTCATCATCTTAGATGT	1277
Db	281	GluArgValIlyAspPheSerTyrrAsnPheGlyTrpGlnHileuGluIleuValAanCys	300
QY	1274	CATCTTAAAGCTTTTCCAAAGCTAGTCACTTTTCTTAAAGTTAGGACTTAACTAC	1333
Db	301	LysPheGlyGlnPheProThrLeuIlySerIlySerLeuIlyAArgLeuThrPheThrIser	320
QY	1334	AAACAGAGATATCAGCTTGTGTGCTCAGTGGCTTGGCAAGTCTCAGATTTATAGATCTT	1399
Db	321	AsnIlyGlyGlyAanAlaPheSerGluValAlaPheLeuProSerLeuGluPheLeuAspLeu	340
QY	1394	AGTGAATATGCATAGCTTATGAGGTGGTCTTTATTTCTGATTTTGGAAACAAAC	1455

Db	341	SerArgAngIylLeuSerPheIysGlyCysSerGlnSerAapPheGlyThrThrSer	360
Qy	1454	CTGAAGTACTAGACCTCAGCTTCAATGTCATCCGATGAAGTCCAACTTACGGGT	1513
Db	361	LeuIysTrpLeuAapLeuSerPheAsnGlyValIleThrMetSerSerAsnPheLeuGly	380
Qy	1514	CTGAAGAGCTGGAAATACCTGGAAGCTTTCAGACCTCCACTTTAAAAAGTCAAGAAATTC	1573
Db	381	LeuGlnGlnLeuGlnIleLeuAapPheGlnIleSerAsnLeuGlySGlnMetSerGlnIuphe	400
Qy	1574	TCAGGTCTTATCTCTTGAAGAAACCTGTTTACCTGTCACCTGTTACATTAATACCAAA	1633
Db	401	SerValPheLeuSerLeuAapAsnLeuIleTrpLeuAapIleSerHisIleHisIleTrpArg	420
Qy	1634	ATTGACTTGAATGGCATATTTCTTGCGCTGATTCAGTCCCAACACTTTAAAAATGGCTGGC	1693
Db	421	ValAlaPheAsnGlyIlePheAsnGlyLeuSerSerLeuGlnValIleuLysMetAlaGly	440
Qy	1694	AATTCCTTCAAGAACAACACCCTTCAAAATGCTTTACAAAACAACAACAACTTAAACATTC	1753
Db	441	AsnSerPheGlnGlnAapPheLeuProAspIlePheThrGlnLeuAapAsnLeuThrPhe	460
Qy	1754	CTGGAATCTTTTAAATGGCAACTGGAACAAGATPheThAGGGGGGATTTGAACAACACTTAC	1813
Db	461	LeuAapLeuSerGlnCysGlnLeuGlnIleLeuSerProThrAlaPheAsnSerLeuSer	480
Qy	1814	AGACTCCAGTATTAACATGATGTCACAACAACCTACGTTTGGATCCATCCATTAAT	1873
Db	481	SerLeuGlnValLeuAsnMetSerHisAsnAsnPhePheSerLeuAapTrpPheProTrp	500
Qy	1874	AAACAGCTGTACTCCCTCAGACCTCTTGATTCAGTTTCAATTCGATAGAGACATCC---	1930
Db	501	LysCysLeuAsnSerLeuGlnValLeuAapTrpSerLeuAsnHisIleMetThrSerLys	520
Qy	1931	AAAGAAATATCTGCACATTTTCCAAAGAGTCTAGCCGCTTCAATCTGACATTAATCTT	1990
Db	521	LysGlnGlnLeuGlnHisPheProSerSerLeuAlaPheLeuAsnLeuThrGlnAsnAap	540
Qy	1991	GTTGGCTGTATATGTGAATATATACAGATTTCTTGACAGTGGGTCAAGACAACAGAAATGTTTC	2050
Db	541	PheAlaCysTrpCysGlnHisIleGlnSerPheLeuGlnTrpIleLysAapGlnArgGlnLeu	560
Qy	2051	TTGTGAATGTTGAACAAAATGAATGTGCATCCCTATAGCATAGAAAGCTCCCTGGTGTG	2110
Db	561	LeuValGlnValGlnArgMetGlnCysAlaThrProSerAapLysGlnGlyLysProVal	580
Qy	2111	TTGGAATTTACGAATTCACCTGTTATATATATACAGACTATACATACAGTATCGGTGGTC	2170
Db	581	LeuSerLeu--AsnIleThrCysGlnMetCysLeuLysTrpIleIleGlyValSerValLeu	599
Qy	2171	AGTGGCTTGTGGTGAACCTGTATACATTTCTGATATACACTTGTATTTTCAACCTGATA	2230
Db	601	SerValLeuValValSerValValAlaValLeuValTrpLysPheTrpPheHisLeuMetC	619
Qy	2231	CTTATTTGCTGGCTGTAAAGATGACAGACAGAGAAAGACATCTATGATGCAATTTGTGATC	2290
Db	621	LeuLeuAlaGlyCysIleLysTrpGlyArgGlyGlnAsnIleTrpAspAlaPheValIle	639
Qy	2291	TACTGTAGCCAGAAATGAGGACTGGGTGAGAAAAGAGCTGGTGTAAAGATTTAGAAAGAGA	2350
Db	641	TrpSerSerGlnAapGlnAapTrpValArgAsnGlnLeuValLysAsnLeuGlnGlnGly	659
Qy	2351	GGGCCCCGGTTTCACTTTGACCTTGATTTACAGGACCTTATTCGCGGTGAGCACTTGGCT	2411
Db	661	ValProProPheGlnLeuCysLeuHisTrpTrpArgAapPheIleProGlyValAlaIleAla	679
Qy	2411	GCCAAATCATATCAGAGAAAGGCTTCCACAAGAGCCGAGAAAGTATATGTGGTGGTCTGAGA	2470
Db	681	AlaAsnIleIleIleHisGlnGlyPheHisLysSerArgLysValIleValValSerGln	699
Qy	2471	CACCTTATTCAGAGCCGTTGGTGTGATCTTTGAATATGAGATTTGCTCAAGATGGCAAGTTT	2531

```

Db      700  HispelleGInSerAArgTrpCyseIlePheGInUryGluIleAlaGlnThrTrpGlnPhe 719
Qy      2531  CTGAATAGCCGCTCTGGCATCATCTTCATTTGTCCTTGAGAAAGTGGAGAAAGTCTTGCTG 2599
Db      720  LeuSerSerAArgAlaGlyIleIlePheIleValLeuGlnUlysValGluUlyThrLeuLeu 739
Qy      2531  AGGACGACGCTCGAATTGCTATTCCTGCTTCTTGACGAACACCTACTCTGAGTGGAGGAC 2655
Db      740  ArgGlnGlnValGlnUlyTrpArgLeuLeuSerAArgAanThrTrpLeuGlnUlyPheLeu 759
Qy      2651  AATGCTTCGGGGAGGACACATCTTCTGAGAGAAAGACTCAAAAAAGCCCTGTGGATGAGAAA 2711
Db      760  SerValLeuGlyArgHsiIlePheThrArgLeuArgLysAlaLeuLeuSerGlyLys 779
Qy      2711  GCCTTGAATCCAGAT-----GAAACATCAGAGAAAGAAAGAAAGCAACTTGG 2766
Db      780  SerTrpAanProGluGlyThrValGlyThrGlyCysAanTrpGlnGluAlaThrSerIle 799

RESULT 6
US-10-114-893-10
/ Sequence 10, Application US/10114893
/ Publication No. US20020193567A1
/ GENERAL INFORMATION:
/ APPLICANT: Jacobs, Kenneth
/ APPLICANT: McCoy, John M.
/ APPLICANT: Lavallee, Edward R.
/ APPLICANT: Collins-Racie, Lisa A.
/ APPLICANT: Evans, Cheryl
/ APPLICANT: Merberg, David
/ APPLICANT: Treacy, Maurice
/ APPLICANT: Bowman, Michael R.
/ APPLICANT: Spaulding, Vikki
/ APPLICANT: Carlin-Duckett, McKeough
/ APPLICANT: Kelleher, Kerry S.
/ APPLICANT: Genetics Institute, Inc.
/ TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
/ FILE REFERENCE: GI 6000-10A
/ CURRENT APPLICATION NUMBER: US/10/114,893
/ CURRENT FILING DATE: 2002-04-02
/ EARLIER APPLICATION NUMBER: 09/413,232
/ EARLIER FILING DATE: 1999-10-06
/ NUMBER OF SEQ ID NOS: 321
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 661
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-114-893-10

Alignment Scores:
Pred. No.: 1,256-48 Length: 661
Score: 609.00 Matches: 194
Percent Similarity: 46.51% Conservative: 133
Best Local Similarity: 27.60% Mismatches: 303
Query Match: 10.25% Indels: 73
Gaps: 21

US-09-396-985B-5 (1-3395) x US-10-114-893-10 (1-661)
Qy      208  TACAGTTGCTATGCTTT-----CTCAGGGCTCCGCTGCTTGACGAAATGCCAG 258
Db      3 PheapValSerCysPhePheTrpValValLeuPheSerAlaGlyCysLys 19
Qy      259  GATGATGCTCTCTTGATCTGGCTGGAGACTCGATGATGAGGATGTTCTCTTCTGCT 318
Db      20 -----ValIleThrSerTrpAapGln-Met----- 27
Qy      319  GAGACAGGAAAGCTTGAATCCTGCGATAGAGGTACTTCTTAATATTACCTACCAATGAT 378
Db      28 -----CysIleGluUysGluAlaLeuLysThrTyrAsnCyseG 40
Qy      379  GGATCAGAAATCTCAGCAAAATCCCTTCATGATCCCTTATTCAACCAAGAACTGATCT 438
Db      111  GATGATGCTCTCTTGATCTGGCTGGAGACTCGATGATGAGGATGTTCTCTTCTGCT 318

```

Db 40 uasnleuglyleuSerGIuileProaspThrleuProasnthrthrIguPheleuGIuPh 60
 QY 439 GAGCTTCAACCCCTGAGATCTTAAAGAAAGCTATAGCTTCAACAATTTCTCAACAATCTCA 498
 Db 60 eSerPheasnheleuprothrIleHisasnrgthrPheSertrgLeuMetAsnleuth 80
 QY 499 GTGGCTGATTTATTCAGAGTGTGAATTTAGACAATTTAGACAAGAGGATGAGCTT 558
 Db 80 rPheleuaspheuthrArgGysgInIleasnthrIleHisgIuaspThrPheGInserH 100
 QY 559 AAACAGCTCTCAACCTTGTGACTGACAGAAACCTTCAAGAGTTTCCCGACGAG 618
 Db 100 sHisGInleuSerthrleuValleuThrGlyAsnProleuIlePheMetAlaGluThrSe 120
 QY 619 TTTTCTGCACTAAACAATTTAGAGAAATCTGTGGCTGTGAGACAACAAATGACCTCT 678
 Db 120 rleuasnIyProlySerleuLyHisleuPheleuIleGInthrGlyIleSerAsnle 140
 QY 679 AGAGGGTTTCCATATTGACAGCTTATATCTTAAAGAACTAAATGTGCTCATATCT 738
 Db 140 uGIuPheIleProValHisasnleuGIuasnleuGIuSerleuYrleuGIuSerAsnH 160
 QY 739 TATACATCTCTTAAAGTTCCTGAATTTTCTTATCTGAACAACCTTGAACATGTGGA 798
 Db 160 sIleSerSerIlelyaspPheProlyaspPhePro--AlaArgAsnleuLyValleuAs 179
 QY 799 TCTTTCTTATCAATATTCACAATCTTCTGCAAGAACTTACAGTTCTTCACTGAAA 858
 Db 179 rPheGInasnasnAlaIleHisrYrIleSerArgIuaspMetArgSerleuGIuGIn- 198
 QY 859 TCCCAACATCAATCTCTTGTAGACCTGTCTTAAACCAATGACATCTCAAGACCCA 918
 Db 199 ----AlaIleasnleuSerleuAsnPheasnIyAsnasnVallysgIyleGIuIeGI 217
 QY 919 AGCCTTTCAGGGAATTAGGCTTCCATGAATTGACTCTTAAAGATTTTAAATAGCTCAA 978
 Db 217 yAlaPheaspSerthrValPheGInSerleu-----AsnPheGlyGIuThrPr 233
 QY 979 TGTAAGTAAATGTGCTTCAAAACATGACGTGTTATCATGTCATGCTGATGCTGGG 1038
 Db 233 oasnleuSerValIlePheasnIyIleuGInasnSerThrthrGInSerleuThrPleuGI 253
 QY 1039 AGAATTTAAATGAAGAAAGATCTGAAAGTTTGAACCGTCTGTCAAGAGAGACTAT 1098
 Db 253 yThrPheGInaspIleaspasp---GluaspIleSerSerIleMetleuLysgIyleuCy 272
 QY 1099 CAATGTGACATGATGAGTTACAGTTTACATATATTAATCATTTTTCAGAT--GATAT 1155
 Db 272 sGluMetSerValGIuSerleuAsnleuGInGIu--HisArgPheSeraspIleSerSe 291
 QY 1156 TTATATCTCAATGTCTTGGCAATATTTTGCATATGCTTTCACAGGTGATCATATAA 1215
 Db 291 rThrThrPheGIncySpherthrGInleuGInGIuIeuspIeuthrAlathrHisleuLy 311
 QY 1216 ACACATGACAGATGTCTTGAAGCAATTTCAAAATGCAATCCTTATCAATCATTAAG 1270
 Db 311 s-----GIuIeuproSerGIuMetlys-----GIuIeupasnleuIeupLySle 326
 QY 1271 -----TGTCATCTTAAGCT-----TTTCCAAA 1293
 Db 326 uValleuSerValasnHisPheaspGInleuCyGInIleSerAlaIleasnPheProSe 346
 QY 1294 GCTGAGTCTACCTTTTCTTAAAGTTGACATTAACTAACCAACAGAGAGATACAGCTT 1353
 Db 346 rleuThrHisleuYrIleArgGly-----AsnVallySlySerleuHisleuGIuYva 363
 QY 1354 TGGTCAGTTG--GCTGTGCAAGTCTCAAGATATCTAGTATGCAATGCAATGAG 1410
 Db 363 IGlyCyIeuleuGIuIySerleuGIuIeuleuGInThrleuaspheSerHisasnApIleGI 383
 QY 1411 CTTTAAAGGTGCTGTCTTATTTCTGATTTTGAACAACAACACTGAAGTATTAAGCT 1470
 Db 383 uAlaSeraspCyCySerleuGInleuLyAsnleuSerHisleuGInThrleuAsnle 403

QY 1471 CAGCTCAATGTGTGATC---CTGATAGTGCACCACTTCACTGAGGTCTAGAAGAGCTGA 1527
 Db 403 uSerHisasnIuProleuGIuIeuleuGInSerGInAlaPheleuSlyCySProGInleuGI 423
 QY 1528 ATACCTGAGCTTTCAGACATCTCCACTTTAAAAAAGTCAACAGAAATTCATGATTTTATC 1587
 Db 423 uleuIeupreuleuAlaPheThrArgleuHisIleAsnAlaProGInSerProPheGInAs 443
 QY 1588 TCTTGAAAACTTCTTCACTGTGACATCTCTTACATTAATTCACAAATTTGACTTGATG 1647
 Db 443 nleuHisPheleuGIuValleuAsnleuThrTyCySpherleuaspThrSerasnGInH 463
 QY 1648 CATATTTCTGGCTTGTGATGACTGCACACACTTTAAATAGTGGCTGAATTTCTTCAAGA 1707
 Db 463 sIeuleuAlaGIuIeuleuProValleuAlaGHisleuAsnleuSlyAsnHisPheGInAs 483
 QY 1708 CAACACCTT-----TCAATATGCTTTTACAAAACAACAACAACTTAACTTCGTGATCT 1761
 Db 483 pGIyThrIlethrIySthrAsnleuGInThrValIGlySerleuGIuValleuIlele 503
 QY 1762 TTTTAAATGCCAAGTGAACAGATTTCTAGAGGGGTATTGACACACTTTCACAGACTCCA 1821
 Db 503 uSerSerCyGIuIeuleuSerIleaspGInGInAlaPheHisSerleuGIuLySmetSe 523
 QY 1822 GTTATTAACATAGTGCACAAACACTTACG-----TTTCTGATGCA---TCCCAATTA 1872
 Db 523 rHisValaspheuSerHisasnSerleuThrCySaspSerIleaspSerleuSerHisSle 543
 QY 1873 TAAACAGCTGTACTCCTCAGAGACTGTGATGCAATTTCAATGCAATGACATGACATCCA 1932
 Db 543 uLyGlyIleTyr-----LeuAsnleuAlaAlaasnSerIleasnIleIleSe 559
 QY 1933 AGGAATCTGCACACTTTTCCAAAAGACTAGCCGTCTTCAATGTGACTATATTTCTGT 1992
 Db 559 rProArgleuIeuproIleuSerGInGInSerThrIleasnleuSerHisasnProle 579
 QY 1993 TGCTTATATGATGATATATGCAATATTCATGAGTGGGTCAAGGACCAAGAAATGTTCTT 2052
 Db 579 uaspCyThrCySerpasnIleHisPheleuThrTyrIlysgIuIeupasnHisSlySle 599
 QY 2053 GGTGAATGTGAACAAATGAAATGTGCATGACCTATGACATGAAAGCCCTCCGTGTTT 2112
 Db 599 uGIuGIuSerGInIuIuThrThrCySAlaasnProproSerleuArgIyVallySleuSe 619
 QY 2113 GGAATTTACGAATTC-----ACCTGTATATATACAGACTATCATCACTGT 2160
 Db 619 rAspVallyleuSerCySgIyleThrAlaIleGlyIlePhePheleuIleValPhele 639
 QY 2161 ATGGGTGTCAGTGTGCTGTGGTGAAGCAGCTGTGACATTTCTGATATACCACTTATTT 2220
 Db 639 uleuIeuleuAlaIleuIeuphePheAlaVallySlyrleuIeupArgIySlyrGI 659
 QY 2221 TCACCTG 2227
 Db 659 nHisIle 661

RESULT 7
 US-10-038-854-134
 / Sequence 134, Application US/10038854
 / Publication No. US20040022781A1
 GENERAL INFORMATION:
 / APPLICANT: Spytek, Kimberly A
 / APPLICANT: Li, Li
 / APPLICANT: Wolenc, Adam R
 / APPLICANT: Verneel, Corine
 / APPLICANT: Riesen, Andrew J
 / APPLICANT: Liu, Xiaohong
 / APPLICANT: Malyankar, Uriel M
 / APPLICANT: Shinkets, Richard A
 / APPLICANT: Tchernev, Velizar
 / APPLICANT: Spaderna, Steven K
 / APPLICANT: Gorman, Linda

```

/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Pattnayaj, Meera
/ APPLICANT: Gusev, Vladimir Y
/ APPLICANT: Gangolli, Esha A
/ APPLICANT: Guo, Xiaojia S
/ APPLICANT: Shenoy, Suresh G
/ APPLICANT: Raestelli, Luca
/ APPLICANT: Caeman, Stacie J
/ APPLICANT: Boldog, Ferenc
/ APPLICANT: Burgess, Catherine E
/ APPLICANT: Edinger, Shlomit R
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Gunther, Erik
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Macougalli, John R
/ TITLE OF INVENTION: Proteins And Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-230
/ CURRENT APPLICATION NUMBER: US/10/038,854
/ CURRENT FILING DATE: 2003-01-22
/ PRIOR APPLICATION NUMBER: 60/258,928
/ PRIOR FILING DATE: 2000-12-29
/ PRIOR APPLICATION NUMBER: 60/259,415
/ PRIOR FILING DATE: 2001-01-02
/ PRIOR APPLICATION NUMBER: 60/259,785
/ PRIOR FILING DATE: 2001-01-04
/ PRIOR APPLICATION NUMBER: 60/269,814
/ PRIOR FILING DATE: 2001-02-20
/ PRIOR APPLICATION NUMBER: 60/279,832
/ PRIOR FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/279,833
/ PRIOR FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/279,863
/ PRIOR FILING DATE: 2001-03-29
/ PRIOR APPLICATION NUMBER: 60/283,889
/ PRIOR FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 60/284,447
/ PRIOR FILING DATE: 2001-04-18
/ PRIOR APPLICATION NUMBER: 60/286,683
/ PRIOR FILING DATE: 2001-04-25
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 411
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 134
/ LENGTH: 661
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-038-854-134

Alignment Scores:
Pred. No.: 1,25e-48 Length: 661
Score: 609.00 Matches: 194
Percent Similarity: 46.51% Conservative: 133
Best Local Similarity: 27.60% Mismatches: 303
Query Match: 10.25% Indels: 73
DB: 15 Gaps: 21

US-09-396-985B-5 (1-3395) x US-10-038-854-134 (1-661)
QY 208 TACAGTTGTCATGCTTT-----CTCAGGCGCTCCGGCTGTTCGAGAAAATGCCAG 258
   :: |||||::: |||||:::
Db 3 PheapValIserCysaSheheTrpValValIleuPheSerIadIyCysIys----- 19
   :: |||||::: |||||:::
QY 259 GATGATGCTCTTCGATCTGGCTGGCTGACCTGATCATGAGCTGTTCCTTTCTGTGCT 318
   :: |||||::: |||||:::
Db 20 -----ValIleTherItpaBgIn-Met----- 27
   :: |||||::: |||||:::
QY 319 GAGACGAGAACTTGAATCCCTGCATAGAGGTACTTCTTAATATTACCTTACCAATGAT 378
   |||||::: |||||:::
Db 28 -----CyeIIleGIuIySgIuIaIaenIyThrTyrIaenIyCysGI 40
   |||||::: |||||:::
QY 379 GGATAGAAATTCAGCAAAATCCCTTCATACATCCCTTATTTCACCAAGAACTAGATCT 438
   |||||::: |||||:::

```

Db	40	uAsnLeuGlyLeuSerGluLeuProAspThrIleuProAsnThrThrgluIleuLeuGluP	60
Qy	439	GAGCTCAACCCCTGAAAGATCTTAAGACGTAAGCTTACCCAAATTTCTCACACTTCA	498
Db	60	eSerPheAsnIleuPheProThrIleHisAsnArgThrPheSerArgIleuLeuAsnLeuTh	80
Qy	499	GTGGCTGGATTATTCACAGCTGTGAAATTTGAGACATTTGAAGACAGGCAATGGCAT	558
Db	80	rPheLeuAspLeuThrArgCysGlnIleAsnTrpIleHisGluAspThrPheGlnSerH	100
Qy	559	AAACCAAGCTCCAACTCTTGACTAGCAGAGAAACCTTAACAAGATTTTCCCAAGAA	618
Db	100	shIleGlnLeuSerThrIleuValIleuThrGlyAsnProIleuIlePheMetAlaGluThr	120
Qy	619	TTTTCTCGACTMAAAATTTAGAGAACTGTGGTGGCTGTGAGACAAATAATGACTCT	678
Db	120	rIleuAsnGlyProIysSerIleuYshIleuPheLeuIleGlnThrGlyIleSerAsnLe	140
Qy	679	AGAGGATTCATATTTGGACAGCTTATATCTTTAAAGAAATAATGTGGCTCATATCT	738
Db	140	uGlnPheIleProValHisAsnLeuGluAsnLeuGlnSerIleuTrpGlySerAsnH	160
Qy	739	TATACATCTCTTAAAGTTGCTCGAAATATTTTCTTAATCTGACAAACCTTAAGACAT	798
Db	160	sIleSerSerIleIysPheProIysAspPhePro--AlaArgAsnLeuIysValLeuAs	179
Qy	799	TCCTTCTTATACATATATTCAAATAATTTCTGTCCAAAGACTACAGTTTCTACGTGAAA	858
Db	179	pPheGlnAsnAsnAlaIleHisTrpIleSerArgGluAspMetArgSerIleuGlnGln--	198
Qy	859	TCCCCAAGTCATCTCTCTTAAAGCTGTCTTAAACCCATGATCTCCATTCAGGCCA	918
Db	199	---AlaIleAsnLeuSerIleuAsnPheAsnGlyAsnAsnValIysGlyIleGluLeuG	217
Qy	919	AGCCTTCAGGGAATTAAGCTCCATGAATGACTCTAAGAAAGTATTTTATATAGCTCAA	978
Db	217	yAlaPheAspSerThrValPheGlnSerLeu-----AsnIleGlyGlyThrPr	233
Qy	979	TGTACTGAAATGTGCTTCAAAACAGTACTGGTTTACATGTCCATCGGTGATCTTGGG	1038
Db	233	oAsnLeuSerValIlePheAsnGlyLeuGlnAsnSerThrThrcIlnSerIleuTrpLeuG	253
Qy	1039	AGAAATTTAAATGAAGAAGATCTGGAAGAATTTGACCGTCTGTCTATGGAAGAAGCTATG	1098
Db	253	yThrPheGluAspIleAspAsp--GluAspIleSerSerAlaMetLeuIysGlyLeuCy	272
Qy	1099	CAATGTGACCTTATATGATGCTCAGGTCAACATATATATATCATCTTCAAGT---GATAT	1155
Db	272	sgIleuSerValGlnSerIleuAsnLeuGlnGlu--HisArgPheSerAspIleSerSe	291
Qy	1156	TTATATATCTCAATTTGCTTGGCAATAATTTCTGCATGTCTTTCACAGGTGATACATATAA	1215
Db	291	rThrThrPheGlnCysPheThrGlnIleuGlnGluLeuAspLeuThrAlaThrHisLeuIy	311
Qy	1216	ACAATAGCAGATGTTCTCTAGGCAATTCAAATGGCAATCCTTATCAATCATTTAGA----	1270
Db	311	s-----GlyLeuProSerGlyMetIys-----GlyLeuAsnLeuLeuIysValSe	326
Qy	1271	-----TGTCACTTAAGGCT-----TTTCCAAA	1293
Db	326	uValLeuSerValAsnHisPheAspGlnLeuCysGlnIleSerAlaAlaAsnPheProSe	346
Qy	1294	GCTGAGTTCACCTTTCTTAAATGTGGACTTTATACCAACCAAGAGATATACACTT	1353
Db	346	rIleuThrHisLeuTrpIleArgGly-----AsnValIysValIleuHisIleuGlyVa	363
Qy	1354	TGGTCACTTG--GCTTCCCAAGTCTCAGATATCTAGATCTTATGTGAATAATGCCATGAG	1410
Db	363	IGlyCysLeuGlnIuysLeuGlyAsnLeuGlnThrIleuAspLeuSerHisAsnAspIleG	383
Qy	1411	CTTTAGAGGTTCGTCTTTATTTCTGATTTTGGAAACAAACAACTGAAGTACTTAAGCT	1470
Db	383	uAlaSerAspCysCysSerIleuGlnLeuIysAsnLeuSerHisIleuGlnThrIleuAsnLe	403

```

QY 1471 CAGCTTCAGTGTGTCATC---CTGATGAGTGCACAACTTCAGGTGAGAGAGCTGA 1527
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 403 usErHiaSnGluIurProeuGlYleuGInSerGlnAlaheYsGluCySProGInleuGl 423
QY 1528 ATACCTGGACCTTTCAGCAGCTCCACTTTAAAAAAGTCAAGAAATTCAGTGTTCTTATC 1587
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 423 uLeuLeuAspLeuAlaPheThrArgLeuHie11eAsnAlaProGInSerProPheGlnAs 443
QY 1588 TCTTGAAGAAACTTCTTACCTGACATCTTACCAATAATCCAAAATGACTTGAATG 1647
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 443 nLeuHiePheLeuGlnValLeuAsnLeuThrTyCySerPheLeuAspThrSerAsnGlnH 463
QY 1648 CATATCTTCTGGCTGATCAGCTTCACAACTTTAAATAAGCTGGCAATCTTCAAGA 1707
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 463 sLeuLeuAlaGluLeuProValLeuArgHieLeuAsnLeuYsGluAsnHiePheGlnAs 483
QY 1708 CAACACCCCTT-----TCAAATGCTTTTCAAAACAAACAACTTACATTCCTGAGATCT 1761
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 483 pGlyThrIleThrIlySerHieLeuGlnThrValGlySerLeuGlnValLeuIleLe 503
QY 1762 TTTCAATGCCAATCGACAGATATCTAGGGGGGATTTGACACACTTCACAGACTCCA 1821
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 503 uSerSerCyGluYleuLeuSerIleAspGlnGlnAlaPheHieSserLeuGluYlsMetSe 523
QY 1822 GTTATTAACATGAGTGCACAACTTCAGTCTG-----TTTCTGATCCAA--TCCCAATTA 1872
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 523 rHieValaSpLeuSerHieSaenSerLeuThrCyAspSerIleAspSerLeuSerHieSle 543
QY 1873 TAAACAGCTGACTCCCTCAGAGACTTTGATTCAGTTTCAATGCGCATAGACATCCAA 1932
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 543 uLyGluYleTyLr-----LeuAsnLeuAlaAlaAsnSerIleAsnIleIleSe 559
QY 1933 AGGAATCTGCAACATTTTCCAAAGAGCTAGCCGCTTCAATGACTATATTTCTGT 1992
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 559 rPrcArgLeuLeuProIleLeuSerGlnGlnSerThrIleAsnLeuSerHieSaenProLe 579
QY 1993 TGCATTATATGTAATATCAGAAATTTCTTCAGTGGGTCAAGAGCAAGAAATGTTCTT 2052
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 579 uAspCySerThrcySerSaenIleHiePheLeuThrTrrPtyGlySgluAsnLeuHieSlySle 599
QY 2053 GGTGAATGTTGACAAATGAATGAATGTGATCACCATTAGACATGAAGGCCCTCGGTGTT 2112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 599 uGluGlySerGluGluThrThrCysAlaAsnProSerLeuArgGlyValYlsLeuSe 619
QY 2113 GGATTTACGAATTC-----ACCTGTTATATATACAGACTATACAGCT 2160
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 619 rAspVallyLeuSerCySglYleThrAlaIleGlyIlePhePheLeuIleValIlePheLe 639
QY 2161 ATCGGTGCTAGTGTGCTTGTGATGACCATGTCATTCCTGATATCACTTCTATTT 2220
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 639 uLeuLeuLeuAlaIleLeuLeuPhePheAlaVallyStryLeuLeuArgTrrlyGly 659
QY 2221 TCACCTG 2227
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 659 nHieIle 661

```

```

APPLICANT: Kekuda, Ramesh
APPLICANT: Paturajan, Meera
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gangolli, Beha A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Raetelli, Luca
APPLICANT: Caeman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Burgess, Catherine B
APPLICANT: Edinger, Shlomit R
APPLICANT: Ellerman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230
CURRENT APPLICATION NUMBER: US/10/038,854
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: 60/258,928
PRIOR FILING DATE: 2000-12-29
PRIOR APPLICATION NUMBER: 60/259,415
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/259,785
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 60/269,814
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/279,832
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,833
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/279,863
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/283,889
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/284,447
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/286,683
PRIOR FILING DATE: 2001-04-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 411
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 135
LENGTH: 661
TYPE: PRT
ORGANISM: Mus musculus
US-10-038-854-135

Alignment Scores:
Pred. No.: 1,57e-47 Length: 661
Score: 597.50 Matches: 187
Percent Similarity: 46.50% Conservative: 125
Best Local Similarity: 27.87% Mismatches: 314
Query Match: 10.05% Indels: 45
DB: 15 Gaps: 15

US-09-396-985b-5 (1-3395) x US-10-038-854-135 (1-661)
QY 293 ATCATGCGATGTGCTTCTTCTCGCTGAGA-----CCAGAGACTGGAATCCCTGCATA 346
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 10 LeuValAlaLeuPheLeuAlaSerCyAsrGAlaThrThrSerSerAspGlnYsCySle 29
QY 347 GAGGTACTTCTTAATATTTACTTACCAATGCATGCATGATAGATTCGACAAATTCCTCAT 406
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 30 GluYsGluValAsnYsThrTyAsnCySgluAsnLeuGluYleuAsnGluIleProGly 49
QY 407 GACATCCCTTATTCACAGACTTCAGTGTGAGTTCAACCCCTGAGATCTTAGA 466
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 50 ThrLeuProAsnSerThrGluCySleGluPheSerHieAsnValleuProThrIleGln 69
QY 467 AGCTATAGCTTCACCAATTTCTGACAACTTCAGTGGCTGATTTATTCAGGTGAAATT 526
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```


Db 70 AsnThrThrPheSerArgLeuIleAsnLeuThrPheLeuAspLeuThrArgCysGlnIle 89
 QY 527 GAGCAATTGAGACCAAGCATGGCATGGCTTAAACCAAGCTTCAACCTTGGTATCTGACA 586
 Db 90 TyrTrpIleHisGluAspThrPheGlnSerGlnHisArgLeuAspThrLeuValLeuThr 109
 QY 587 GGAACCCCTATCAGAGTTTTCGCCAGAGATTTTTCGACATACCAATTTAGAGAT 646
 Db 110 AlaAsnProLeuIlePheMetAlaGluThrAlaLeuSerGlyProlyValAlaLeuHis 129
 QY 647 CTGGTGGCTGGAGACAAAATGATACCTCTAGAGGTTTCCATATTGACACCTTATA 706
 Db 130 LeuPhePheIleGlnThrGlyIleSerSerIleAspPheIleProLeuHisAsnGlnHis 149
 QY 707 TCTTAAAGAACTTAATGGCTCATATATCTTATACCTTCTTAAGTCCGGAATAT 766
 Db 150 ThrLeuGluSerLeuTyrLeuGlySerAsnHisIleSerSerIleLeuProlyGly 169
 QY 767 TTTTCTATCTGACAAACCTAGAAACATGGATCTTTCTTATATCTATATCAACTAT 826
 Db 170 PheProThr---GluLeuValLeuAspPheGlnAsnAsnAlaIleHisTyrLeu 188
 QY 827 TCTGTCAAGACTTACAGTTTCTACGTGAAAATCCCAAGTCAATCTCTTATAGACCTG 886
 Db 189 SerIysGluAspMetSerSerLeuGlnGln-----AlaThrAsnLeuSerLeuAsnLeu 206
 QY 887 TCTTAAACCAATTGACTCCATTCAGCCCAAGCTTTCAGGAAATTAGGCTCCATGAA 946
 Db 207 AsnAlaAsnAspIleAlaGlyIleGluProGlyAlaPheAspSerAlaValPheGlnSer 226
 QY 947 TTGACTCTAGAGATTTTAAATAGCTCAATAGTCAAAATAGTGGCTTCAAAACAT 1006
 Db 227 Leu-----AsnPheGlyGlyThrGlnAsnLeuValIlePheIysGlyLeu 242
 QY 1007 ACTGGTTACATGTCATCGGTGATCTTGGAGAAATTGAAAAGAAAGATCTGGAA 1066
 Db 243 LysAsnSerThrIleGlnSerLeuTrpLeuGlyThrPheGln---AspMetAspAspIle 261
 QY 1067 AGTTTGAACCGTTCGTATGAGAGATATGCAATGAGCATTTGATGAGTTA 1126
 Db 262 AspIleSerProAlaValPheGlnGlyLeuCysGluMetSerValGluSerIleAsnLeu 281
 QY 1127 ACATATATAATCATTTTTCAGATGATATTTAATCATTCATTTGGCAATATTTCT 1186
 Db 282 GlnIysHisTyrPhePheAsnIleSerSerAsnThrPheHisCysPheSerGlyLeuGln 301
 QY 1187 GCAAATGCTTTCACAGGTGATCATATTAACAACATAGACAGAT----- 1228
 Db 302 GluLeuAspLeuThrAlaThrHisLeuSerGluLeuProSerGlyLeuValGlyLeuSer 321
 QY 1229 -----GTTCTTAGGCATTTCAATGGCAATCTTATCATATCATTAAGAT 1273
 Db 322 ThrLeuIysIysLeuValLeuSerAlaAsnIysPheGluAsnLeu-----Cys 337
 QY 1274 CATCTTAAGCCT-----TTTCCAAAGCTGAGTCACTTTCTTAAAGTTGACTTTA 1327
 Db 338 GlnIleSerAlaSerAsnPheProSerLeuThrHisLeuSerIleIysGly----- 354
 QY 1328 ACTACCAACAGAGAGATATCAGCTTTGGTACATGGTGCCT---CTGCCAAGTCTCAGATAT 1384
 Db 355 AsnThrIysIysGluGlnLeuGlyThrGlyCysLeuGluAsnLeuGluAsnLeuArgGln 374
 QY 1385 CTAGATCTTAGTGAAGATGCCATGAGCTTTAGAGGTTGCTGTTTCTTATTCGATTTTGA 1444
 Db 375 LeuAspLeuSerHisAspAspIleGluThrSerAspCysAsnLeuGlnLeuArgAsn 394
 QY 1445 ACAAAACAACCTGAGTATAGACTCAGCTTCACTGATGATGATC---CTGATGATGATC 1501
 Db 395 LeuSerHisLeuGlnSerLeuAsnLeuSerTyrAsnGluProLeuSerLeuIysThrGln 414
 QY 1502 AACTTCATGGGTCTTGAAGAGCTGGAATATCTGCACTTTCAGACACTCACTTAAAAAAG 1561
 Db 415 AlaPheIysGluCysProGlnLeuGluLeuLeuAspLeuAlaPheThrArgLeuIysVal 434

QY 1562 GTACAGAAATTCAGAGTTCTTATGCTTGAAGAACTTCTTACCTTGACATGCTTAC 1621
 Db 435 LysAspAlaGlnSerProGlnAsnLeuHisLeuLeuIysValLeuAsnLeuSerHis 454
 QY 1622 ACTAATATCAAAATGATCTTGTAGTGCATATTTCTTGGCTTGATCAGTCCAACTTTA 1681
 Db 455 SerLeuLeuAspIleSerSerGlnGlnLeuPheAspGlyLeuProAlaLeuGlnHisLeu 474
 QY 1682 AAAATGGCTGGCAATTTCTTGAAGACACACCTT-----TCAATGCTTTTCAAAAC 1735
 Db 475 AsnLeuGlnIysAsnHisPheProIysGlyAsnIleGlnIysThrAsnSerLeuGlnThr 494
 QY 1736 ACAAAACAACCTGAGTATGATCTTGAAGAACTTGAAGCAAGATATGAGGAGG 1795
 Db 495 LeuGlyArgLeuGluIleLeuValLeuSerPheCysAspLeuSerSerIleAspGlnHis 514
 QY 1796 GTATTGACACACTTACAGACTCCAGTTATTTAAACATGATGACAAACATTAAGTGT 1855
 Db 515 AlaPheThrSerLeuIysMetMetAsnHisValAspLeuSerHisAsnArgLeuThrSer 534
 QY 1856 CTGGAT-----CCATCCATTTAAACAGCTGATCCCTCAGGACTTTGATGTC 1906
 Db 535 SerSerIleGlnAlaLeuSerHisLeuIysGlyIleTyr-----LeuAsnLeu 550
 QY 1907 AGTTTCAATGCAATGAGACATCCAAAGAAATCTGCAACATTTTCCAAAGAGCTAGCC 1966
 Db 551 AlaSerAsnHisIleSerIleIleLeuProSerLeuLeuProIleLeuSerGlnGlnArg 570
 QY 1967 GTCTTCAATGCAATTAATATCTGTGCTTGTATATGTAATGCAATTTCTTGCAG 2026
 Db 571 ThrIleAsnLeuArgGlnAsnProLeuAspCysThrCysSerAsnIleTyrPheLeuGln 590
 QY 2027 TGGGTCAAGACCAAGAAATGTTCTTGGTGAATTTGAACAAATGTAATGATGATCAGCT 2086
 Db 591 TrpTyrIysGluAsnMetGlnIysLeuGluAspThrGlnAspThrLeuCysGluAsnPro 610
 QY 2087 ATAGACATGAAGGCTCCCTCGTGGTGAATTTTATGCAATTTCCACCTGTAT----- 2137
 Db 611 ProLeuLeuArgGlyValArgLeuSerAspValThrLeuSerCysSerMetAlaAlaVal 630
 QY 2138 ---ATATACAAAGATATCATCAGTATCGGTGTCAGTGTGCTTGTAGACCATGTA 2194
 Db 631 GlyIlePhePheLeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePheAlaVal 650
 QY 2195 GCATTTCTGATATACCATTTTATTTCACTG 2227
 Db 651 LysTyrPheLeuArgTyrIysTyrGlnHisIle 661
 RESULT 9
 US-10-037-417-107
 ; Sequence 107, Application US/10037417
 ; Publication No. US20040052806A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kekuda, Rameesh
 ; APPLICANT: Alsebrook II, John P
 ; APPLICANT: Tchernenov, Velizar T
 ; APPLICANT: Liu, Xiaodong
 ; APPLICANT: Spytek, Kimberly A
 ; APPLICANT: Paturajan, Meera
 ; APPLICANT: Grose, William M
 ; APPLICANT: Lepley, Denise M
 ; APPLICANT: Burgess, Catherine E
 ; APPLICANT: Verne, Corine A.M.
 ; APPLICANT: Li, Li
 ; APPLICANT: Gorman, Linda
 ; APPLICANT: Edinger, Shlomit R
 ; APPLICANT: Sciore, Paul
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Maiyanekar, Uziel M
 ; APPLICANT: Rothenberg, Mark
 ; APPLICANT: Stone, David J
 ; APPLICANT: Boldog, Ferenc L

QY 1736 ACACAAACTTAACATTCCTGATCTTTTAATCCACATCGAACAGATATCTAGGGGG 1795
 DB 495 LeuGlyArgLeuGluIleValIleuSerPheCybAspLeuSerSerIleAspGlnHis 514
 QY 1796 GTATTGACACACTCTACAGACTGATTATTAACATGAGTCACAAACACTCTGCTTT 1855
 DB 515 AlaIleHisSerLeuLysMetMetAsnHisValAspLeuSerHisAsnArgLeuThrSer 534
 QY 1856 CTGAT-----CCATCCCATTTATTAACAGCTGTATCTCCACAGACTCTTGATTGC 1906
 DB 535 SerSerIleGluAlaLeuSerHisLeuLysGlyIleTy-----LeuAsnLeu 550
 QY 1907 AGTTTACATCCGACAGACATCCAAAGATACTGCACATTTCCAAAGACTGAGCC 1966
 DB 551 AlaSerAsnHisIleSerIleIleLeuProSerLeuLeuProIleLeuSerGlnArg 570
 QY 1967 GTCTTCATCTGACTAATTAATTCCTGCTGTATATGTAATATCAGAAATTTCTTGAC 2026
 DB 571 ThrIleAsnLeuArgGlnAsnProLeuAspCybThrCybSerAsnIleTyPheLeuGlu 590
 QY 2027 TGGGTCAAGACCAAGAAATTTCTGTGTAATGTGAACAAATGAATGTGCATCACT 2086
 DB 591 TrpTyrlsGluAsnMetGlnLysLeuGluAspThrGluAspThrLeuCybGluAsnPro 610
 QY 2087 ATAGACATGAAGGCTCCCTGCTGTGATTTTACGATTTCCACTCTGTAT----- 2137
 DB 611 ProLeuLeuArgGlyValArgLysSerAspAlaThrLeuSerCybSerMetAlaVal 630
 QY 2138 --ATATACAGACTATCATCATGATATCGGTGTCAGTGTCTGTGTAGCCACTGTA 2194
 DB 631 GlyIlePhePheLeuIleValPheLeuLeuValPheAlaIleLeuLeuIlePheAlaVal 650
 QY 2195 GCATTTCTGATATACCACTTCTATTTTCACTG 2227
 DB 651 LysTyrlPheLeuArgTrpLysTyrlGlnHisIle 661
 RESULT 10
 US-09-954-987B-192
 ; Sequence 192, Application US/09954987B
 ; Publication No. US20030104523A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stefan Bauer
 ; APPLICANT: Grayson B. Lipford
 ; APPLICANT: Herman Wagner
 ; TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
 ; FILE REFERENCE: C1041/7016 (AMS)
 ; CURRENT APPLICATION NUMBER: US/09/354, 987B
 ; CURRENT FILING DATE: 2001-09-17
 ; PRIOR APPLICATION NUMBER: US 60/233, 035
 ; PRIOR FILING DATE: 2000-09-15
 ; PRIOR APPLICATION NUMBER: US 60/263, 657
 ; PRIOR FILING DATE: 2001-01-23
 ; PRIOR APPLICATION NUMBER: US 60/291, 726
 ; PRIOR FILING DATE: 2001-05-17
 ; PRIOR APPLICATION NUMBER: US 60/300, 210
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 230
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 192
 ; LENGTH: 1032
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-954-987B-192
 Alignment Scores:
 Pged. No.: 2,69e-45 Length: 1032
 Score: 575.00 Matches: 242
 Percent Similarity: 40.93% Conservatve: 153
 Best Local Similarity: 25.08% Mismatches: 318
 Query Match: 9.68% Indels: 252
 DB: 10 Gaps: 40

US-09-396--985B-5 (1-3395) x US-09-954-987B-192 (1-1032)
 QY 353 CTTCCTAATATTACCTTACCAATGATGATCAGAAAT---CTGAGCAAAATCCCTCATGAC 409
 DB 120 LeuArgAsnLeuThrValLeuLeuLeuGluAspAsnGlnLeuTyThrIleProAlaGly 139
 QY 410 ATCCCTTATTCACCAAGAACTAGATCTGAGCTTCAC--- 448
 DB 140 LeuProGluSerLeuLysGluLeuSerLeuIleGlnAsnAsnIlePheGlnValThrLys 159
 QY 448 ----- 448
 DB 160 AsnAsnThrPheGlyLeuArgAsnLeuGluArgLeuTyIleuGlyTrpAsnCybTyPhe 179
 QY 449 ----- 449
 DB 180 LysCybAsnGlnThrPheLysValGluAspGlyAlaPheLysAsnLeuIleHisLeuLys 199
 QY 458 ATCTTAAGAGCTATAGCTTACCAATTTCC-----TCACA 493
 DB 200 ValLeu---SerLeuSerPheAsnAsnLeuPheTyValProProLysLeuProSerSer 218
 QY 494 CTTCAGTGTGCTGATTTATTCAGGTGTGAATTTGACAAATGAGCAAGCATGGCAT 553
 DB 219 LeuArgLysLeuPheLeuSerAsnAlaLysIleMetAsnIleThrGlnGluAspPheLys 238
 QY 554 GCGTTAAACACGCTCTCAACCTTGTTCTGACAGGAAC----- 592
 DB 239 GlyLeuGluAsnLeuThrLeuLeuAspLeuSerGlyAsnCybProArgCybTyAsnAla 258
 QY 593 ----- 622
 DB 259 ProPheProCybThrProCybLysGluAsnSerSerIleHisIleHisProLeuAlaPhe 278
 QY 623 TCTGACATAACAAATTTAGAAATCTGTGCTGTGAGCAAAATGACCTCTTAGAG 682
 DB 279 GlnSerLeuThrGlnLeuLeuTyIleAsnLeuSerSerThrSerLeuArgThrIlePro 298
 QY 683 GGTTCATATTGACAGCTTATATCTTAAAGAAATGAGTGGCTCAATAT---CTT 739
 DB 299 SerThrTrpPheGluAsnLeuSerAsnLeuGlyIleGlnHisIleGlnPheAspTyLeu 318
 QY 740 ATACATTCCTTTAAGTTCGCTGAATATTTTCTAATCTGACAAACCTAGAACATGGAT 799
 DB 319 ValGlnGluIleAlaSerGlyAlaPheLeuThrLysLeuProSerLeuGlnIleLeuAsp 338
 QY 800 CTTCCTATAAC-----TATATTCAACTATTCTGTC----- 832
 DB 339 LeuSerPheAsnPheGlnTyLysGluTyIleGlnIlePheIleAsnIleSerSerAsnPhe 358
 QY 832 ----- 832
 DB 359 SerLysLeuArgSerLeuLysLysLeuHisIleuArgGlyTyValPheArgGlyLeuLys 378
 QY 833 ---AAGACTTACAGTTTACAGTGAATCCCAAGCTCAATCTCTTAGACCTGTCT 889
 DB 379 LysLysHisIlePheGlnHisIleGlnSerLeuProAsnLeu---AlaThrIleAsnLeuGly 397
 QY 890 TTAACCCCAATGATCTCATTCAGCCCAAGCCTTTCAGGGAATGAGCTCATGAATG 949
 DB 398 IleAsnHeIleGluLysIleAspPheLysAlaPheGln----- 410
 QY 950 ACTGTAAAGAGTAATTTTATAGCTCAAAATGTACTGAAATGTGCTTCACAAACATGACT 1009
 DB 411 -----AsnPheSerLysLeuAspValIle-----TyIleSer 421
 QY 1010 GGTTCATATGTCATGCTGATCTTGGA---GAATTTAAATGAAGGAATCTG--- 1063
 DB 422 GlyAsnArgIleAlaSerValLeuAspGlyThrAspTyIleSerSerThrPheArgAsnArgLeu 441
 QY 1064 -----GAAAGTTTTCAC----- 1075

Db 442 ArglyspProLeuSerThrAspAspArgLupheAspProHisValAsnPhetYrHisSer 461
Qy 1076 ---GGTTGTCATGGAAGACTATGACATGATGACATTTGACGTTACATAT 1132
Db 462 ThrlyspProLeuIlelyspProGlnCysThrAlaYrGlyLysAlaLeuAspSerLeu 481
Qy 1133 ATAAATCATTTT-----TCAGATGATATTATATCT 1165
Db 482 AsnLeuIlePheIleIleGlyLysSerGlnPheGlnGlyPheGlnAspIleIleCysLeu 501
Qy 1166 AATTGCTGGCAATATTTCGCAATGTCCTTTCACAGGTGATATATAACACATAGCA 1225
Db 502 AsnLeuSerPheAsnAlaAsnThrGlnValPheAsnGlyThrGluPheSer----- 518
Qy 1226 GATGTTCTAGGCAATTCGAATGCAATCCTTATCAATTCATTCATTCATTCAGCT 1285
Db 518 ----- 518
Qy 1286 TTTCGAAGCTGATCTACTTTTCTTAAAGTTGACATTAACCAACAGAGAGAT 1345
Db 519 -----SerMetProHisIleIleYrIleAspLeuPheThrAsnAsnArgLeuAsp 534
Qy 1346 ATC-----AGCTTGGTCATGTTGGCTGCTGCCAAGCTGCAGATATCTAGATCTT 1393
Db 535 PheAspAspAsnAlaPheSerAsp-----LeuHisAspLeuGluValLeuAspLeu 552
Qy 1394 AGTAGAATGGC-----ATGAGCTTTAGAGTTCCTGCTTCTATTCGATTTTGAAACA 1447
Db 553 SerHisAsnAlaHisIleYrPheSerIleAlaGlyValThrHisAspArgLeuGlyPheIleGln 572
Qy 1448 AAC-----AACCTGAAGTACTAGCTCAGCTTCATGAGTGTGCTGAGT--- 1498
Db 573 AsnLeuIleAsnLeuArgValLeuAsnLeuSerHisAsnGlyIleYrThrLeuThrGlu 592
Qy 1499 -----GCCAATTCATGAGTGTGCTGAGAGCTGGAATACCTGAGCTTCACGACTCC 1549
Db 593 GluSerGluLeuYrSerIleSerLeuYsgluValPheSerGlyAsnArgLeuAsp 612
Qy 1550 ACTTTAAAAAGTCACAGAA-----TTCTCAGTGTCTTATCTCTTGAATAACTT 1600
Db 613 HisLeuYrAsnAlaAsnAspGlyYrIleYrTrpSerIlePheYsgluGlnAsnLeu 632
Qy 1601 CTTTACCTTCATCTCTTACCTATACCAAAATTCGATTCGATTCCTTGGC 1660
Db 633 IleArgLeuAspLeuSerYrAsnAsnLeuGlnGlnIleProAsnGlyAlaPheLeuAsn 652
Qy 1661 TTG---ATCAGTCTCAACACTTTAAAAATGCGTGCATTCCT-----TTCAAGACAAC 1711
Db 653 LeuProGlnSerLeuGlnGluLeuLeuIleSerGlyAsnLysLeuArgPheAsnTrp 672
Qy 1712 ACCCTTTCATATGTCCTTTACAAACACAACTTAATTCCTGATCTTTTAAATGC 1771
Db 673 ThrLeuLeuGlnYrPhe-----ProHisLeuHisLeuAspLeuSerHisArgAsn 689
Qy 1772 CAATCGAAGACAGATATCTAGGGGGGATTTGACACACTCTCAGACCTCAGCTATTAAC 1831
Db 690 GluLeuYrPheLeuProAsnCysLeuSerYrPheAlaHisSerLeuGlnThrLeuLeu 709
Qy 1832 ATGAGTCACAACAACCTACTGTTCTGATCCATCCATTTAAACAGCTGACTCCCTC 1891
Db 710 LeuSerHisAsnHisPheSerHisLeuProSerGlyPheLeuSerGluAlaArgAsnLeu 729
Qy 1892 AGGACTCTTGATTTGCACTTTCAATGCGCTAGAG--ACATCCAAAGCAATCTGCACAT 1948
Db 730 ValHisLeuAspLeuSerPheAsnThrIleYsgluMetIleAsnLysSerSerLeuGlnThr 749
Qy 1949 TTTCGAAG---AGCTCAGCGTCTTCAATCGACTATATATTCGTTGCTGTATATGT 2005
Db 750 LysMetYrThrAspLeuSerIleLeuGluLeuHisGlyAsnYrPheAspCysThrCys 769
Qy 2006 GAATATACGAATTTCTTGACGTGGTCAAGACAGCAAAATGTTTC-----TTG 2053
Db 770 AspIleSerAspPheArgSerTrpLeuAspGluAsnLeuAsnIleThrIleProLysLeu 789

Qy 2054 GTGAATGTTGAACAATGAATGTCATCACCTATAGACATGAAGGCTCCCTGGTGTG 2113
Db 790 ValAsnVal-----IleCysSerAsnProGlyAspGlnYsgluSerLysSerIleMet 806
Qy 2114 GATTTTACGAATTCACCTGT-----TATATATACAAAGCT 2149
Db 807 SerLeuAspLeuThrThrCysValSerAspThrThrAlaValAlaLeuPhePheLeuThr 826
Qy 2150 ATCATCAGTGTATGGGTGTCAGTGTCTTGTGTAGCAGCTATAGCAATTTCTGATATAC 2209
Db 827 PheLeuThrThrSerMet-----ValMetLeuAlaIleValHisIleLeuPheYr 844
Qy 2210 -----CACTCTATTTTCACCTG-----ATACTATGCTGGCTGTAAAAAGTAC 2254
Db 845 TrpAspValTrpPheIleYrHisMetCysSerAlaLysLeuYsglyYrArgThrSer 864
Qy 2255 AGCAGAGAGAAAGCATCTATGATGATGATTTGTGATCTGACGACCAAGAT----- 2305
Db 865 SerThrSerGlnThrPheYrAspAlaYrIleSerYrAspThrLysAspAlaSerVal 884
Qy 2306 GAGACTGGGTGGAACAGAGCTGTAAAGATTTAGAAAGAGATGCCCGC---TTT 2362
Db 885 ThrAspTrpValIleAsnGluLeuArgYrHisLeuGluGluSerGluAspLysSerVal 904
Qy 2363 CAGCTTGGCTTCATTCAGGAGCTTATTCCTGCTGAGCCATTCGTCGAACATATC 2422
Db 905 LeuLeuCysLeuGluGluArgAspTrpAspProGlyLeuProIleIleAspAsnLeuMet 924
Qy 2423 CAGAAAGGCTTCACAAGAGCCGAAAGATTATGTGTGTGTGTAGACACTTTATTCAG 2482
Db 925 Gln---SerIleAsnGlnSerLysLeuThrIlePheValLeuThrLysLeuYr----- 941
Qy 2483 AGCCGTGTGTATCTTGAATATGAAATTCCTCAGACATGCGAGTTTCGAGT----- 2536
Db 942 -----AlaLysSerTrpAsnPhetYrAlaPhe 951
Qy 2537 -----AGCGCTCTGCAATCTTCATTCATTCCTT 2566
Db 952 TyrLeuAlaLeuGlnArgLeuMetAspGluAsnMetAspValIleIlePheIleLeuLeu 971
Qy 2567 GAGAAATGAGAGAGTCTGCTGAGCAGCAGCTGCAATGTATTCGCTTTCAGCAGA 2626
Db 972 GluProValLeuGln-----TyrSerIleYrLeuArgLeuArgGlnArgIleCysLys 989
Qy 2627 AACACTTACTCGATGAGGAGAGACATGCTCTGGGAGGACATCTTGGAGAAAGACTC 2686
Db 990 SerSerIleLeuGlnTrpProAsnAsnProLysAlaGluAsnLeuPheTrpGlnSerLeu 1009
Qy 2687 AAAAAGCCCTGTG 2701
Db 1010 LysAsnValValLeu 1014

RESULT 11
US-10-272-502A-31
; Sequence 31, Application US/10272502A
; Publication No. US20030139364A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Vollmer, Jörg
; APPLICANT: Bauer, Stefan
; TITLE OF INVENTION: METHODS AND PRODUCTS FOR ENHANCING IMMUNE RESPONSES USING
; FILE REFERENCE: CO1039, 70065, US
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,208
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1

[illegible][illegible]

```

Db 710 LeuSerHisAsnHisPheSerHisIleuProSerGlyPheLeuSerGluAlaArgAsnLeu 729
QY 1892 AGCACTTTGATGCGAGTTTCAATGCATAGAG---ACATCGAAAGAAATGCAATCAT 1948
Db 730 ValHisIleuAspLeuSerPheAsnThrIleLeuSerIleAsnLysSerSerLeuGlnThr 749
QY 1949 TTTCGAAG---AGTCAAGCCGCTTCATCTGCAATTAATTAATTCGTGCTGTTATATGT 2005
Db 750 LysMetLysThrAsnLeuSerIleLeuGlnLeuHisGlyAsnIlePheAspCysThrGly 769
QY 2006 GAATATTCAGAAATTTCTGCACTGGCTCAAGACAGAAATGCTC-----TTG 2053
Db 770 AspiLeSerAspPheArgSerThrLeuAspGlnLeuAsnIleThrIleProLysLeu 789
QY 2054 GTGATGTGTGAACAATGAATGTCATCACCCTATAGACATGAAGAGCCCTCCCTGCTGTG 2113
Db 790 ValAsnVal-----IleCysSerAsnProGlnAspGlnLysSerLysSerIleMet 806
QY 2114 GATTTTACGAATTCACCTGT-----TATATATACAGACT 2149
Db 807 SerLeuAspLeuThrThrCysValSerAspThrThrAlaValLeuPhePheLeuThr 826
QY 2150 ATCATCAGTGTATGCGTGTGTCAGTGTGCTGTGAGCCACTGTACATTTCTGATATAC 2209
Db 827 PheLeuThrThrSerMet-----ValMetLeuAlaIleValHisIleLeuPheTyr 844
QY 2210 -----CACTTCTATTTTACCTG-----ATACTTATGCTGCTGTGTAAGAACATC 2254
Db 845 TrpAspValTrpPheIleTyrHisMetCysSerAlaLysLeuLysGlyTyrAspThrSer 864
QY 2255 AGCAGAGAGAGAACATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2305
Db 865 SerThrSerGlnThrPheTyrAspAlaTyrIleSerTyrAspThrLysAspAlaSerVal 884
QY 2306 GAGACCTGGGTGAGAAACGAGCTGTGTAAGAAATTTAGAAGAAAGAGTCCCGCC---TTT 2362
Db 885 ThrAspTrpValIleAsnGlnLeuArgTyrHisLeuGlnGlnSerGlnAspLysSerVal 904
QY 2363 CAGTTTGCCTTCAATTACAGGAGCTTATTCCTGCTGAGCCATGCTGCTGCCAATCATC 2422
Db 905 LeuLeuCysLeuGlnGlnArgAspTrpAspProGlyLeuProIleIleAspAsnLeuMet 924
QY 2423 CAGGAGAGCTTCACAAGAGCCGAAAGTTATTTGCTGCTGTGCTGCTGCTGCTGCTGCTGCT 2482
Db 925 Gln---SerIleAsnGlnSerLysLysThrIlePheValLeuThrLysLysTyr----- 941
QY 2483 AGCGGTGGTGTATCTTGAATATGAGATTGCTCAGACATGCGAGTTTCTGAGT----- 2536
Db 942 -----AlaLysSerTrpAsnPheLysThrAlaPhe 951
QY 2537 -----AGCGCTTGGCATCATTTCTTATTGCTT 2566
Db 952 TyrLeuAlaLeuGlnArgLeuMetAspGlnLysMetAspValIleIlePheIleLeuLeu 971
QY 2567 GAGAAAGTGAAGAGTCTGCTGAGCAGAGCTGATGATGATGATGATGATGATGATGATGATG 2626
Db 972 GlnProValLeuGln-----TyrSerGlnTyrLeuAspGlnArgIleCysLys 989
QY 2627 AACACCTACCTCGATGAGGAGACAAATGCTGTGGAGGACAACTTCTGAGAAAGACTC 2686
Db 990 SerSerIleLeuGlnTyrProAsnAsnProLysAlaGlnLeuAsnLeuPheTrpGlnSerLeu 1009
QY 2687 AAAAAAGCCCTGTG 2701
Db 1010 LysAsnValValLeu 1014

```

```

; TITLE OF INVENTION: Immunostimulatory G,U-Containing Oligoribonucleotides
; FILE REFERENCE: C01041.70037.US
; CURRENT APPLICATION NUMBER: US/10/407,952
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/421,966
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 60/370,515
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1032
; TYPE: PRN
; ORGANISM: Mus musculus
; US-10-407-952-32

Alignment Scores:
Pred. No.: 2,69e-45 Length: 1032
Score: 575.00 Matches: 242
Percent Similarity: 40.93% Conservative: 153
Best Local Similarity: 25.08% Mismatches: 318
Query Match: 9.68% Indels: 252
DB: 15 Gaps: 40

US-09-396-985b-5 (1-3395) x US-10-407-952-32 (1-1032)

QY 353 CTTCCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 409
Db 120 LeuArgAsnLeuThrValLeuLeuLeuGlnAspAsnGlnLeuTyrThrIleProAlaGly 139
QY 410 ATCCCTATTTCACCAACCAAGAACTGATGCTGCTTCAAC----- 448
Db 140 LeuProGlnSerLeuLysGlnLeuSerLeuIleGlnAsnIlePheGlnValThrLys 159
QY 448 ----- 448
Db 160 AsnAsnThrPheGlyLeuArgAsnLeuGlnArgLeuTyrLeuGlnTyrTrpAsnCysTyrPhe 179
QY 449 -----CCCTGAG 457
Db 180 LysCysAsnGlnThrPheLysValGlnAspGlyAlaPheLysAsnLeuIleHisLeuLys 199
QY 458 ATCTTAAGAACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 493
Db 200 ValLeu---SerLeuSerPheAsnAsnLeuPheTyrValProProLysLeuProSerSer 218
QY 494 CTTCAGTGTGCTGATTTATTCAGGTGTGAATTAAGAACTTGAAGAACTGAGCAT 553
Db 219 LeuArgLysLeuPheLeuSerAsnAlaLysIleMetAsnIleThrGlnGlnAspPheLys 238
QY 554 GGCCTTAACCAAGCTCTCAACCTTGCTGACAGAAAC----- 592
Db 239 GlnLeuGlnAsnLeuThrIleLeuAspLeuSerGlnAsnCysProArgCysTyrAsnAla 258
QY 593 -----CCATCAAGAGTTTTC-----CCAGAAAGTTT 622
Db 259 ProPheProCysThrProCysLysGlnAsnSerSerIleHisIleHisPheLeuAlaPhe 278
QY 623 TCTGAGTAAACAATTTAGAATCTGTGCTGTGAGACAAATAGACCTCTAGAG 682
Db 279 GlnSerLeuThrGlnLeuLysTyrLeuAsnLeuSerSerThrSerLeuArgThrIlePro 298
QY 683 GGTTCATATTTGAGACAGCTTATATCTTAAAGAACTTAATATGCTCATTAAT---CTT 739
Db 299 SerThrTrpPheGlnLeuLeuSerAsnLeuLysGlnLeuHisIleLeuGlnPheAsnTyrLeu 318
QY 740 ATACATTCCTTTAAGTTCCTGAATATTTCTAATTTGAACAACTGAGAACTGAGAT 799
Db 319 ValGlnIleIleAlaSerGlyAlaPheLeuThrLysLeuProSerLeuGlnIleLeuAsp 338
QY 800 CTTCCTTATAAC-----TATATTCAAACTATTTCTGTC----- 832
Db 339 LeuSerPheAsnPheGlnTyrLysGlnTyrLeuGlnPheIleAsnIleSerSerAsnPhe 358

```

RESULT 12

US-10-407-952-32

; Sequence 32, Application US/10407952

; Publication No. US20030232074A1

; GENERAL INFORMATION:

; APPLICANT: Lipford, Grayson

; APPLICANT: Bauer, Stefan

QY	832	-----	832
Db	359	SeRiLVleAUGSeRleUyLVleUhiVleUyrgIyUyValPheArGyIleUyLV	378
QY	833	---AAAGACTTAAGATTCTTACAGTAAATCCCAAGCAATCTCTTTAGACCTGCT	889
Db	379	LVyLVyVhiVehPheGluhiVleUdGlnSeRleUyProAmeU---LVthiLVleAmeUdly	397
QY	890	TTAAACCAATTTGACTCCATTCACAGCCCAAGCCTTTACGGAAATTAAGGCTCCATGAATTG	949
Db	398	lLeAmePheLVleGluLVleAlaAPhLeUyLVAlaPheGln-----	410
QY	950	ACTTAAGAGATTTATTTAAAGCTCAATATGAGTCAAAATGAGAAATGTGCTTCAAAACATGACT	1009
Db	411	-----AAsPheSeRleUyLeUAsPValIle-----TyrLeUSeR	421
QY	1010	GGTTTACATGTCATCGGTTGATCTTTGGGA---GAATTTAAAAATGAAGGAATCTG---	1063
Db	422	GLyAmeArGILleAlaSeRValleUmePryLihXrAPeUyTyrSeRSeRTTPrArGAlaPheU	441
QY	1064	-----GAAAGTTTGAAC-----	1075
Db	442	ArgLVsPProLeUSeRTThsPAsPAsPryLVleAPhSeRProhiVAlaAmePheTyrhiSeR	461
QY	1076	---CGTTCTGTCATGAAGAGACTTAATGATGTCAGATTCGATTCGATTCAGGTTAAACATAT	1132
Db	462	ThiLVsPProLeUhiLVleYProGlnCyehThiAlaTyrGlyLVAlaLeUAsPLeUSeRleU	481
QY	1133	ATAAATCAATTT-----TCAGATGATATTTAAATCTC	1165
Db	482	AsnAmeLVlePheLVleLVleGlyLVleSeRglnPheGlnGlyPheGlnAsPILAlaCySeU	501
QY	1166	AATTCTTGAGCAATATTTCTGCATATGCTTTACAGAGGTACATATATAAACACATAGCA	1225
Db	502	AsnLeUSeRPheAsnAlaASeRThcLVAlaPheAmeGlyThiGlnPheSeR-----	518
QY	1226	GATGTCTTACGGACTTCAATGCGAATCTTATATCATATTAAGATGCATCTTAAGCCT	1285
Db	518	-----	518
QY	1286	TTTCCAAAGCTGAGTCACTTTCTTTCTTAAAGTTGAGATTATACACAGAGAGAGAT	1345
Db	519	-----SeRMeCProhiVleLVleUyTyrLeUAsPLeUThhAsnAsPArGLeUAsP	534
QY	1346	ATC-----AGCTTTGTCATGTGGCTGCGCAAGCTCTCAGATATCTAGATCTT	1393
Db	535	PheAsPAsPAsnAlaASeRSeRAsP-----LeUhiVAsPLeUgLVAlleUAsPLeU	552
QY	1394	AGTAGAAATGCC-----ATGAGCTTTAGAGGTTCTGCTTCTTATTCGATTTTGGAA	1447
Db	553	SeRhiVAsnAlaASeRTyrPheSeRlLeAlaGlyValThihiVAsPLeUgLVPhelLeGln	572
QY	1448	AAC-----AACCTGAAGTACTTAAACCTCAAGCTTCAAGGTGATCTCTGAAGAGT---	1498
Db	573	AsnLeUhiVleAmeUArGyValleUAsnLeUSeRhiVAsnGlyLVleTyrThiLeUThcLVleU	592
QY	1499	-----GCCAAGCTTATGAGGTCTGAGAAGAGCTGAATACCTGAGACTTTCAGACACTCC	1549
Db	593	GlUsSeRgLVleUySeRlLeSeRleUySeRgLVleUValPheSeRgLVAsnArGLeUAsP	612
QY	1550	ACTTTAAAAAAGTGCACAGA-----TTCTGAGGTCTTATTCCTTTGAAAAAATT	1600
Db	613	hiSLeUThTPAsnAlaAsnAsPryLVyTyrThiSeRlLePheLVSeRLeUglnAsnLeU	632
QY	1601	CTTTACCTTGACATCTTTTACACTATACCAAAATTTGACTTTGAGGATATTTCTTGAC	1660
Db	633	lLeArGLeUAsPLeUSeRTThsAmeUmeUglnGlnlLeProAmeGlyAlaPheLeUAsn	652
QY	1661	TTTG---ATCAGTCTCAACATTTAAAAATGCTGCGCAATCTC-----TTCAAGACAAAC	1711
Db	653	LeUProGlnSeRLeUglnGlnleUleUSeRgLVyAmeLVleUArGyPhePheSeRThiP	672

[illegible]

```

Db      1010 LysasValValleu 1014
RESULT 13
US-09-954-987B-175
Sequence 175, Application US/09954987B
Publication No. US20030104523A1
GENERAL INFORMATION:
APPLICANT: Stefan Bauer
APPLICANT: Grayson B. Lipford
APPLICANT: Hermann Wagner
TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
TITLE OF INVENTION: CPG-BASED IMMUNO-AGONIST/ANTAGONIST
FILE REFERENCE: C1041/7016 (AMS)
CURRENT APPLICATION NUMBER: US/09/954,987B
CURRENT FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: US 60/233,035
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/263,657
PRIOR FILING DATE: 2001-01-23
PRIOR APPLICATION NUMBER: US 60/291,726
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: US 60/300,210
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 230
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 175
LENGTH: 1050
TYPE: PRT
ORGANISM: Mus musculus
US-09-954-987B-175

Alignment Scores:
Pred. No.: 9.18e-44 Length: 1050
Score: 559.00 Matches: 265
Percent Similarity: 38.45% Conservative: 153
Best Local Similarity: 24.38% Mismatches: 327
Query Match: 9.41% Indels: 342
DB: 10 Gaps: 52

US-09-396-985B-5 (1-3395) x US-09-954-987B-175 (1-1050)
QY      269 CTCCTGATGCTGGCTGGAGCTGATGATGCTGCTTCTGCTGAGACAGCA 328
      |||::: ||| |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      13 LeuileheleuamMetleuValSerArgValheglPheArgTrpPheProlys 32
QY      329 AGCTTGATCCCTGATAGAGTACTTCTTAATTT-----ACCTACCA 373
      ::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      33 Thrleu---ProCys---GluValLysValAsnIleProGluAlaHisValIleValAsp 50
QY      374 TGCATGATGAGATCTCAGCAAAATCCCTCATGACATCCCTTATTGACCAAGAACTA 433
      ||| |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      51 CysThrAspLysHisLeuThrGluIleProGluIleProThrAsnThrThrAsnLeu 70
QY      434 GATCTGAGCTTCAACCCCTGAGAGATCTTAAGAGTATAGCTTCAACCAATTTCTCAAA 493
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      71 ThrleuThrIleAsnHisIleProSerIleSerProAspSerPheArgLysLeuHis 90
QY      494 CTCAGTGGCTGATTTA-----TCAGGTGTGAA 523
      |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      91 LeuGluAlaLeuIleAspLeuArgCysAsnGlyValProValLeuLeuGluSerLysAlaAsn 110
QY      524 ATTGAGCA-----ATTGAGACAGAGCAAGGCTTAAACAGCTTCA 571
      ::| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      111 ValCysThrLysArgLeuGluIleArgProGlySerPheSerGlyLeuSerAspLeuLys 130
QY      572 ACCCTGACTACAGAGAAACCTATCAAGATTTC-----CCAGGAGTTT 622
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      131 AlaLeuLysLeuAspGlyAsnGluLeuLeuGluIleProGluAspLeuProSerSerLeu 150
QY      623 TCTGAGCAACAATTAGAG-----AATCTGGTGGCTGTGAG-----ACA 664
      ||| |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      151 His---LeuLeuSerLeuGluAlaAsnAsnIlePheSerIleThrLysGluAsnLeuThr 169

```

```

QY      665 AAAATGACCTCTAGAGGTTTCCATATTGACAG----- 700
      ::|::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      170 GluLeuValAsnIleGluThrLeuLysLeuGlyGlyAsnGlySerTyrTrpAsnProCys 189
QY      701 -----CTTATA 706
Db      190 AsnValSerLysSerIleGluLysAspAlaPheLeuValMetArgAsnLeuLysValleu 209
QY      707 TCCCTTAAGAACTAAATGTGGCT-----CATATCTT 730
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      210 SerLeuLysAspAsnValThrAlaValProThrThrLeuProProAsnLeuGlu 229
QY      731 -----CATATCTT 739
      ::|::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      230 LeuTyrLeuTyrAsnAsnIleIleLysLysIleGluGluAsnAspPheAsnLeuAsn 249
QY      739 ----- 739
Db      250 GluLeuGluValLeuAspLeuSerGlyAsnGlyProArgCysTyrAsnValProTyrPro 269
QY      739 ----- 739
Db      270 CysThrProCysGluAsnAsnSerProLeuGluIleHisAspAsnAlaPheAsnSerLeu 289
QY      740 -----ATACATTCTTAACTG-----CCTGAATAT 766
      ::|::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      290 ThrGluLeuLysValLeuArgLeuHisSerAsnSerLeuGluHisValProProThrTrp 309
QY      767 TTTTCTAATCTGACAAACCTAGAACATGTGATCTTTCTTAATCAATATTAATCAAACTATT 826
      ||| |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      310 PheLysAsnMetArgAsnLeuGluIleLeuAspLeuSerGluAsnTyrLeuAlaArg--- 328
QY      827 TCTGTCAAAAGCTTACAGTTTCTACGTGAATAATCCCAAGTCAATCTCTTTAGACTG 886
      ::|::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      329 GluIleGluGluAlaLysPheLeuHisPheLeuProAsnLeu---ValGluLeuAspPhe 347
QY      887 TCTTTAAACCAATGATGATCTCATTCAGCCAGCCTTTAGGGGAATTAGGCTCCAGAA 946
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      348 SerPheAsn-----TyrGluLeuGluValTyrHisAla-----Ser 359
QY      947 TTGACTCTTAAGAGTATTTTAATAGCTCAATGTACTGAATAATGTGC----- 994
      ::|::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      360 IleThrLeuProHisSerLeuSerSerLeuGluAsnLeuLysIleLeuArgValLysGly 379
QY      995 -----CTTCAAAACATGACTGCTGTATCATCTCCATCGCTTG----- 1030
      ::|::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      380 TyrValPheLysGluLeuLysAsnSerSerLeuSerValLeuHisLysLeuProArgLeu 399
QY      1031 -----ATCTTGGGGAATTTAAAT 1051
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      400 GluValLeuAspLeuGlyThrAsnPheIleLysIleAlaAspLeuAsnIlePheLysHis 419
QY      1052 GAAAGGATCTGGAAGTTTGAACGTTCTGTGATGAA----- 1090
      ||| |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      420 PheGluAsnLeuLysLeuIleAspLeuSerValAsnLysIleSerProSerGluGluSer 439
QY      1091 -----GAGTATGC-----AATGTAGCATGATGATTCAGG----- 1123
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      440 ArgGluValGlyPheCysProAsnAlaGluThrSerValAspArgHisGlyProGluVal 459
QY      1124 TTAACATATATTAATGATTTTCAGATGATTAATTAATTCGAATGC-----TTGGCAAT 1180
      ||| |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      460 LeuGluAlaLeuHisTyrTrpPheArgTyrAspGluTyrAlaArgSerCysArgPheLysAsn 479
QY      1181 ATTCTGCATATCTTTCAAGGTGTACATATTAACACATACAGATGTTCTTAGCAT 1240
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      480 LysGluProProSerPheLeuProLeuAsn-----AlaAspCys-----His 493
QY      1241 TTCAAAATGGCAATCTTATCATATCATTAATGATGCAT-----CTTAAGCTTTTCCA 1291
      ||| |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||
Db      494 IleTyrGlyGluThrLeuAspLeuSerArgAsnAsnIlePhePheIleLysProSerAsp 513

```


Query	Local Similarity	24.38*	Mismatches	327
DB:	9.41*	Gaps:	52	
US-09-396-985B-5 (1-3395) x US-10-272-502A-22 (1-1050)				
Qy	269	CTCTGATGATGGCTGGAGACTGATGATGATGGATGGTCTTCTGCTGGACGACGA	328	
Db	13	LeuIleheLeuSnmMetLeuLeuValSerArgValPheGlyPheArgTyrPheProLys	32	
Qy	329	AGCTTGATATCCCGCATAGAGACTCTTAATTT-----ACCTACCA	373	
Db	33	Thrlenu---ProCys---GluValLysValAsnIleProGluAlaHisValIleValAsp	50	
Qy	374	TGCATGATCAGATCTCAGCAAAATCCCTCATGACATCCCTTATTCACCAAGACCTA	433	
Db	51	CysThrAspLysHisLeuThrGluIleProGluGlyIleProThrAsnThrThrsLeu	70	
Qy	434	GATCTGAGCTTCAACCCCTGAAAGACTTAAAGACCTAGCTTACCAATTTCTCAAA	493	
Db	71	ThrlenuThrIleAsnHisIleProSerIleSerProAspSerPheArgArgLeuAsnHis	90	
Qy	494	CTTCAGGCTGGATTTA-----TTCAGGCTGGAA	523	
Db	91	LeuGluGluIleAspLeuArgCysAsnGlyValAlaProValLeuLeuGlySerLysAlaAsn	110	
Qy	524	ATTGAGACA-----ATTGAGACAAGCATGGATGGCTTAAACAGCTCTCA	571	
Db	111	ValCysThrLysArgLeuGluIleArgProGlySerPheSerGlyLeuSerAspLeuLys	130	
Qy	572	ACCTGGTACTGACAGAAACCCCTATCAAGATTTTCC-----CCAGAGATTTT	622	
Db	131	AlaLeuLysIleuAspGlyAsnGluLeuLeuGluIleProGluAspLeuProSerSerLeu	150	
Qy	623	TCGTGATTAACAATTTAGAG-----AATCGTGGCTGGTGGAG-----ACA	664	
Db	151	His---LeuLeuSerLeuGluAlaAsnHisIlePheSerIleThrLysGluAsnLeuThr	165	
Qy	665	AAATGACCTCTCTAGAGGTTTCCATATTTGACAG-----	700	
Db	170	GluLeuValAsnIleGluThrLeuLysGluGlnAsnCysTyrTyrArgAsnProCys	189	
Qy	701	-----CTTATA	706	
Db	190	AsnValSerTyrSerIleGluLysAspAlaPheLeuValMetArgAsnLeuLysValLeu	209	
Qy	707	TCCTTAAAGAACTAATATGGCT-----	720	
Db	210	SerLeuLysAspAsnValThrAlaValProThrThrlenuProProAsnLeuLeuGlu	229	
Qy	731	-----CATATCTT--	739	
Db	230	LeuTyrLeuTyrAsnAsnIleIleLysLysIleGluGluAsnAspPheAsnAsnLeuAsn	249	
Qy	739	-----	739	
Db	250	GluLeuGluValLeuAspLeuSerGlyAsnCysProArgCysTyrAsnValProTyrPro	269	
Qy	739	-----	739	
Db	270	CysThrProCysGluAsnAsnSerProLeuGluIleHisAspAsnAlaPheAsnSerLeu	289	
Qy	740	-----ATCATCTTTAAGTTG-----CTCGAATAT	766	
Db	290	ThrGluLeuLysValLeuArgLysHisSerIleAsnSerLeuGluHisValAlaProProThrTyr	309	
Qy	767	TTTTCTAATGACAAACCTAGAACATGTGATCTTTCTTAACTATATCAAACTATT	826	
Db	310	PheLysAsnMetArgAsnLeuGluGluLeuAspLeuSerGlnAsnTyrLeuAlaArg---	328	
Qy	827	TCGTGAAAGACTTAAGTTCTAGCTGAAATCCCAAGCAATCTCTTAGACTG	866	
Db	329	GluIleGluIleValLysPheLeuHisPheLeuProAsnLeu---ValGluLeuAspPhe	347	

OY	887	TCCTTAAACCCAAATTGATCCATTCATTAACGCCCAAGCTTTCACAGGAATTAGGCTCCATGAA	946
Db	348	SerPheAn-----TyrGluLeuGlnValTyrHisAla-----Ser	359
OY	947	TTGACTCTTAACAAGTAATTTAATTAATGCTCAAAATGTATGAAAAATGTGC-----	994
Db	360	IleThrLeuProHisSerLeuSerSerSerLeuGlnAenLeuLyIleLeuLysValLysGly	379
OY	995	-----CTTCAAAACATGACTGTGTTTACATGTCCATCCGCTTG-----	103
Db	380	TyrValPheLysGluLeuLysAlaSerSerLeuSerValLeuHisLysLeuProArgLeu	399
OY	1031	-----ATCTGGAGAAATTTAAAAAT	105
Db	400	GluValLeuAspLeuGlyTyrAsnPheIleLysIleAlaAspLeuAsnIlePheLysHis	419
OY	1052	GAAGAAGATCTGGAAGTTTTCACCGCTTCTGTCAATGAA-----	109
Db	420	PheGlnAenLeuLysLeuIleAspLeuSerValAlaenLysIleSerProSerGluGlnSer	439
OY	1091	-----GGACTATGC-----AATGTGACATGTGATGAGTTCAAG-----	112
Db	440	ArgGluValGlyPheCysProAsnAlaGlnThrSerValAspArgHisGlyProGlnVal	459
OY	1124	TTAACATATTAATTAATCATTTTTCACATGATGATATTTTAATCTCAATTCG-----TTGGCAAAAT	118
Db	460	LeuGlnAlaLeuHisIleTyrPheArgTyrAspGlnTyrAlaArgSerCysArgPheLysAsn	479
OY	1181	ATTTCCTGCAATGTCTTTTCACAGGTGTACATATMAAACATATGACAGATGTTCTTAGGCAT	124
Db	480	LysGlnProProSerPheLeuProAsn-----AlaAspCys-----His	493
OY	1241	TTCAAAATGCAATCCCTTATCATCATTTGATGTCTAT-----CTTAAGCTTTTCCA	129
Db	494	IleTyrGlyGlnThrLeuAspLeuSerArgAsnAlaIlePhePheIleLysProSerAsp	513
OY	1292	AAGCTGAGTCAACCTTTCTTAAAAAGTTGAGCATTTATACCAAGAGAGATATACAG	135
Db	514	PheGlnHisLeuSerPheLeuLysCysLeuAsnLeuSerGlyAsn-----Thr	529
OY	1352	TTTGGTCACTTG-----GCTCTGCCAAGTCTCAGATATCTAGAT	139
Db	530	IleGlyGlnThrLeuAsnGlySerGlnLeuTyrProLeuArgGlnLeuArgTyrLeuAsp	549
OY	1391	CTTAGTAAGTAATGCCATGACGCTTAAAGAGTTGCTGTCTTATTCGATTTTGGAAACAAC	145
Db	550	PheSerAsnAlaArgLeuAsp-----	556
OY	1451	AACCTGAAGTACTTAGACCTCAGCTTCAATGGTGCATCCTGATAGTCCAACTTCATG	151
Db	557	-----LeuLeuTyrSerThrAlaPheGln	564
OY	1511	GGCTTAGAAGACCTGGAAATCCTGAC-----TTTCAGCACTCC	154
Db	565	GluLeuGlnSerLeuGlnValLeuAspLeuSerSerAsnSerHisTyrPheGlnAlaGln	584
OY	1550	ACTTTAAAAAAGGTCAAGATTCCTCAGATGTTCTATCT-----CTTGAAAACTTCTTAC	160
Db	585	GlyIleThrHisLeuLeuAsnPheThrLysLysValLeuArgLeuLeuAspLysLeuMetCst	604
OY	1607	-----CTTGAATCTCTTACATATATCAAA-----ATTGACTTTGGCATATTTCTT	165
Db	605	AsnAspAsnAspIleSerThrSerAlaSerArgThrMetGlnSerAsp-----	620
OY	1658	GGCTTGATCAGTCTTCACACATTTAAAAAATGGCTGGCAATTTCTTCAA-----	170
Db	621	-----SerLeuArgIleLeuGlnPheArgGlyAlaHisLysAspValLeuTyrArg	637
OY	1706	-----GACACACACCCCTTTCAAAATCTTTTCAAAACAACAACATTTAACTTCTGAT	175
Db	638	AlaGlyAspAsnAlaGlyTyrLeuAspPhePheLysAsnLeuPheAsnLeuGlnValLeuAsp	657

[illegible][illegible]

```

Db      170 GluLeuValAsnIleGluThrLeuTyrLeuGluGlnAsnGlyTyrTyrArgAsnProCys 189
Qy      701 -----CTTATA 706
Db      190 AsnValSerTyrSerIleGluLysAspAlaPheLeuValMetArgAsnLeuValLeu 209
Qy      707 TCTTAAAGAACTAATATGTGGCT----- 730
Db      210 SerLeuLysAspAsnValThrAlaValProThrThrLeuProProAsnLeuGlu 229
Qy      731 -----CATATCTT 739
Db      230 LeuTyrLeuTyrAsnAsnIleIleLysLysIleGlnGlnAsnAspPheAsnAsnLeuAsn 249
Qy      739 ----- 739
Db      250 GluLeuGlnValLeuAspLeuSerGlyAsnGlyProArgCysTyrAsnValProTyrPro 269
Qy      739 ----- 739
Db      270 CysThrProCysGluAsnAsnSerProLeuGlnIleHisAspAsnAlaPheAsnSerLeu 289
Qy      740 -----ATACATTCCTTAAATTG-----CTGAATAT 766
Db      290 ThrGluLeuLysValLeuArgLeuHisSerAsnSerLeuGlnHisValProProThrTyr 309
Qy      767 TTTTCTATCTGACAACTTGAAACATGTGATCTTTTATTAATCTATTTCAACTATTT 826
Db      310 PheLysAsnMetArgAsnLeuGlnGluLeuAspLeuSerGlnAsnTyrLeuAlaArg 328
Qy      827 TCTGTCAAGACTTACAGTTCTACGTGAATAATCCCAAGCATCTCTCTTGAAGCTG 886
Db      329 GluIleGlnGluAlaLysPheLeuHisPheLeuProAsnLeuValGlnLeuAspPhe 347
Qy      887 TCTTTAAACCCCAATGTGATCTCCATTCAGCCCAAGCCTTTCAGGAAATTAGGCTCATGAA 946
Db      348 SerPheAsn-----TyrGluLeuGlnValTyrHisAla-----Ser 359
Qy      947 TTGACTCTAGAGACTAATTTTAAATGCTCAAAATGCTAGAAATGTGC----- 994
Db      360 IleThrLeuProHisSerLeuSerLeuGlnLysLeuLysIleLeuArgValLysGly 379
Qy      995 -----CTTCAAAACATGACGTGTTTACATGTCATCGGTG----- 1030
Db      380 TyrValPheLysGluLeuLysAsnSerLeuSerValLeuHisLysLeuProArgLeu 399
Qy      1031 -----ATCTTGGAGAAATTTAAAT 1051
Db      400 GluValLeuAspLeuGlyThrAsnPheIleLysIleAlaAspLeuAsnIlePheLysHis 419
Qy      1052 GAAAGCAATCTGAAAGTTTTCACCGCTTGTGATGAA----- 1090
Db      420 PheGluLysLeuLysIleAspLeuSerValAsnLysIleSerProSerGluGluSer 439
Qy      1091 -----GGACATATGC-----AATGTGAGCATGTAGTGTAGC----- 1123
Db      440 ArgGluValGlyPheCysProAsnAlaGlnThrSerValAspArgHisGlyProGlnVal 459
Qy      1124 TTAACATATATTAATCAATTTTTCAGATGATATTTATATCTCAATGTC-----TTGCAAT 1180
Db      460 LeuGluAlaLeuHisTyrPheArgTyrAspGluTyrHisAlaArgSerGlyAspPheLysAsn 479
Qy      1181 ATTTTCTGCATGTCTTTTCACAGGTGTACATATTAACAACATAGCATGTTCTTAGCAT 1240
Db      480 LysGluProProSerPheLeuProLeuAsn-----AlaAspCys-----His 493
Qy      1241 TTCAATAGCAATCTTATCATCATATGATGAT-----CTTAACGCTTTTCCA 1291
Db      494 IleTyrGlyGlnThrLeuAspLeuSerArgAsnAsnIlePhePheIleLysProSerAsp 513
Qy      1292 AAGCTGAGTTCATCTTTCTTAAAGTTGACTTAACTACCAACAGAGAGATATCAAC 1351

```

```

Db      514 PheGlnHisLeuSerPheLeuLysCysLeuAsnLeuSerGlyAsn-----Thr 529
Qy      1352 TTTGTGACATTTG-----GCTGTGCCAACTCTCAGATATCTGAT 1390
Db      530 IleGlyGlnThrLeuAsnGlySerGluLeuTyrProLeuArgGluLeuArgTyrLeuAsp 549
Qy      1391 CTTAGTAGAAATGCGCATGAGCTTTAGAGTTGCTGTTCTTATCTGATTTTGGAAACAAC 1450
Db      550 PheSerAsnAsnAlaGluLeuAsp----- 556
Qy      1451 AACCTGAAGTACTTGAACCTTCAAGCTTCAATGCTGTCAATCTGATAGTCCCACTTCATG 1510
Db      557 -----LeuLeuTyrSerThrAlaPheGlu 564
Qy      1511 GGTCTGAAGAAGCTGAATACCTTGAC-----TTTCAACAGCTCC 1549
Db      565 GluLeuGlnSerLeuGlnValLeuAspLeuSerSerAsnSerHisTyrPheGlnAlaGlu 584
Qy      1550 ACTTTAAAAAAGGCACAGAAATTCAGATGTTCTATCT-----CTTGAAAAATCTTTTAC 1606
Db      585 GlyIleThrHisMetLeuAsnPheThrLysLysLeuArgLeuLeuAspLysLeuMetMet 604
Qy      1607 -----CTGACATCTCTTACACTAATACCAAA--ATGACTTTGATGGCATATTTCTT 1657
Db      605 AsnAspAsnAspIleSerThrSerAlaSerArgThrMetGluSerAsp----- 620
Qy      1658 GGCCTTGAATGCTCCACACTTTTAAATAGCTGGCAATCTTTCAAA----- 1705
Db      621 -----SerLeuArgIleLeuGluPheArgGlyLysAsnHisLeuAspValLeuTyrArg 637
Qy      1706 -----GACAAACACCTTTCAAAATGCTTTTAAACAACCAACAACTTACCTGAT 1759
Db      638 AlaGlyAspAsnAlaGlyTyrLeuAspPhePheLysAsnLeuPheAsnLeuGlnValLeuAsp 657
Qy      1760 CTTTCTAATGCGCAACTGGAACAGATATCTAGGGGGTATTTGAC----- 1804
Db      658 IleSerArgAsnSerLeuAsnSerLeuProGluValPheGluGlyMetProProAsn 677
Qy      1804 ----- 1804
Db      678 LeuLysAsnLeuSerLeuAlaLysAsnGlyLeuLysSerPhePheTyrAspArgLeuGln 697
Qy      1805 ACACTTACAGACTCCGATTTTAAACATGATGACAAACAACCTTA----- 1849
Db      698 LeuLeuLysHisLeuGluIleLeuAspLeuSerHisAsnGlnLeuThrLysValProGlu 717
Qy      1850 -----CTGTTTCTGATTCATCCATTAATAA 1876
Db      718 ArgLeuAlaAsnGlySerLysSerLeuThrThrLeuIleLeuLysHisAsnGlnIleArg 737
Qy      1877 CAGCTG-----TACTCCCTCAGAGCTTTGATGATGCAATTC 1912
Db      738 GlnLeuThrLysTyrPheLeuGlnAspAlaLeuGlnIleuLysTyrLeuAspIleSerSer 757
Qy      1913 AATGCAATGAGACATCCAAAGAAATCTGAA-----CATTTCCAAAG----- 1957
Db      758 AsnLysIleGln-----ValIleGlnLysThrSerPheProGluAsnValLeu 773
Qy      1958 ---AGTCAACCGCTTCAATCTGACTAATTAATTTCTGCTTGTATATGTAATATCAG 2014
Db      774 AsnAsnLeuGlnMetLeuValLeuHisHisAsnAspArgPheLeuCysAsnGlyAspAlaVal 793
Qy      2015 AATTTCTGCAAGTGGGTCGAAGACACCAAAATGTTCTTGGTGAATGTT---GAAACAATG 2071
Db      794 TyrPheValIleTyrValAsnHisThrAspValThrIleProTyrLeuAlaThrAspVal 813
Qy      2072 AAATGTCATCAGCTATAGACATGAAGAGCTCCCTGGTGTGATTTTACGAATTTCAAC 2131
Db      814 ThrCysValGlyProGluAlaHisLysGlyGlnSerValIleSerLeuAspLeuTyrThr 833
Qy      2132 TGTATATATACAGACT-----ATCATCAGTATATGCTGATGCTGATGCTT--- 2179
Db      834 CysGluLeuAspLeuThrAsnLeuIleLeuPheSerValSerIleSerSerValLeuPhe 853

```

```
QY 2180 -----GTGGTAGCCACTGTAGCATTTCTGATA-----TACCACTTCTAT 2218
      ||||| ||| :|||
Db 854 LeuMetValValMetThrThrSerHisLeuPhePheThrPaspMetTrpTyrIleTyr 873
      ||||| ||| :|||
QY 2219 TTTCACCTGATACCTTATTTGCTGTGATAAAAGTACAGACAGAGAGAAAGCATCTATGAT 2278
      ||||| ||| :|||
Db 874 PheTrpValAlaLysIleLysGlyTyrClnHisLeuGlnSerMetGlnSerCysTyrAsp 893
      ||||| ||| :|||
QY 2279 GCATTTTGTGATCTACTGAGCCAGAAATGAG-----GACTGGGTGAGAAACGAGCTG 2329
      ||||| ||| :|||
Db 894 AlaPheIleValTyrAspThrLysAsnSerAlaValThrGlnTrpValLeuGlnGlnLeu 913
      ||||| ||| :|||
QY 2330 GTAAGAATTATTAAGAAGAAGAGTGCCCGC-----TTTCAGCTTTGCTTCATTAC 2380
      ||||| ||| :|||
Db 914 ValAlaLysLeuGlnAsp-----ProArgGlnLysHisPheAsnLeuCysLeuGlnGlu 931
      ||||| ||| :|||
QY 2381 AGGAGCTTTATTCCTGTGTGTAGCCATGTGCGCAACATCATTCAGAAAGCTTCACAG 2440
      ||||| ||| :|||
Db 932 ArgAspTrpLeuProGlyGlnProValLeuGlnAsnLeuSerGln---SerIleGlnLeu 950
      ||||| ||| :|||
QY 2441 AGCCGAAAGTTATTTGTGTGTGTCTAGACATTTATCCAGAGCCGTTGTGTATCTTT 2500
      ||||| ||| :|||
Db 951 SerLysLysThrValPheValMetThrGlnLysTyrAlaLysThrGlnSerPheLysMet 970
      ||||| ||| :|||
QY 2501 GAATATGAGATTGTGCTCAGACATGCGCAATGTCGCTGCGCATCATCTTCATT 2560
      ||||| ||| :|||
Db 971 AlaPheTyrLeuSerHisGln---ArgLeuLeuAspGlnLysValAspValIleIleLeu 989
      ||||| ||| :|||
QY 2561 GTCCTTGAGAAAGTGAGAGAGTCTGCTGAGGAGCAG--GTGCAATTGTATCGCCTT 2617
      ||||| ||| :|||
Db 990 IlePhe-----LeuGlnLysProLeuGlnLysSerLysPheLeuGlnLeuArgLysArg 1007
      ||||| ||| :|||
QY 2618 CTTAGCAAGAAACACCTACCTGAGTGGAGAGACATGCTCTGGGAGGACATCTCTGG 2677
      ||||| ||| :|||
Db 1008 LeuCysArgSerSerValLeuGlnLysProAlaAsnProGlnAlaHisProTyrPheTrp 1027
      ||||| ||| :|||
QY 2678 AGAAGACTCAAAAAAGCCCTG 2698
      ||||| ||| :|||
Db 1028 GlnCysLeuLysAsnAlaLeu 1034
      ||||| ||| :|||
```

Search completed: March 30, 2005, 04:42:10
Job time : 223.93 secs